

From: Swope, Sheridan
Sent: Friday, January 28, 2005 3:36 PM
To: STIC-Biotech/ChemLib
Subject: 10/029,345

For 10/029,345, pls interference search only:

SID 108, residues 538-2532, against the NT data bases
SID 108, residues 538-1443, against the NT data bases
SID 108, full-length, oligo search (at least 1419 NTs), against the NT data bases

SID 109, full-length, against the NT & AA data bases
SID 109, residues 1-302, against the NT & AA data bases
SID 109, full-length, oligo search (at least 473 AAs), against the NT & AA data bases

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)

5/1/2001

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109: 1/2-665
1/2-302
>473

108: 538-2532
541-2532
538-1443
541-1443
>1419

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Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 15, 2005, 02:21:00 ; Search time 361.039 Seconds
(without alignments)
9041.598 Million cell updates/sec

Title: US-10-029-345A-108_COPY_538_2532
Perfect score: 1995.538
Sequence: 1@cgccatgagatgagatcg...cggaatcattgaggtctc1995

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818136359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:
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2: /cgn2_6/ptodata/1/1na/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/1na/PTCDS_COMB.seq:*
6: /cgn2_6/ptodata/1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1991.8	99.8	1998	4 US-09-816-494-3	Sequence 3, Appli
2	1991.8	99.8	3544	4 US-09-816-494-1	Sequence 1, Appli
3	387.8	19.4	2377	4 US-09-920-668-3	Sequence 3, Appli
4	386.2	19.4	2351	4 US-09-949-016-3250	Sequence 3250, Ap
5	294.6	14.8	333	4 US-09-513-999C-2877	Sequence 2877, Ap
6	223	11.2	279	4 US-09-016-434-91	Sequence 91, Appli
7	187.8	9.4	378	4 US-09-513-999C-3684	Sequence 3684, Ap
8	124.6	6.2	1830	4 US-09-557-921-1	Sequence 91, Appli
9	106.8	5.4	2283	4 US-09-949-016-4617	Sequence 4617, Ap
10	106.8	5.4	2303	4 US-09-922-146-3	Sequence 3, Appli
11	96.2	4.8	2109	4 US-09-016-434-1135	Sequence 1135, Ap
12	96.2	4.8	2109	4 US-09-023-655-946	Sequence 946, App
13	96.2	4.8	2475	4 US-09-949-016-2615	Sequence 2615, Ap
14	94.6	4.7	1208	4 US-09-023-655-347	Sequence 347, App
15	93.6	4.7	1619	4 US-09-702-705-801	Sequence 801, App
16	93.6	4.7	1619	4 US-09-736-457-801	Sequence 801, App
17	93.6	4.7	1619	4 US-09-614-124B-801	Sequence 801, App
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ALIGNMENTS

RESULT 1					
US-09-816-494-3					
Sequence 3, Application US/09816494					
Patent No. 6664089					
GENERAL INFORMATION:					
APPLICANT: Meyers, Rachel A.					
TITLE OF INVENTION: 38692 And 21117, NOVEL DUAL SPECIFICITY					
FILE REFERENCE: 10448-030002					
CURRENT APPLICATION NUMBER: US/09/816,494					
PRIOR APPLICATION NUMBER: 2001-03-23					
PRIORITY FILING DATE: 2000-03-24					
NUMBER OF SEQ ID NOS: 10					
SOFTWARE: FASTSEQ for Windows Version 4.0					
SEQ ID NO 3					
LENGTH: 1998					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-09-816-494-3					
Query Match					
Best Local Similarity 99.8%; Score 1991.8; DB 4; Length 1998;					
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
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DB	61	AGTGAAGGAAAAAGTCTCTAATTGATAGCCGCGCATTTGTGAATACATATCATCC	120		
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DB	241	TGCACTGAGAAAGTTGATTAAGATCAAGAGCTCCCAAGATGTTGCTCTCTTCA	300		
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QY 721 CTAGTGCATGTTTGTGCTGAGATCTCCGCTCCGCAACATGCTATGCTGCTGCTGCTG 780
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QY 781 AAGAGATGACATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 840
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QY 841 ATATCTCCAAATTTTCTGAGGCAATCTCTGCACTATGAGAAAGAAAGAAAGAAAG 900
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Db 1729 AGTGGGCTGCACTGTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1788

QY 1201 TCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGCGAGCATCTTACATGCTTC 1260
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Db 1909 AAGCTATGCGAGTTTCTCCCTGTTTCAAGAACTATTTGGAGAGAGAGAGAGAGAG 1968
QY 1381 GATTAAG 1440
Db 1969 GATTAAG 2028
QY 1441 AGCAAGCAGATTGCTTCTGCTGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
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QY 1921 AGCTCAGCGGAG 1980
Db 2509 AGCTCAGCGGAG 2568
QY 1981 ATCATTGAGTCTCC 1995
Db 2569 ATCATTGAGTCTCC 2583

RESULT 3
US-09-920-668-3
; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Coweart
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RUS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2377
; TYPE: DNA

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (135) ... (2012)
 US-09-920-668-3

Query Match 19.4%; Score 387.8; DB 4; Length 2377;
 Best Local Similarity 59.9%; Pred. No. 2.6e-119;
 Matches 716; Conservative 0; Mismatches 453; Indels 27; Gaps 3;

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DB 225 GACAGCGGCTCTTCTGTGAGTACACAGCTGGATGTCTCAAGCTCTGTAATCTGTC 284
QY 148 TGTCTCAAGCTTATGAAGCCGAAAGTTGCAACAGACAAAGTGTAAATTACAGACTCAT 207
DB 285 TGTCTCAAGCTGTGGAAGCGCGCGCTGCAAGGGCAAGGTGACATGTGCGAGCTCATC 344
QY 208 CAGCATTCAGCGAAACATTAAGTTGATGATTTGACAGTGAAGTTGATTTGATTCAT 267
DB 345 CAGCGGCTGACGACGACCGAGTGGAGCTACGAGCCACAGGACGTTGGTGTATATGAC 404
QY 268 CAAAGCTCCCAAGATGTGCTCTCTCTCTTCAAGACTGTTTCTCACTGATCTTGGGT 327
DB 405 CAGAGCAGCGGGAGCGCCAGCTGTGGCGCGAGACAGCTTCTTCCATCTGCTGAGC 464
QY 328 AAAGCTGAGAAAGCTTCAACTGTGTACCTGCTTGCAGGTGGTTGCTGATCTCT 387
DB 465 AAGCTGACGCGCTGTGCAAGCGTGGCCATCTTCACTGGGGGCTTCCCACTCTTCC 524
QY 388 CGTTGTTTCCCTGGCTCTGTGAAAGAAAATCCACT---CTAGTCCCTACCTGCATTTCT 444
DB 525 TCTGCTTCCCGGCTCTGCGAGGCGCAAGCTGCTGCTGCTACATGAGCTCTTCC 584
QY 445 CAGCTTGTCTTACTCTGTGGCAACATTTGGGCCAACCCGAATCTTCCCATCTTATCTT 504
DB 585 CAGCTTGTCTGCTGTGCGCCAGCGTGGGCTGACCCGCTGCTGCTGCTGCTGCTGCT 644
QY 505 GGTGCGCAGCAGATGTCTTCAACAAAGAGCTGATACAGCAAAATGGGATTTGTTATGTC 564
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QY 565 TTAAATGCCAGCTATATCTGTCCAAAGCTGATTTATCCCGAGTCTCATTTCTGCGGT 624
DB 705 CTCAACGCGCAGCACTCTGCCCCCAAGCTGATCTTCACTGTGAGAGCGCTTCAATGCG 764
QY 625 GTGCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCTGTGGTGAACAATTCAGTATGAT 684
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QY 685 TTCAATGAGAAAGCAAAAGCTTCAATGATGTGTCTAGTGCACTGTTTGAAGTGGATC 744
DB 825 TTCAATGATTAAGCAAGCTCTCAAGCTGCAAGTCAATGCTGCTGCTGCTGCTGCTGCT 884
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DB 885 TCCGCTGTGCAACATGTGCTATGCTTCAATCAATGAAGCAATGAGCAATGTCTCTGAC 944
QY 805 GAAAGCTTCAAGATTTGTGAAGAAAGAAAGAAAGCTTATCTATCTCAAACTTCAATTTCTG 864
DB 945 GAGCGCTACAGGTTCTGTGAAGAAAGAGGCGCGCTGCTCACTGTGCGCAACTTCACTTCTG 1004
QY 865 GCGCAATCTCTGCACTATGAGAAAGATTAAGAACGACCTGAGGATCAGGAGCCAAAG 924
DB 1005 GCGCAGCTGTGAGTACGAGCGCAGCTGAGAGTGTGCGCGCGCTGAGGAGCGACCG 1064
QY 925 AGCAAACTCAAGCTGTGCACTGTGAGAAAGCAATTAACCTGTCTCTGTGCTGAGAG 984
DB 1065 GCGA-----CCCTCTCAGGAGCGCGAGGCTCTGCGCTGCTGCGCGG 1112

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DB 1173 GC-----CAGGAGGCGCGCTGAGCGCGGCGGAGCGCCCGCGCGCC 1220
QY 1105 TCGCTGTTAGAGGACAGCGCGCTGTGACAGCGCTGACAGTGGGCTGACACTTCCGAC 1164
DB 1221 AGCGCCCGGCGGACCGAGCGCACTGTAGCAGAGGCGCTGCGCGCTGTGCACTTCTCGAG 1280
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RESULT 4

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US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0.001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250

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Query Match 19.4%; Score 386.2; DB 4; Length 2351;
 Best Local Similarity 59.8%; Pred. No. 9.1e-119;
 Matches 715; Conservative 0; Mismatches 453; Indels 27; Gaps 3;

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DB 259 TGTCTCAAGCTGTGTAAGCGGCGCTGCGAGGCAAGTGTGCAATTTGCGAACTCATC 318
QY 208 CAGCAATTCAGGAAACATTAAGTTGATGATTTGCAAGTGTGATTTAGAT 267
DB 319 CAGCGGCTGCAACGAGCAGAGTGAAGGCTACGAGCCACAGAGCGTGTGTATGAC 378
QY 268 CAAAGCTCCCAAGAGTTGCTCTCTCTTCAAGCTGTTTCTCACTGTATCTTGGGT 327
DB 379 CAGAGTACCGGAGCGCGAGCTGTGCGCGCAACAGCTTCTCTCATCTGCTGAGC 438
QY 388 AAAGCTGAGAAAGCTTCACTGTGTTCACTGCTTCAAGTGGGTTTGTGAGTTCT 387
DB 439 AAGCTGACGCGCTGCTTGAACAGGTGGCAATCTCACTGGGGCTTCCGCACTTCTCC 488
QY 388 CGTTGTTTCCCTGGCTCTGTGAAAGAAAATCCACT---CTAGTCCCTACCTGATTTCT 444

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Db      559 CAGCCCTGTCTCTGTGGTCCAGCGTGGGCGCTGAGCCCGATCTGTGCTTCACTTACCTG 618
QY      505 GGCCTGCAGCAGAGATGTCTCAACAAGAGCGTATCAACACAGATGGGATTTGGTATATG 564
Db      619 GGCTGCAGAGAGAGCGTCTTAACAAGAGATCTGATGACGCAAAATGGAAATGACTACGTC 678
QY      565 TTAAATGCCAGCTATATACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTTCTCGCT 624
Db      679 CTCAAGCGCAGCAACTCTCGCCCAAGCCTGACTTCTATCTGGAGAGCCGCTTCATGCGG 738
QY      625 GTGCCTGTGATATGACAGCTTTTGTGTGAGAAATTTTGGCTGTGTGACAAATCAATGAT 684
Db      739 GTCCCATCAACGACAACTACTGTGAAAATCTGTGCTCCCTGGCTGGACAAGTCCATCGAG 798
QY      665 TTCAATTGAGAAAGCAAAAGCCTCCAAATGATATGTGTTCTATGTGCACTGTTTACTGGAGATC 744
Db      799 TTCAATCGAATAAAGCCAAAGCTCTCCAGCTGCAAGTATGTGCACATGTCGTGCTGCAATC 858
QY      745 TCCCGCTCCGSCCAACCATCGTATATGCGCTATCATATGAAGAGATGGACATGCTTTATGAT 804
Db      859 TCCGCTCTGCGCAACATCGCCATCGCTATCATATGAGACCAATGGGCAATGCTCTCCAG 918
QY      805 GAACTTACAGATTTGTGAAAAGAAAAGACCTATATATCTCCAACTTCAATTTTCTG 864
Db      919 GACGCTTACAGGTTCTGTGAAGGACAGGGCCCGCTCATCTGGCCCAACTTCAACTTCTG 978
QY      865 GGCCTCACTCTGAGCTATATGAGAAAGATTAAAGAACCAAGCTGAGACATCAGGGCCAAAG 924
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QY      985 GGTGACAGAAAAGGAGAGCGCCCTCACTAGTCCACCTGTGCGCACTGTGCTACTCTCAGAG 1044
Db      1087 GCGCCGCTGCGCACGGCTGTGCACACTACCTGACAGAGGGCTGTGCCACAGGAGATGGGCT 1144
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Db      1147 GC-----CAGGAGGGGCGGCTGAGACGGGCGGAGAGCCCGCCGCGCCCGC 1199
QY      1105 TCGCTGTTAAGAGACAGCCCGCTGTGTGACAGGGGCTCAATGAGGGCTGCACCTGTCCGAGAC 1166
Db      1195 ACGCCCCCGGCGACCGAGCTGTGACAGAGGGCTGTGGGGCTGTGACTTCTCTGTGGAC 1255
QY      1165 AGGCTGAGAGACAGCAATTAAGCTCAAGCGTGTCTTCTCTGTGATATCAATCAG 1219
Db      1255 CGCTGCAGAGACCTAACCGGCTCAAGCGCTCTTCTCTGTGACATCAAGTCTG 1309

RESULT 5
US-09-513-999C-2877
: Sequence 2877, Application US/09513999C
: Patent No. 6783961
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Ducleat, A.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
: Patent No. 6783961
: FILE REFERENCE: 59, US2, REG
: CURRENT APPLICATION NUMBER: US/09/513, 999C
: CURRENT FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/122, 487
: PRIOR FILING DATE: 1999-03-26
: NUMBER OF SEQ ID NOS: 36681
: SOFTWARE: Patent.pm
: SEQ ID NO 2877

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; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 127..333
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17
; OTHER INFORMATION: h=a or c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 19
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 36
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 58
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 237
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 37
; OTHER INFORMATION: Xaa=His or Gln
US-09-513-999C-2877
Query Match          14.8%; Score 294.6; DB 4; Length 333;
Best Local Similarity 97.3%; Pred. No. 1.6e-88;
Matches 326; Conservative 5; Mismatches 0; Indels 4; Gaps 3
QY      34 ACTGAGAGTGTGGCGCTCTGTCGTAAGTGGAACG-AAAAGGCTGCTAATTGATAG 92
DB      1  ACTGAGAGTGTGGGAT--KCTGAAAGTGGAACGNAAAAAGTGCTGCTAATTGATNR 58
QY      93 CCGGCATTGTGGGAATA-CATACATCCCACTTTTGAAGCCATTATATCAACTGCT 151
DB      59 CCGGCATTGTGGGAATCCATATCATCTCCACATTTTGAAGCCATTATATCAACTGCT 118
QY     152 CGAAGCTTATGAAGCGAAGTTGCCAACAGACAAGAAGTGTAAATTACAGAGCTCATCCAGC 211
DB     119 CGAAGCTTATGAAGCGAAGTTGCCAACAGACAAGAAGTGTAAATTACAGAGCTCATCCAGC 178
QY     212 ATTACGCGAAACATTAAGTTGACATGTAATTGCACTGACAGAAAGTTGTAGTTTACATCAA 271
DB     179 ATTACGCGAAACATTAAGTTGACATGTAATTGCACTGACAGAAAGTTGTAGTTTACATCAA 238
QY     272 GCTCCCAAGATGTTGCCCTCTCTCTCTTGAAGCTGTTTCTGACTGTACTTCTGGSTAAC 331
DB     239 GCTCCCAAGATGTTGCCCTCTCTCTCTTGAAGCTGTTTCTGACTGTACTTCTGGSTAAC 298
QY     332 TGGAGAAAGCTTCAACTCTGTTCACCTGCTTGA 366
DB     299 TGGAGAAAGCTTCAACTCTGTTCACCTGCTTGA 333
RESULT 6
US-09-016-434-91
; Sequence 91, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
```


Qy 638 ACAGCTTTGTGAGAAAATTTTGGCGGTGGACAAATCAGTAGATTCAATTGAGAAAG 697
Db 1216 ACAGCAACAGAGAACTCGGCGCAGTACTTTGAAAGAGGCTTTTGTAGTTCAATGAGAAAG 1275
Qy 698 CAAAAGCTCCAAATGATGTGTCTAGTGCATCTTTTACGTGGATCTCCGCTCCGCCA 757
Db 1276 CTCACAGTGTGGAGAGGGGCTTCTCATCTCGACGCTGGGGGTGTCCGCTCCGCCA 1335
Qy 758 CCATGCTATGCGCTCATCATCAAGAGATGACATGCTTTTGTAGTAGAGCTTACAGAT 817
Db 1336 CCATGCTATGCTTACTTGTATGAAGACACTCGGATACATGACTATGATTATTAAT 1395
Qy 818 TTGTGAAGAAAAGAAAGCCTATATATCTCCAAATTTTCTGGGCCAACTCTGG 877
Db 1396 TTGTCAAAAGCAAGCAATATATCTCCAACTTACTTCAATGGGCGAGTTGCTAG 1455
Qy 878 ACTATGAGAGAGATTTAAGAAC 900
Db 1456 AGTTCAGAGAAAGACCTTAACAAC 1478

RESULT 9

US-09-949-016-4617
; Sequence 4617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4617
; LENGTH: 2283
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4617

Query Match 5.4%; Score 106.8; DB 4; Length 2283;
Best Local Similarity 55.3%; Pred. No. 2.1e-24;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTTTCCCAATCTTATTTGGCTGCCAGCGAGATCTCAACAAGAG 534
Db 723 CCTGTCCAGATCTGCCCACTCTATCTGGCGAGTCCCGGAAATTCGCAATTTGGAG 782
Qy 535 CTGATACAGCAGAAATGGGATGTATGTATTAATGCGAGCTATACCTGTCCAAA---G 591
Db 783 AGCTGGCCAACTGGGCGATCCGCTACATCTCATGTGACCCCAACCTCCCAAACTTC 842
Qy 592 CCGTACTTATCCCGAGTCTCATTTCTGTGCTGTGCTGTGAATGACAGCTTTTGTAG 651
Db 843 TTGAGAAAGATGTGATCTTCACTACAGAGATCCCACTCCGACACTGGAGCCAG 902
Qy 652 AAAATTTTGGCGGTGGAGCAAAATCAGTAGATTTCATTGGAAGCAAAAGCTCCCAAT 711
Db 903 AACCTGTGCGGTTCTTCCGAGGCCATGATGATTAATGAGGCTTGTCCAGAAC 962
Qy 712 GGATGTGTCTTAGTCACTGTTTAGTGGAGATCTCCGCTCCGACCATGCTATGCGC 771
Db 963 TCGGGGTGCTGTCTCACTGTGGCGGGGTCAAGCCCTTGTGACCGTCACTGTGGCC 1022
Qy 772 TACATCATGAAGAGATGACATGTCTTTAGATGAGCTTACAGATTTGTGAAAAGAAAA 831
Db 1022 TACATCATGAAGAGATGACATGTCTTTAGATGAGCTTACAGATTTGTGAAAAGAAAA 831

Db 1023 TACCTCATGAGAAAGCTCCACTCTCTCTCAACAGATGCTTATGACTGTGAGAGAG 1082
Qy 832 AGACCTACTATATCTCAAACTTCAATTTTGTGGCGCAACTCTGACTATAG 885
Db 1083 AAGCTAACATCTCCCACTTCACTTCAATGGGCGAGTTGCTGACTTTGAG 1136

RESULT 10

US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RUS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 2303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114)...(1268)
US-09-922-146-3

Query Match 5.4%; Score 106.8; DB 4; Length 2303;
Best Local Similarity 55.3%; Pred. No. 2.1e-24;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTTTCCCAATCTTATTTGGCTGCCAGCGAGATCTCAACAAGAG 534
Db 723 CCTGTCCAGATCTGCCCACTCTATCTGGCGAGTCCCGGAAATTTGGAG 782
Qy 535 CTGATACAGCAGAAATGGGATGTATGTATTAATGCGAGCTATACCTGTCCAAA---G 591
Db 783 AGCTGGCCAACTGGGCGATCCGCTACATCTCATGTGACCCCAACCTCCCAAACTTC 842
Qy 592 CCGTACTTATCCCGAGTCTCATTTCTGTGCTGTGCTGTGAATGACAGCTTTTGTAG 651
Db 843 TTGAGAAAGATGTGATCTTCACTACAGAGATCCCACTCCGACACTGGAGCCAG 902
Qy 652 AAAATTTTGGCGGTGGAGCAAAATCAGTAGATTTCATTGGAAGCAAAAGCTCCCAAT 711
Db 903 AACCTGTGCGGTTCTTCCGAGGCCATGATGATTAATGAGGCTTGTCCAGAAC 962
Qy 712 GGATGTGTCTTAGTCACTGTTTAGTGGAGATCTCCGCTCCGACCATGCTATGCGC 771
Db 963 TCGGGGTGCTGTCTCACTGTGGCGGGGTCAAGCCCTTGTGACCGTCACTGTGGCC 1022
Qy 772 TACATCATGAAGAGATGACATGTCTTTAGATGAGCTTACAGATTTGTGAAAAGAAAA 831
Db 1023 TACCTCATGAGAGATGACATGTCTTCAACAGATGCTTATGACTGTGCAAGAGAAAG 1082
Qy 832 AGACCTACTATATCTCAAACTTCAATTTTGTGGCGCAACTCTGACTATAG 885
Db 1083 AAGCTAACATCTCCCACTTCACTTCAATGGGCGAGTTGCTGACTTTGAG 1136

RESULT 11

US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

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/
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,434
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0002 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1135:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2109 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g1418933
/
/ US-09-016-434-1135
/
Query Match 4.8%; Score 96.2; DB 4; Length 2109;
Best Local Similarity 53.8%; Pred. No. 7,6e-21;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
/
QY 484 ATTCTTCCCAATCTTTATCTTGTGCTGCAGCGAGATGTCCTCAACAAGAGCTGATACG 543
DB 979 ATCTTGCCCTTCTCTACTTGCGCTGTGCCAAGACTCCACCACTTGACGTGTGGAG 1038
QY 544 CAGAAATGGAGTTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGC---CTGACTTT 600
DB 1039 GAATTCGGCATCAAGTACATCTTGAACGTCAACCCCAATTTGCCGAATCTTTGAGAAC 1098
QY 601 ATCCCGAGTCTCATTTCTCGCTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660
DB 1099 GCAGAGAGTTTAAATACAGAAATCCCATCTCGATCACTGAGCCAAACCTGTCC 1158
QY 661 CCGTGTGGACAATAATCAGATATTTCATTTGAGAAAGCAAAAGCCTCCATGATGTGT 720
DB 1159 CAGTTTTTCCGAGGCCATTTCTTCAATATAGAACCCGGGCAAGAACTGTGTGTC 1218
QY 721 CTAGTGCATGTTTACTGCTGAGATCTCCGCTCCGCCAATCGCTATGCGCTTACATCATG 780
DB 1219 TTGGTACATTTCTTGCTGCGCATTTAGCCGCTCAGTCACTGTGAGCTTGACCTTAATG 1278
QY 781 AAGAGATGACATGCTTTAGATGAGAGCTTACAGATTTGTGAGAAAAGAAAGCTACT 840
DB 1279 CAGAAAGCTCAATCTGTGATCAAGATGCTATACATTTGCAAAATGAAAATCCMAC 1338
QY 841 ATATCTCCAAATCTCAATTTTCTGGGCCAACTCTGAGACTATGAGAGAAAT 893
DB 1339 ATATCCCTTACTTCAATCTTCAATGAGTCAAGTGTGAGACTTTCAGAGAGACGCT 1391
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RESULT 12
US-09-023-655-946
/ Sequence 946; Application US/09023655
/ Patent No. 6607879
```

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/
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 946:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2109 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g1418933
/
/ US-09-023-655-946
/
Query Match 4.8%; Score 96.2; DB 4; Length 2109;
Best Local Similarity 53.8%; Pred. No. 7,6e-21;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
/
QY 484 ATTCTTCCCAATCTTTATCTTGTGCTGCAGCGAGATGTCCTCAACAAGAGCTGATACG 543
DB 979 ATCTTGCCCTTCTCTACTTGCGCTGTGCCAAGACTCCACCACTTGACGTGTGGAG 1038
QY 544 CAGAAATGGAGTTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGC---CTGACTTT 600
DB 1039 GAATTCGGCATCAAGTACATCTTGAACGTCAACCCCAATTTGCCGAATCTTTGAGAAC 1098
QY 601 ATCCCGAGTCTCATTTCTCGCTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660
DB 1099 GCAGAGAGTTTAAATACAGAAATCCCATCTCGATCACTGAGCCAAACCTGTCC 1158
QY 661 CCGTGTGGACAATAATCAGATATTTCATTTGAGAAAGCAAAAGCCTCCATGATGTGT 720
DB 1159 CAGTTTTTCCGAGGCCATTTCTTCAATATAGAACCCGGGCAAGAACTGTGTGTC 1218
QY 721 CTAGTGCATGTTTACTGCTGAGATCTCCGCTCCGCCAATCGCTATGCGCTTACATCATG 780
DB 1219 TTGGTACATTTCTTGCTGCGCATTTAGCCGCTCAGTCACTGTGAGCTTGACCTTAATG 1278
QY 781 AAGAGATGACATGCTTTAGATGAGAGCTTACAGATTTGTGAGAAAAGAAAGCTACT 840
DB 1279 CAGAAAGCTCAATCTGTGATCAAGATGCTATACATTTGCAAAATGAAAATCCMAC 1338
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Qy 841 ATATCTCCAACTTCAATTTCTGGGCCAACTCTGAGCTATGAGAGAAGAT 893
Db 1339 ATATCCCTTAATCTCACTTATGAGTGTGAGCTGCTGAGACTTGAAGAGAGCGCT 1391

RESULT 13
US-09-949-016-2615

/ Sequence 2615, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 2615
/ LENGTH: 2475
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-2615

Query Match 4.8%; Score 96.2; DB 4; Length 2475;
Best Local Similarity 53.8%; Pred. No. 8.7e-21;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
Qy 484 ATCTTCCCAATCTTATCTTGGCTGCCAGGAGATGCTCAACAGAGCTGATACAG 543
Db 1068 ATCTTCCCTCTCTCTACTTGGCTGTGCCAAGACTCCACCACTTGAAGTGGAG 1127
Qy 544 CAGATGGGATTTGTTAGTGTAAATCCAGCTATACCTGTCCAAAC---CTGACTTT 600
Db 1128 GAATTCGGCATCAAGTACATCTTGAAAGCTCAACCCCAATTTGCCCAATCTTTGAGAAC 1187
Qy 601 ATCCCGAGTCTCATTTCTCGTGTGCTGGAATGACAGCTTTTGTGAGAAATTTTG 660
Db 1188 GCAGAGAGTTTAATATACAGCAATCCCATCTGAGTACCTGAGACCAAACTGTGCC 1247
Qy 661 CCGTGTGGAACAATCAGATGATTTCATGAGAAAGCAAAAGCCTCCATGATGTGTT 720
Db 1248 CAGTTTTCCTGAGGCCATTTCTTCAATGATGAGCCGGGGCAAGAACTGTGTGTC 1307
Qy 721 CTAGTGCACTGTTTACGTGGGATCTCCGGCTCCGACCAATCGCTATGCTTACATCATG 780
Db 1308 TTGATGACATTCCTTGGCTGGGATTAAGCCGCTCAGTCACTGTGCTTACCTTATG 1367
Qy 781 AAGGAGATGACATGCTTTTATGATGAGCTTACAGATTGTGAAAGAAAGAAAGCTTACT 840
Db 1368 CAGAACTCAATCTGTCAATGACATGCTTATGACATTTGCAAAATATAAAATTCACAC 1427
Qy 841 ATATCTCCAACTTCAATTTCTGGGCCAACTCTGAGCTATGAGAGAAGAT 893
Db 1428 ATATCCCTTAATCTCACTTATGAGTGTGAGCTGCTGAGACTTGAAGAGAGCGCT 1480

RESULT 14
US-09-023-655-347
/ Sequence 347, Application US/09023655
/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ EXPRESSION

/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HERewith

/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166

/ INFORMATION FOR SEQ ID NO: 347:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1208 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear

/ IMMEDIATE SOURCE:
/ LIBRARY: THYNOT03
/ CLONE: 1444245
US-09-023-655-347

Query Match 4.7%; Score 94.6; DB 4; Length 1208;
Best Local Similarity 64.3%; Pred. No. 1.7e-20;
Matches 142; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 680 TAGATTCATGAGAAAGCAAAAGCCTCCATGATGATGTTCTAGTCACTGTTAGCTG 739
Db 4 TTGATTCATGAGAAAGCTCACAAGTGTGGAAGGCTTCTCATCTGACCTGCAAGGCTG 63
Qy 740 GGATCTCCCGTCCGCCACATCGCTATCGCTACATCATGAGATGAGATGTCTT 799
Db 64 GGGTGTCCCGTCCGCCACATCGCTATCGCTTATGATGAGACACCTGAGTACCA 123
Qy 800 TAGATGAAGCTTACAGATTGTTGTGAAGAAAGAAAGCACTACTATATCTCCAACTCAATT 859
Db 124 TGACTGATGCTTATTAATTTGTCAAGGCAAAAGCAACATATCTCCCAAACTTAAT 183
Qy 860 TTCTGGGCCAACTCTGAGCTATGAGAAAGATTAGAAC 900
Db 184 TCATGGGGCAGTGTCTAGAGTTGAGAGAAAGCTTAACAC 224

RESULT 15
US-09-702-705-801
/ Sequence 801, Application US/09702705
/ Patent No. 6504010
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvik, Tom
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane

```
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 801
/ LENGTH: 1619
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-702-705-801
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Query Match      4.7%; Score 93.6; DB 4; Length 1619;
Best Local Similarity 52.3%; Pred. No. 4.6e-20;
Matches 232; Conservative 0; Mismatches 209; Indels 3; Gaps 1;

QY 484 ATCTTCCCAATCTTATCTTGCTGCGCAGAGATGTCCTCACAAGAGCTGATACG 543
Db 320 ATCTTCCCTTCTCTACTCGCAGTGCTACATGCTGCCGAGAGACATGCTGAGC 379

QY 544 CAGATGGGATGGTTATGTGTTAAATGCCACTATACCTGTCCAAAGCTGACTTTATC 603
Db 380 GCCCTGGGATCAGCGCTCTGTGATGTCCTCGAGCTGCCCAACC--ACTTTGAA 436

QY 604 CCCGAGTCTATTTCTGCGTGTGCTGTGAATGACAGCTTTGTGAGAAATTTTGGCG 663
Db 437 GGACACTATCAGTACAGAGCATCCCAAGTGAAGATTAACACAGGCCGACATCAGCTCC 496

QY 664 TGGTTGACAAATCAGTAGATTTCATGTGAAAGCAAAAGCCTCCATGATGTGTTCTA 723
Db 497 TGGTTCATGGAAGCCATAGATGATCATGATGCGGTGAAGACTGCGGTGGGGCGTGCTG 556

QY 724 GTGCACTGTTAGCTGGGATTCCTCCGCTCCGCCACCATGCTATGCTTACATCATGAG 783
Db 557 GTGCACTGCGAGCGCGGATCTGCGGTGCGGCACCATCTGCTGCTTACTCTGATGATG 616

QY 784 AGGATGACATGTCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACTTACTATA 843
Db 617 AAGAAACGGGTGAGGCTGAGAGAGGCTTCGAGTTGTTAAGCAGCGCCGACGATTATC 676

QY 844 TCTCAAACTTCAATTTTCTGGGCCAATCTCTGACATAGAGAGAGATTAAAGAACCG 903
Db 677 TCGCCCACTTCAGCTTCATGGGGCAGCTGCTGACGTTCAGATCCAGAGTGTGGCCACG 736

QY 904 ACTGAGCATCAGGGCCAAAGAGC 927
Db 737 TCTGTGCTGCGAGGCTGCTAGC 760
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Search completed: February 15, 2005, 11:51:06
Job time : 363.039 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	1991.8	99.8	1998	9	US-09-816-494-3	Sequence 3, Appl1
2	1991.8	99.8	1998	17	US-10-377-072-27	Sequence 21, Appl
3	1991.8	99.8	1998	18	US-10-377-072-27	Sequence 27, Appl
4	1991.8	99.8	3059	17	US-10-257-026-1	Sequence 1, Appl
5	1991.8	99.8	3496	9	US-09-964-277-1	Sequence 1, Appl
6	1991.8	99.8	3521	18	US-10-370-715B-261	Sequence 261, Appl
7	1991.8	99.8	3544	9	US-09-616-494-1	Sequence 1, Appl
8	1991.8	99.8	3544	17	US-10-377-072-25	Sequence 25, Appl
9	1991.8	99.8	3544	18	US-10-377-072-25	Sequence 25, Appl
10	1991.8	99.8	3635	17	US-10-422-114-26234	Sequence 26234, A
11	1991.8	99.8	3766	17	US-10-343-357-17	Sequence 17, Appl

12	1991.8	99.8	5490	18	US-10-648-593-115	Sequence 115, April
13	1991.8	99.8	5145	18	US-10-357-930-20824	Sequence 20824, A
14	1991.8	99.8	5145	18	US-10-357-930-20969	Sequence 20969, A
15	1991.8	99.8	5145	18	US-10-357-930-21071	Sequence 21071, A
16	1991.8	99.8	5145	18	US-10-357-930-21083	Sequence 21083, A
17	1991.8	99.8	5145	18	US-10-357-930-21303	Sequence 21303, A
18	1991.8	99.8	5145	18	US-10-357-930-21307	Sequence 21307, A
19	1991.8	99.8	5145	18	US-10-357-930-22820	Sequence 22820, A
20	1991.8	99.8	5145	18	US-10-357-930-26669	Sequence 26669, A
21	1991.8	99.8	5145	18	US-10-357-930-26815	Sequence 26815, A
22	1991.8	99.8	5145	18	US-10-357-930-26912	Sequence 26912, A
23	1991.8	99.8	5145	18	US-10-357-930-26923	Sequence 26923, A
24	1991.8	99.8	5145	18	US-10-357-930-27145	Sequence 27145, A
25	1991.8	99.8	5145	18	US-10-357-930-27149	Sequence 27149, A
26	1991.8	99.8	5145	18	US-10-357-930-28675	Sequence 28675, A
27	1990.2	99.8	2732	17	US-10-168-506-2	Sequence 2, April
28	1988.6	99.7	2102	17	US-10-094-749-6-73	Sequence 673, April
29	1988.6	99.7	2866	17	US-10-286-115-520	Sequence 520, April
30	1962.2	98.4	2071	17	US-10-072-012-257	Sequence 257, April
31	1906.8	95.6	2200	17	US-10-072-012-255	Sequence 255, April
32	1653.8	82.9	3332	9	US-09-964-277-20	Sequence 20, April
33	879.4	44.1	1216	17	US-10-108-260A-2429	Sequence 2429, April
34	417.2	20.8	425	18	US-10-357-930-10717	Sequence 10717, A
35	415.2	20.8	467	18	US-10-357-930-31909	Sequence 31909, A
36	415.2	20.8	467	18	US-10-357-930-40688	Sequence 40688, A
37	415.2	20.8	467	18	US-10-357-930-41017	Sequence 41017, A
38	411.2	20.6	418	18	US-10-357-930-11243	Sequence 11243, A
39	410.2	20.6	461	18	US-10-357-930-32416	Sequence 32416, A
40	410.2	20.6	461	18	US-10-357-930-41000	Sequence 41000, A
41	410.2	20.6	461	18	US-10-357-930-41048	Sequence 41346, A
42	401.2	20.1	408	18	US-10-357-930-31089	Sequence 10898, A
43	399.2	20.0	438	18	US-10-357-930-32077	Sequence 32077, A
44	395.4	19.8	427	18	US-10-357-930-10878	Sequence 10878, A
45	382	19.1	2453	13	US-10-005-558-1	Sequence 1, April

ALIGNMENTS

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RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Query Match          99.8%; Score 1991.8; DB 9; Length 1998;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY      1  ATGGGCCCATGAGATGATATGGAACCTCAATTTGTACTAGAGAGCTTGCGCTCGTGGAA 60
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DB       1  ATGGGCCCATGAGATGATGGAACCTCAATTTGTACTAGAGAGCTTGCGCTGGAA 60
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QY      61  AGTGGACGGAAGAAAAGTCTCTAATTGATAGCCGGCATTTGTGGAATCAATACATCC 120
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DB       61  AATGGACGGAAGAAAAGTCTCTAATTGATAGCCGGCATTTGTGGAATCAATACATCC 120
        |||

QY      121  CACATTTTGAAGACCATTAATATCACTGCTCCAGACTTATGAAGCAAGTTGCAACAG 180
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DB       121  CACATTTTGAAGACCATTAATATCACTGCTCCAGACTTATGAAGCAAGTTGCAACAG 180
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Db 121 CACATTTGGAAAGCCATTAATATCAATGCTCCAGGTTATGAAAGCCAAAGTTGCAACAG 180
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Qy 241 TGCAGTCAAGAGTTAGTTATGATCAAAAGCTCCCAAGATGTTGCTCTCTCTCA 300
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Qy 301 GACTGTTTCTCACTGTACTTTGAGTAACTGAGAAAGACTTCAACTCTGTTCACTG 360
Db 301 GACTGTTTCTCACTGTACTTTGAGTAACTGAGAAAGACTTCAACTCTGTTCACTG 360
Qy 361 CTGACAGTGGGTTTGTGAGTTCTCTGCTGTTTCCCTGAGCTCTGTGAGAAATCC 420
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Qy 421 ACTCTAGTCCCTACCTGATTTCTCAGCCCTTGCCTTACCTGTTGCAAACTGGGCCAAC 480
Db 421 ACTCTAGTCCCTACCTGATTTCTCAGCCCTTGCCTTACCTGTTGCAAACTGGGCCAAC 480
Qy 481 CGAATCTTCCCAATCTTTATCTTGGCTGCGACGAGATGCTCTCAACAGAGCTGAT 540
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Db 721 CTAGTGCATGTTTATGCTGGGATCTCCGCTCCGCAACCATGCTATGCTTACATCAG 780
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Db 781 AAGAGATGAGATGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 840
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Db 841 ATATCTCCAACTTCAATTTTCTGGGCAATCCCTGGAATGATGATGATGATGATGAT 900
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Db 901 CAGACTGAGATCAAGGAGCAAAAGCAAACTCAAGTGTGACCTTGAAGAGCAAAAT 960
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Db 1321 AAGCTATGCTGATTTTCCCTGTTTCAAGAACTATGAGAGAGATCTCCGAAACAGTCT 1380
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Db 1381 GATAAGAGAGAGAGAGAGATGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
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Db 1561 CTTTCCAG 1620
Qy 1621 TCGATATCTTGGGCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
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Db 1741 GCTTACAGCTGAG 1800
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Db 1861 AAGCAATTTTAAAGCAAG 1920
Qy 1921 AGGTCAAG 1980
Db 1921 AGGTCAAG 1980
Qy 1981 ATCATTGAGTCTCC 1995
Db 1981 ATCATTGAGTCTCC 1995

RESULT 2
US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-yang
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: AND USES THEREFOR
; FILE REFERENCE: MP103-01BOWNIM

CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27

Query Match 99.8%; Score 1991.8; DB 17; Length 1998;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGCCCATGAGTATTTGGAATTTGTTACTGAGAGTGGTGGCTCTGCTGAA 60
1 ATGGCCCATGAGTATTTGGAATTTGTTACTGAGAGTGGTGGCTCTGCTGAA 60
61 AGTGAACGGAAGAGTCTGCTAATTTAGAGCGGCAATTTGTAATACATATC 120
61 AGTGAACGGAAGAGTCTGCTAATTTAGAGCGGCAATTTGTAATACATATC 120
121 CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAAAGGTTGCAAC 180
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181 GACAAAGTATTATTAAGAGTCTATCCAGCATTCAGGAAACATTAAGTTGAT 240
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OY	1621	TCGAAATATCTGGCCCCCCAGACCTCTACCCCTTCCCTGACCCAGACGCTGGTAATTTGGCC	1680
Db	1621	TCCGAATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCCAGACGCTGGTAATTTGGCC	1680
OY	1681	ACAGAGTCTCTACACTTCTCTACTCTGACGCATCTACGGAGAGGCGAGTGCAGATTACTCT	1740
Db	1681	ACAGAGTCTCTACACTTCTCTACTCTGACGCATCTACGGAGAGGCGAGTGCAGATTACTCT	1740
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Db	1741	GCTTACAGCTGCAGCCAGCTGCCCCATTGCGAGACCAAGTCTATTCTGTGTCGACGCGG	1800
OY	1801	CAGAAGCCAATGACAGAGCTGACTTCGGCGCGAGCTGCACTGAAGAGAGCCCTTTGAA	1860
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OY	1921	AGGTTCACGGGGAAGAGCTGGGGGAAAGTGGGCACTGACTGACTTTTGGGGCAGACATGGAA	1980
Db	1921	AGGTTCACGGGGAAGAGCTGGGGGAAAGTGGGCACTGACTGACTTTTGGGGCAGACATGGAA	1980
OY	1981	ATCATTTGAGGTCTCC	1995
Db	1981	ATCATTTGAGGTCTCC	1995

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RESULT 3
US-10-377-072-27
Sequence 27, Application US/10377072
Publication No. US20040157221A9
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Miyoung
APPLICANT: Tsai, Feng-Ying
TITLE OF INVENTION: NOVEL 25669, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MPI03-0180MINT
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27

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; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1998)
;
US-10-377-072-27

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Query Match	99.8%	Score 1991.8;	DB 18;	Length 1998;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1993; Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;

QY	1	ATGGGCCATGAGATGATGTAAGTAACAAATTGTATCTGAGAAGGTGTGGCTCTGCTGGAA	60
Db	1	ATGGGCCATGAGATGATGTAAGTAACAAATTGTATCTGAGAAGGTGTGGCTCTGCTGGAA	60
QY	61	ACGTGAACGGAAAAAGTGTCTGTAATTGATAGCCGGCAATTTGTGGAATACAAATACATCC	120
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QY	121	CACATTTTGGAAAGCCATTATATCAACGTCTCCAAAGCTTATGAAAGCGAAGTTGCAACAG	180
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QY	181	GACAAAGTGTAAATTAACAAGCTCACCCAGCATTCAGCGAAACATAAGTTGATGATGAT	240
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Db	241	TGCAGTCMAAGGTGTGATTTACATCAAAAGCTCCMAAGATGTGGCTCTCTCTCTTCA	300
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Db	301	GACTGTATTCTCACTGTACTTCTGGGTAACTGAGAAAGCTTCAACTCTGTTCACCTG	360
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QY	481	CGAATCTTCCCAATCTTTATCTTGAGTGCACAGAGATGCTCTCAACAAAGAGCTGAT	540
Db	481	CGAATCTTCCCAATCTTTATCTTGAGTGCACAGAGATGCTCTCAACAAAGAGCTGAT	540
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Db	541	CAGCAGATGGGATTTGGTATATGCTTAAAGCCAGCTATATCTGTGCCAAAGCTGACTTT	600
QY	601	ATCCCGAGTCTCATTTCTCGCGTGTGCCTGTGAATGACAGCTTTGTGAGAAAAATTTTG	660
Db	601	ATCCCGAGTCTCATTTCTCGCGTGTGCCTGTGAATGACAGCTTTGTGAGAAAAATTTTG	660
QY	661	CCGTGTGTGACAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCTCCATGAGATGTGT	720
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QY	721	CTAGTGCAGTTTATGCTGGGATCTCCCGGTCCGACACATGCGTATGCGCTACATCAG	780
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QY	781	AAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAAAGAACTACT	840
Db	781	AAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAAAGAACTACT	840
QY	841	ATAATCTCAAACCTTCAATTTTCTGGGCCAACTCTTGACATATGAGAGAAGAAATTTAAGAC	900
Db	841	ATAATCTCAAACCTTCAATTTTCTGGGCCAACTCTTGACATATGAGAGAAGAAATTTAAGAC	900
QY	901	CAGACTGAGACATCAGGGCCAAAGAGCAAACTCAAGCTGTCTCAGCTGAGAAAGCCAAAT	960

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Qy 781 AAGAGATGACATGTCCTTATAGATGAAAGCTTACAGATTTGTGAAAAGAAAAGACCTACT 840
Db 907 AAGAGATGACATGTCCTTATAGATGAAAGCTTACAGATTTGTGAAAAGAAAAGACCTACT 966
Qy 841 ATATCTCAAACTTCAATTTTCTGGGCAACTCTGGACTATGAGAAAGATTAAGAAC 900
Db 967 ATATCTCAAACTTCAATTTTCTGGGCAACTCTGGACTATGAGAAAGATTAAGAAC 1026
Qy 901 CAGACTGAGACATCAGGGCCAAAGAGCAATCAGCTGCTGACCTGGAGAAAGCCAAAT 960
Db 1027 CAGACTGAGACATCAGGGCCAAAGAGCAATCAGCTGCTGACCTGGAGAAAGCCAAAT 1086
Qy 961 GAACCTGTCTCTGTCTCAGAGGGTGAACAAGAAAGGAGACGCCCCCTCAGTCCACC 1020
Db 1087 GAACCTGTCTCTGTCTCAGAGGGTGAACAAGAAAGGAGACGCCCCCTCAGTCCACC 1146
Qy 1021 TGAGCCGACTCTGCTACCTCAGAGGAGAGCAAGAGCCCGTGTATCCCCCAGCTG 1080
Db 1147 TGAGCCGACTCTGCTACCTCAGAGGAGAGCAAGAGCCCGTGTATCCCCCAGCTG 1206
Qy 1081 CCCAGGCTGCCCAGCGCTGACGCGTGTGTTAGAGAGCAGCCGCTGTTACAGGCGCTC 1140
Db 1207 CCCAGGCTGCCCAGCGCTGACGCGTGTGTTAGAGAGCAGCCGCTGTTACAGGCGCTC 1266
Qy 1141 AGTGGGCTGACACTGTGCCGACAGAGGCTGGAAGACAGCAATTAAGCTCAGGTTCTTC 1200
Db 1267 AGTGGGCTGACACTGTGCCGACAGAGGCTGGAAGACAGCAATTAAGCTCAGGTTCTTC 1326
Qy 1201 TCTCTGATATCAAAATCAGTTTCAATTCAGCCAGATGAGCAATCTCTACAGGCTTC 1260
Db 1327 TCTCTGATATCAAAATCAGTTTCAATTCAGCCAGATGAGCAATCTCTACAGGCTTC 1386
Qy 1261 TCTCTATCAGAAAGATGCTTTGGAATTAACAACCTTCCACTCTGATGAGACCAAC 1320
Db 1387 TCTCTATCAGAAAGATGCTTTGGAATTAACAACCTTCCACTCTGATGAGACCAAC 1446
Qy 1321 AAGCTATGCGAGTTTCCCTGTGAGAGCAATATGAGAGCAGACTCCGAAACAGTCTCT 1380
Db 1447 AAGCTATGCGAGTTTCCCTGTGAGAGCAATATGAGAGCAGACTCCGAAACAGTCTCT 1506
Qy 1381 GATAAGAGAGAGCCAGCATCCCAAGAGCTGACAGCCGACGAGCTTTCAGACAGCAG 1440
Db 1507 GATAAGAGAGAGCCAGCATCCCAAGAGCTGACAGCCGACGAGCTTTCAGACAGCAG 1566
Qy 1441 AGCAAGGATGCAATTCGCTGAGAACAGAGCAGAGTGGACCGCCCAAGAGTCCCTTTTA 1500
Db 1567 AGCAAGGATGCAATTCGCTGAGAACAGAGCAGAGTGGACCGCCCAAGAGTCCCTTTTA 1626
Qy 1501 TCTCCACTGATCCAAAGTGGAGCGTGGAGAGCAATTAACAACAACAATCTTTTGGGC 1560
Db 1627 TCTCCACTGATCCAAAGTGGAGCGTGGAGAGCAATTAACAACAACAATCTTTTGGGC 1686
Qy 1561 CTTTTCACACGACGACAGCACTTCAGAAAGTCTGCTGAGCTTGAAGGCTGGCAG 1620
Db 1687 CTTTTCACACGACGACAGCACTTCAGAAAGTCTGCTGAGCTTGAAGGCTGGCAG 1746
Qy 1621 TCGGATATCTTGGCCCCCAGACCTTAACCTTCCCTGACACAGAGCTGTATTTTGGC 1680
Db 1747 TCGGATATCTTGGCCCCCAGACCTTAACCTTCCCTGACACAGAGCTGTATTTTGGC 1806
Qy 1681 ACAGAGTCTCAACTTTCTACTCTGCTCAGCACTTAACGAGGAGAGTGCATTTA 1740
Db 1807 ACAGAGTCTCAACTTTCTACTCTGCTCAGCACTTAACGAGGAGAGTGCATTTA 1866
Qy 1741 GCCTAAGCTGACGACGCTGCCCCCTTGGAGAGCAAGCTTAATCTGTGCGCAGGCGG 1800

Db 1867 GCCTAAGCTGACGACGCTGCCCACTTGCAGAGCAAGCTTAATCTGTGCGCAGGCGG 1926
Qy 1801 CAGAAAGCAAGTGAAGAGAGTGAAGTCTGCGCGGAGAGTGGATGAAGAGGCCCTTTGAA 1860
Db 1927 CAGAAAGCAAGTGAAGAGAGTGAAGTCTGCGCGGAGAGTGGATGAAGAGGCCCTTTGAA 1986
Qy 1861 AAGCATTTAAACGACAGAGCTGCCAAATTTGAGAGAGCAATCTGACAGAAC 1920
Db 1987 AAGCATTTAAACGACAGAGCTGCCAAATTTGAGAGAGCAATCTGACAGAAC 2046
Qy 1921 AGTCAAGGAGAGAGTGGGAAAGTGGAGAGTGAAGTGAAGTGGGAGAGAGTGAAG 1980
Db 2047 AGTCAAGGAGAGAGTGGGAAAGTGGAGAGTGAAGTGAAGTGGGAGAGAGTGAAG 2106
Qy 1981 ATCAATGAGTCTCC 1995
Db 2107 ATCAATGAGTCTCC 2121

RESULT 5
US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucbe, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Query Match 99.8%; Score 1991.8; DB 9; Length 3496;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGCCATGAGATGATGAACTCAATTTGTTACTGAGAGGTGGCTGCTGGTGA 60
Db 562 AAGGCCATGAGATGATGAACTCAATTTGTTACTGAGAGGTGGCTGCTGGTGA 621
Qy 61 AGTGAACCGAAAAAGTCTGCTAATTGATAGCCGACATTTGTGAATACATATCATCC 120
Db 622 AGTGAACCGAAAAAGTCTGCTAATTGATAGCCGACATTTGTGAATACATATCATCC 681
Qy 121 CACATTTGGAAGCCATTATATCAACTGCTCCAGCTTATGAGCGAAGGTTGCAAG 180
Db 682 CACATTTGGAAGCCATTATATCAACTGCTCCAGCTTATGAGCGAAGGTTGCAAG 741
Qy 181 GACAAAGTGTATTAACAGAGCTATCCAGCAATTCAGGAAACATTAAGTTGACATTGAT 240
Db 742 GACAAAGTGTATTAACAGAGCTATCCAGCAATTCAGGAAACATTAAGTTGACATTGAT 801
Qy 241 TGCAGTCAAGAGGTGTGTTTAAAGATCAAGAGTCCCAAGATGTGCTCTCTCTTCA 300
Db 802 TGCAGTCAAGAGGTGTGTTTAAAGATCAAGAGTCCCAAGATGTGCTCTCTCTTCA 861
Qy 301 GACTGTTTCTCACTGATCTTGGGTAACTGAGAAAGACTTCAACTCTGTCACTG 360
Db 862 GACTGTTTCTCACTGATCTTGGGTAACTGAGAAAGACTTCAACTCTGTCACTG 921
Qy 361 CTTGAGAGTGGGTTTGTGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC 420
Db 922 CTTGAGAGTGGGTTTGTGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC 981
Qy 421 ACTTAAGCTCTACCTGATTTCTCAGCTTGTCTTACTGTTGCAACATTTGGGCAACC 480
Db 982 ACTTAAGCTCTACCTGATTTCTCAGCTTGTCTTACTGTTGCAACATTTGGGCAACC 1041

Db 684 CACATTTTGAAAGCCATTATATCACTGCTCCAAAGCTTATGAAAGCGAAGGTTGCACAG 743
Qy 181 GACAAAGTGAATTAATTAAGAGCTGATCCAGATTCACAGAAACATAAGGTTGACATTGAT 240
Db 744 GACAAAGTGAATTAATTAAGAGCTGATCCAGATTCACAGAAACATAAGGTTGACATTGAT 803
Qy 241 TGCAGTCAGAAAGGTTGATGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
Db 804 TGCAGTCAGAAAGGTTGATGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 863
Qy 301 GACGTTTTCTCATCTGATCTTCTGGGTAATCTGGAAGAGCTTCAACTCTGTTCACTTG 360
Db 864 GACGTTTTCTCATCTGATCTTCTGGGTAATCTGGAAGAGCTTCAACTCTGTTCACTTG 923
Qy 361 CTTCAGAGTGGGTTGCTGAGTTCTCTGTTGTTCCCTGGGCTCTGTGAAAGAAATCC 420
Db 924 CTTCAGAGTGGGTTGCTGAGTTCTCTGTTGTTCCCTGGGCTCTGTGAAAGAAATCC 983
Qy 421 ACTCTAGTCCCTTACCTGATCTTCTGAGCTTTCCTTTCCTGTTGCCAAATGGGCCAAC 480
Db 984 ACTCTAGTCCCTTACCTGATCTTCTGAGCTTTCCTTTCCTGTTGCCAAATGGGCCAAC 1043
Qy 481 CGAATTCCTCCCAATCTTATCTTGGCTGCAAGAGATGCTCTCAAGAGAGCTGATG 540
Db 1044 CGAATTCCTCCCAATCTTATCTTGGCTGCAAGAGATGCTCTCAAGAGAGCTGATG 1103
Qy 541 CAGCAGATGAGATGTTGTTATGTTTAAATGCGAGCTATACCTGTCAAAGCCTGACTT 600
Db 1104 CAGCAGATGAGATGTTGTTATGTTTAAATGCGAGCAATACCTGTCAAAGCCTGACTT 1163
Qy 601 ATCCCGAGTCTCATCTTCTGCTGCTGCTGCTGATGACAGCTTTTGTGAAATTTTG 660
Db 1164 ATCCCGAGTCTCATCTTCTGCTGCTGCTGCTGATGACAGCTTTTGTGAAATTTTG 1223
Qy 661 CCGTGTGTTGAGCAAAATCAGTATGTTTCTTGAAGAAAGCCCTCAATGGAGTGT 720
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Qy 721 CTATGTCATCTTGTAGCTGGGATCTCCGCTCCGCCACCATGCTATGCTTACATCAG 780
Db 1284 CTATGTCATCTTGTAGCTGGGATCTCCGCTCCGCCACCATGCTATGCTTACATCAG 1343
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Db 1344 AAGAGATGAGATGCTTATGATGAGGTTACATATTTGCAAGAAAGAAAGAAAGCTTCT 1403
Qy 841 ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACCTATGAGAGAAATTAAGAC 900
Db 1404 ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACCTATGAGAGAAATTAAGAC 1463
Qy 901 CAGACTGAGAGATCAGGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGAGAGCCCAAT 960
Db 1464 CAGACTGAGAGATCAGGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGAGAGCCCAAT 1523
Qy 961 GAACTGTCTCCTGCTGCTCTCAGAGGGTGAAGAGAAAGAGAGAGAGAGAGAGAGAG 1020
Db 1524 GAACTGTCTCCTGCTGCTCTCAGAGGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
Qy 1021 TGTGCGCATCTGCTGCTCTCAGAGGCAAGCAAAAGCCCTGCTGATCCCGCAGAGCTG 1080
Db 1584 TGTGCGCATCTGCTGCTCTCAGAGGCAAGCAAAAGCCCTGCTGATCCCGCAGAGCTG 1643
Qy 1081 CCGAGCGTGGCCAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1644 CCGAGCGTGGCCAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
Qy 1141 AGTGGGCTGACCTGTCCGAGAGAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1704 AGTGGGCTGACCTGTCCGAGAGAGAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
Qy 1201 TCTCTGATATCAATCAAGTTTCAATTTCAAGCCAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1764 TCTCTGATATCAATCAAGTTTCAATTTCAAGCCAGAGAGAGAGAGAGAGAGAGAGAG 1823

Qy 1261 TCTCATCAAGAGATGCTTGGATATCAAAACCTTCCACTGATCTGATGGAGCAAC 1320
Db 1824 TCTCATCAAGAGATGCTTGGATATCAAAACCTTCCACTGATCTGATGGAGCAAC 1883
Qy 1321 AAGCTATGCGAGTTTCTCCCTGTTTCAAGAGATATGAGAGAGAGAGAGAGAGAGAG 1380
Db 1884 AAGCTATGCGAGTTTCTCCCTGTTTCAAGAGATATGAGAGAGAGAGAGAGAGAGAG 1943
Qy 1381 GATTAAG 1440
Db 1944 GATTAAG 2003
Qy 1441 AGCAAGCCATTTGATTTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 2004 AGCAAGCCATTTGATTTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063
Qy 1501 TCTCCACTGATCAAG 1560
Db 2064 TCTCCACTGATCAAG 2123
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Db 2184 TGGATATCTTGGGCCCCAG 2243
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Db 2244 ACAGAGTCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2303
Qy 1741 GCTTACAGCTGCAAG 1800
Db 2304 GCTTACAGCTGCAAG 2363
Qy 1801 CAG 1860
Db 2364 CAG 2423
Qy 1861 AAGCAGTTTAAAGCAG 1920
Db 2424 AAGCAGTTTAAAGCAG 2483
Qy 1921 AGGTACAGGAG 1980
Db 2484 AGGTACAGGAG 2543
Qy 1981 ATCATTGAGGTCTCC 1995
Db 2544 ATCATTGAGGTCTCC 2558

RESULT 7
US-09-816-494-1
Sequence 1, Application US/09816494
Patent No. US2002034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FaalSeo for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2583)
US-09-816-494-1

Query Match 99.8%; Score 1991.8; DB 9; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATATTGGAACCTCAAAATTTGTTACTGAGAGGTGTGTGCTGTGGA 60
DB ATGGCCCATGAGATATTGGAACCTCAAAATTTGTTACTGAGAGGTGTGTGCTGTGGA 648
QY 61 AGTGGACGGAAGAAAGTCTGCTAAATGATAGCCGCAATTTGTGAAATACAAATACATCC 120
DB AGTGGACGGAAGAAAGTCTGCTAAATGATAGCCGCAATTTGTGAAATACAAATACATCC 708
QY 121 CACATTTTGAAGCCATTAAATCACTGCTCCAAAGCTTATGAGAGCGAAGTTGCAACAG 180
DB CACATTTTGAAGCCATTAAATCACTGCTCCAAAGCTTATGAGAGCGAAGTTGCAACAG 768
QY 181 GACAAAGTTTAAATTAAGAGCTCATCAAGCATTCAGAGGAAACATAAGTTGACATTAAT 240
DB GACAAAGTTTAAATTAAGAGCTCATCAAGCATTCAGAGGAAACATAAGTTGACATTAAT 828
QY 241 TGCAGTCAGAAAGTTGATTTACGATCAAAAGCTCCCAAGATGTTGCCCTCTCTCTTCA 300
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QY 301 GACTGTTTTCTCACTGTAATTCTGAGGTAACGTGAAGAAAGCTTCAACTCTGTTCACCTG 360
DB GACTGTTTTCTCACTGTAATTCTGAGGTAACGTGAAGAAAGCTTCAACTCTGTTCACCTG 948
QY 361 CTGTCAGAGTGGGTTTGTGAGATTTCTCTGTTTCTCCCTGCTCTGTGAAGAAATCC 420
DB CTGTCAGAGTGGGTTTGTGAGATTTCTCTGTTTCTCCCTGCTCTGTGAAGAAATCC 1008
QY 421 ACTCAGTCCCTACCTGCAATTTCTGAGCTGCTTACCGTTGSCCAACATTTGGGCAAC 480
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QY 481 GCAATCTTCCCAATCTTATCTTGGCTGCCAGCAGATGTCCTCAACAGAGCTGATA 540
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QY 541 CAGCAGAAATGGGATGTTATGTTAAATGCAAGCTTACTGTCTCAAAAGCTGACTTT 600
DB CAGCAGAAATGGGATGTTATGTTAAATGCAAGCTTACTGTCTCAAAAGCTGACTTT 1188
QY 601 ATCCCGAGTCTCAATTTCTGAGTGTGCTGTAATGACAGTTTGTGAAGAAATTTTG 660
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QY 661 CCGTGTGTTGACAAATCAGTGAATTCATTGGAAGAAAGAAAGCTCCCAATGATGTGT 720
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QY 781 AAGGAGTGAAGCATGCTTTTGAATGAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 840
DB AAGGAGTGAAGCATGCTTTTGAATGAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 1428
QY 841 ATATCTCCAAATTTCTGAGGCAATCTCTGCACTATGAGAAAGATTTAAGAAC 900
DB ATATCTCCAAATTTCTGAGGCAATCTCTGCACTATGAGAAAGATTTAAGAAC 1488
QY 901 CAGACTGAGCATCAGGCGCAAGCAAACTCAAGCTGTGACCTGAGAGACCAAT 960
DB CAGACTGAGCATCAGGCGCAAGCAAACTCAAGCTGTGACCTGAGAGACCAAT 1548

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DB TGTGCGCATCTGTCTACTCAGAGGACAGAGCAAAAGCCCTGTGATTCGCCGACGGT 1668
QY 1081 CCGAGCTGCCAGGCTGACGCGGTGCTGTTAAGAGCAGCCGCTGATACAGGCGCTC 1140
DB CCGAGCTGCCAGGCTGACGCGGTGCTGTTAAGAGCAGCCGCTGATACAGGCGCTC 1728
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DB AGTGGCTGCACTGTCCGAGACAGGCTGGAAGA CAGCAATTAAGCTCAAGGTTCTTC 1788
QY 1201 TCTGTGAATATCAATCAGTTTCAATTTCAAGCAGCATGAGCATCTTACATGCTTC 1260
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QY 1621 TCGAATATCTTGGCCCCCAACCTTACCCCTTCCGACCAAGAGCTGATTTTGC 1680
DB TCGAATATCTTGGCCCCCAACCTTACCCCTTCCGACCAAGAGCTGATTTTGC 2268
QY 1681 ACAGAGTCTCACTTCTACTCTGCTCAGACCAATCTACGAGAGGAGTGCAGTTACTCT 1740
DB ACAGAGTCTCACTTCTACTCTGCTCAGACCAATCTACGAGAGGAGTGCAGTTACTCT 2328
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QY 1861 AAGCAGTTTAAACGAGAGCTGCAAAATGGAATTTGAGAGAGCATGATCAGAGAAC 1920
DB AAGCAGTTTAAACGAGAGCTGCAAAATGGAATTTGAGAGAGCATGATCAGAGAAC 2508
QY 1921 AGGTCAAGGAAAGAGCTGGGAAAGTGGGCAAGTCAAGCTTTTCGGGACAGATGGA 1980
DB AGGTCAAGGAAAGAGCTGGGAAAGTGGGCAAGTCAAGCTTTTCGGGACAGATGGA 2568
QY 1981 ATCAATTGAGTCTCC 1995
DB ATCAATTGAGTCTCC 2583

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RESULT 8
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Gluckmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND US$ THEREFOR
; FILE REFERENCE: MEI03-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; PRIOR APPLICATION NUMBER: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895, 860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Query Match          99.8%; Score 1991.8; DB 17; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGCCCATGAGATGGAATCTCAATTTGTAAGAGAGTTGTGGCTCTCTGCGAAA 60
DB      589  ATGGCCCATGAGATGGAATCTCAATTTGTAAGAGAGTTGTGGCTCTCTGCGAAA 648
QY      61  AGTGAAGCGAAAAGTGTCTGTAATGATAGCCGGCCCATTTTGTGGAATACATACATCC 120
DB      649  AGTGAAGCGAAAAGTGTCTGTAATGATAGCCGGCCCATTTTGTGGAATACATACATCC 708
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DB      709  CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAAGCGAAGTTGCAACAG 768
QY      181  GACAAAGTTAATTAACAGAGCTCATCCAGATTACAGGAAACATAAGTTGACATTGAT 240
DB      769  GACAAAGTTAATTAACAGAGCTCATCCAGATTACAGGAAACATAAGTTGACATTGAT 828
QY      241  TGCACTGAGAAAGTTGTATGTTACGATCAAGAGCTCCAAAGATGTGCTCTCTCTTCA 300
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QY      301  GACTGTTTTCACATGATCTTCTGGGTAACTGGAAGAGACTTCAATCTGTTCACCTG 360
DB      889  GACTGTTTTCACATGATCTTCTGGGTAACTGGAAGAGACTTCAATCTGTTCACCTG 948
QY      361  CTTCGAGGTGGTTTGTGATGATCTCTGTGTTTCCCTGAGCTCTGTGAAGAAATTC 420
DB      949  CTTCGAGGTGGTTTGTGATGATCTCTGTGTTTCCCTGAGCTCTGTGAAGAAATTC 1008
QY      421  ACTCAATGCCCTACCTGATTTCTCAGCTGCTTCTTACTGTCGCAACATTGGCCCAAC 480
DB      1009  ACTCAATGCCCTACCTGATTTCTCAGCTGCTTCTTACTGTCGCAACATTGGCCCAAC 1068
QY      481  CGAATTCCTCCCAATCTTATCTTGGCTGCCAGGAGATGTCCTCAACAGAGCTGATA 540
DB      1069  CGAATTCCTCCCAATCTTATCTTGGCTGCCAGGAGATGTCCTCAACAGAGCTGATA 1128
QY      541  CAGCAAAATGGATTTGTTATGTTAAATGCCAGCTATACCTGTCAAAGCTGACTTT 600
DB      1129  CAGCAAAATGGATTTGTTATGTTAAATGCCAGCAATACCTGTCAAAGCTGACTTT 1188
QY      601  ATCCCGAGTCTCATTTCCGCGCTGCTGCTGTAATGACAGCTTTTGTGAATAATTTTG 660
DB      1189  ATCCCGAGTCTCATTTCCGCGCTGCTGCTGTAATGACAGCTTTTGTGAATAATTTTG 1248
QY      661  CCGTGTGTGACAAATAGTAGATTTTCATTGAGAAAGCAAAACCTTCAATGATGTGT 720
DB      1249  CCGTGTGTGACAAATAGTAGATTTTCATTGAGAAAGCAAAACCTTCAATGATGTGT 1308
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DB      1309  CTACTGACATGTTTAACTGAGGATCTCCCGCTCCGCCACCATGCTTACGCTTACATCATG 1368
QY      781  AAGAGATGACATGTTCTTAAATGATGAAGCTTACAGATTTGTGAAGAAAGAAACCTACT 840
DB      1369  AAGAGATGACATGTTCTTAAATGATGAAGCTTACAGATTTGTGAAGAAAGAAACCTACT 1428
QY      841  ATATCTCAAAATCTCAATTTTCTGGGCCAACTCTGGAATAGAGAAAGATTAAGAAC 900
DB      1429  ATATCTCAAAATCTCAATTTTCTGGGCCAACTCTGGAATAGAGAAAGATTAAGAAC 1488
QY      901  CAGACTGGAGCACTCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACTGGAAGAACCAAT 960
DB      1489  CAGACTGGAGCACTCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACTGGAAGAACCAAT 1548
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DB      1549  GAACTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAGAGAGAGCCCTCTCAGTCAACC 1608
QY      1021  TGTGCCGATCTGTCTTACCTCAGAGGCAAGAGCAAAAGGCCCTGTGATCCGACGCTG 1080
DB      1609  TGTGCCGATCTGTCTTACCTCAGAGGCAAGAGCAAAAGGCCCTGTGATCCGACGCTG 1668
QY      1081  CCCAGGCTCCAGAGCGTGCAGCGCTGCTGTAAGAGGACAGCGCCCTGTAAAGGCGCTC 1140
DB      1669  CCCAGGCTCCAGAGCGTGCAGCGCTGCTGTAAGAGGACAGCGCCCTGTAAAGGCGCTC 1728
QY      1141  AGTGGGCTGACCTGTCCGACAGACAGCTGAGAGACAGCAATTAAGCTCAAGGTTCTTC 1200
DB      1729  AGTGGGCTGACCTGTCCGACAGACAGCTGAGAGAGCAAGCAATTAAGCTCAAGGTTCTTC 1788
QY      1201  TCTCTGGAATATCAATTCATTTCAAGCAGACATGGCAGCATCTTACATGAGCTTC 1260
DB      1789  TCTCTGGAATATCAATTCATTTCAAGCAGACATGGCAGCATCTTACATGAGCTTC 1848
QY      1261  TCTCATCAGAAAGCTTTGGAAATACAAACCTTCACATCTCTGGAATGGAGCAAC 1320
DB      1849  TCTCATCAGAAAGCTTTGGAAATACAAACCTTCACATCTCTGGAATGGAGCAAC 1908
QY      1321  AAGCTATGCAATTTCTCCCTGTTCAGGAACATATCGAGAGACTCCGGAACCAAGTCT 1380
```

Db	1909	AAGCATATGCACTTCTCCCTGTTACGAACTATCGAGAGACAGTCCCGAAACAAGTCT	1968
Qy	1381	GATTAAGGAGGAGCCAGCATTCCTCCCAAGAGCTGACACCCGCGCTTTCAGACAGCCAG	1440
Db	1969	GATTAAGGAGGAGCCAGCATTCCTCCCAAGAGCTGACACCCGCGCTTTCAGACAGCCAG	2028
Qy	1441	AGCAAGCATTCATTCGCTGAGAAACACAGACAGTGGACCGCCGAGAGGTCCCTTTTA	1500
Db	2029	AGCAAGCATTCATTCGCTGAGAAACACAGACAGTGGACCGCCGAGAGGTCCCTTTTA	2088
Qy	1501	TCTCCACTGCATCGAAGTGGAGCGCTGAGAGCAATTACACACAGACTTCCTTTTCGCG	1560
Db	2089	TCTCCACTGCATCGAAGTGGAGCGCTGAGAGCAATTACACACAGACTTCCTTTTCGCG	2148
Qy	1561	CTTTCCACACAGCCAGACAGCACTCAGAGTGTGCTGCGCTTGCGCTTAAGGCTGGCAC	1620
Db	2149	CTTTCCACACAGCCAGACAGCACTCAGAGTGTGCTGCGCTTGCGCTTAAGGCTGGCAC	2208
Qy	1621	TCCGATATCTGGCCCCCGACAGCTTACCCCTCCCTGACAGACAGCTGTATTTTGCC	1680
Db	2209	TCCGATATCTGGCCCCCGACAGCTTACCCCTCCCTGACAGACAGCTGTATTTTGCC	2268
Qy	1681	ACAGAGTCTCTCACATTTCTACTCTGCTCAGCCATCTAAGAGGCGAGTGCAGTTACTCT	1740
Db	2269	ACAGAGTCTCTCACATTTCTACTCTGCTCAGCCATCTAAGAGGCGAGTGCAGTTACTCT	2328
Qy	1741	GCTTACAGCTGACGCCAGCTGCGCACTTGGCGAGACCAAGTCTATTCTGTGCGCAGCGG	1800
Db	2329	GCTTACAGCTGACGCCAGCTGCGCACTTGGCGAGACCAAGTCTATTCTGTGCGCAGCGG	2388
Qy	1801	CAGAACCCAGAGTGAAGAGCTGACCTGCGCGCGGAGCTGGCATGAAAGAGCCCTTTGAA	1860
Db	2389	CAGAACCCAGAGTGAAGAGCTGACCTGCGCGCGGAGCTGGCATGAAAGAGCCCTTTGAA	2448
Qy	1861	AAGCAGTTTAAACGAGAGAGTGCCTCAATGAAATTTGAGAGAGCATCATGTCAGAGAC	1920
Db	2449	AAGCAGTTTAAACGAGAGAGTGCCTCAATGAAATTTGAGAGAGCATCATGTCAGAGAC	2508
Qy	1921	AGGTTCACGCGAAGAGCTGGGGAAGTGGGCACTGACTTTCCTTTTCGGGACAGATGAA	1980
Db	2509	AGGTTCACGCGAAGAGCTGGGGAAGTGGGCACTGACTTTCCTTTTCGGGACAGATGAA	2568
Qy	1981	ATCATTTAGGTCTCC	1995
Db	2569	ATCATTTAGGTCTCC	2583
RESULT 9			
US-10-377-072-25			
Sequence 25, Application US/10377072			
Publication No. US20040157221A9			
GENERAL INFORMATION:			
APPLICANT: Millennium Pharmaceuticals Inc.			
APPLICANT: Curtis, Rory A.J.			
APPLICANT: Logan, Thomas Joseph			
APPLICANT: Glucksmann, Maria A.			
APPLICANT: Meyers, Rachel E.			
APPLICANT: Williamson, Mark J.			
APPLICANT: Rudolph-Owen, Laura A.			
APPLICANT: Chun, Miyoung			
APPLICANT: Tsai, Fong-Ying			
TITLE OF INVENTION: NOVEL 25669, 25934, 26335, 50365, 21117,			
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES			
FILE REFERENCE: MP103-0180NM1			
CURRENT APPLICATION NUMBER: US/10/377, 072			
CURRENT FILING DATE: 2003-02-27			
PRIOR APPLICATION NUMBER: US 09/895,860			
PRIOR FILING DATE: 2001-06-29			
PRIOR APPLICATION NUMBER: US 60/215,370			
PRIOR FILING DATE: 2000-06-29			
PRIOR APPLICATION NUMBER: US 09/723,806			
PRIOR FILING DATE: 2000-11-28			

QY	1	ATGGCCATGAGTGAATTTGGAACCTCAAAATTTGTTCTGAGAGGTTGGTGGCTCTGCTGAA	60
DB	589	ATGGCCCATGAGTGAATTTGGAACCTCAAAATTTGTTCTGAGAGGTTGGTGGCTCTGCTGAA	648
QY	61	AGTGAACGGAAAAAGGCTGCTAAATTGATGACGGGCAATTTGGTAATACATATCAATCC	120
DB	649	AGTGAACGGAAAAAGGCTGCTAAATTGATGACGGGCAATTTGGTAATACATATCAATCC	708
QY	121	CACATTTTGAAGCCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAGTTGCCAAG	180
DB	709	CACATTTTGAAGCCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAGTTGCCAAG	768
QY	181	GACAAAGTTTAATTACAGAGCTCATCCAGATTCAAGGAAACATAAGTTGACATTGAT	240
DB	769	GACAAAGTTTAATTACAGAGCTCATCCAGATTCAAGGAAACATAAGTTGACATTGAT	828
QY	241	TGACGTACGAAGGTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA	300
DB	829	TGACGTACGAAGGTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA	888
QY	301	GACTGTTTCTCACTGTACTTCTGGGTAACCTGAGAAAGAGCTTCAACTCTGTTCACTG	360
DB	889	GACTGTTTCTCACTGTACTTCTGGGTAACCTGAGAAAGAGCTTCAACTCTGTTCACTG	948
QY	361	CTTGCAAGTGGGTTTGTGAGATTCTCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC	420
DB	949	CTTGCAAGTGGGTTTGTGAGATTCTCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC	1008
QY	421	ACTCTAGTCCCTTACCTGCAATTTCTCAAGCTTGTCTTACTCTGTGGCAACATTGGGCCAAC	480
DB	1009	ACTCTAGTCCCTTACCTGCAATTTCTCAAGCTTGTCTTACTCTGTGGCAACATTGGGCCAAC	1068
QY	481	CGAATTCCTCCCAATCTTTATCTTGGGTGCGACGAGATGTCCTCAACAAGAGCTGATA	540
DB	1069	CGAATTCCTCCCAATCTTTATCTTGGGTGCGACGAGATGTCCTCAACAAGAGCTGATA	1128
QY	541	CACGAGATGGATGGTTATGTTTAAATGCAAGCTATACCTGTCCAAAGCTGACTTT	600
DB	1129	CACGAGATGGATGGTTATGTTTAAATGCAAGCTATACCTGTCCAAAGCTGACTTT	1188
QY	601	ATCCCGAGCTCTAATTTCTCGCTGGCTCTGTGAATACAGCTTTTGTGAATAATTTTG	660
DB	1189	ATCCCGAGCTCTAATTTCTCGCTGGCTCTGTGAATACAGCTTTTGTGAATAATTTTG	1248

QY 661 CCGTGTGTGACAAATCAGTATTTGATGAGAAAGCAAAAGCTCCAAATGATGTGTT 720
DB 1249 CCGTGTGTGACAAATCAGTATTTGATGAGAAAGCAAAAGCTCCAAATGATGTGTT 1308
QY 721 CTAAGTGCATGTTTAACTGGAGATCTCCGCTCCGCCACAATCGCTATCGCTCATCATG 780
DB 1309 CTAAGTGCATGTTTAACTGGAGATCTCCGCTCCGCCACAATCGCTATCGCTCATCATG 1368
QY 781 AAGAGATGACATGCTTTAGATGAGCTTACAGATTTTGTGAAAGAAAAGACTACT 840
DB 1369 AAGAGATGACATGCTTTAGATGAGCTTACAGATTTTGTGAAAGAAAAGACTACT 1428
QY 841 ATATCTCCAACTTCAATTTTGTGGGCCAACTCCGTGACTATGAGAAAGATTAAAGAC 900
DB 1429 ATATCTCCAACTTCAATTTTGTGGGCCAACTCCGTGACTATGAGAAAGATTAAAGAC 1488
QY 901 CAGACTGAGACATCAAGGCCCAAGAAAGCAAACTGAGCTGTGACCTGAGAAAGCCAAAT 960
DB 1489 CAGACTGAGACATCAAGGCCCAAGAAAGCAAACTGAGCTGTGACCTGAGAAAGCCAAAT 1548
QY 961 GAACTGTCTCCGTGCTCTCAGAGGGGTGACAGAAAGAGAGAGCCGCTCAGTCCACCC 1020
DB 1549 GAACTGTCTCCGTGCTCTCAGAGGGGTGACAGAAAGAGAGAGCCGCTCAGTCCACCC 1608
QY 1021 TGTGCGGACTGTGCTTACTCAGAGGCAAGCAAAAGCCGTGATCCGCCAGCGTG 1080
DB 1609 TGTGCGGACTGTGCTTACTCAGAGGCAAGCAAAAGCCGTGATCCGCCAGCGTG 1668
QY 1081 CCCAGGCTGCCAGCGGTGAGCCGCTGTGAGAGACAGCCCGTGTGATCAGGCGCTC 1140
DB 1669 CCCAGGCTGCCAGCGGTGAGCCGCTGTGAGAGACAGCCCGTGTGATCAGGCGCTC 1728
QY 1141 AGTGGCTGCACTGTCCGACAGAGCTGAGAAAGCAAGATTAAGTCAAGGCTTCTTC 1200
DB 1729 AGTGGCTGCACTGTCCGACAGAGCTGAGAAAGCAAGATTAAGTCAAGGCTTCTTC 1788
QY 1201 TCTCTGGAATTCAAATCAATTTCAATTTCAAGCCAGATGAGCATCTTACATGAGCTTC 1260
DB 1789 TCTCTGGAATTCAAATCAATTTCAATTTCAAGCCAGATGAGCATCTTACATGAGCTTC 1848
QY 1261 TCTCTATCAGAAAGATCTTTGGAATTAATCAAACTCCACTCACTCTGATGAGCAAC 1320
DB 1849 TCTCTATCAGAAAGATCTTTGGAATTAATCAAACTCCACTCACTCTGATGAGCAAC 1908
QY 1321 AAGCTATGCACTTCTCCCTGTGAGAACTATCGAGAGCACTCCGAAAACAGTCTCT 1380
DB 1909 AAGCTATGCACTTCTCCCTGTGAGAACTATCGAGAGCACTCCGAAAACAGTCTCT 1968
QY 1381 GATTAAGAGAGAAAGCCAGATCCCAAGAAAGCTGCGACCCGACGCTTCAAGACGACG 1440
DB 1969 GATTAAGAGAGAAAGCCAGATCCCAAGAAAGCTGCGACCCGACGCTTCAAGACGACG 2028
QY 1441 AGCAAGCGATTCATTCGATGAGAAAGCAAGAGTGGCAACGCGCAAGAGGTCCCTTTTA 1500
DB 2029 AGCAAGCGATTCATTCGATGAGAAAGCAAGAGTGGCAACGCGCGCAAGAGGTCCCTTTTA 2088
QY 1501 TCTCTACATGCAATCGAAGTGGAGGCTGAGAGCAATTAACAACAGCTTCTTTTGGGC 1560
DB 2089 TCTCTACATGCAATCGAAGTGGAGGCTGAGAGCAATTAACAACAGCTTCTTTTGGGC 2148
QY 1561 CTTTTCACACGACGACGACCTCAACGAAGTCTGCGCTGAGACGACGACGCTGTATTTGGC 1620
DB 2149 CTTTTCACACGACGACGACCTCAACGAAGTCTGCGCTGAGACGACGACGCTGTATTTGGC 2208
QY 1621 TCGGATATCTTGGCTCCCGACAGCTTACCCCTTCCCTGACAGACGACGCTGTATTTGGC 1680
DB 2209 TCGGATATCTTGGCTCCCGACAGCTTACCCCTTCCCTGACAGACGACGCTGTATTTGGC 2268
QY 1681 ACAGAGTCTCAACCTTCTAATCTGCTCAGCCATCTAAGAGGAGGCTGCAAGTTACTCT 1740
DB 2269 ACAGAGTCTCAACCTTCTAATCTGCTCAGCCATCTAAGAGGAGGCTGCAAGTTACTCT 2328

QY 1741 GCTTACAGCTGAGGCACTGCTGCCACTTGCAGAGCAAGTCTATTTCTGTGCGAGGCGG 1800
DB 2329 GCTTACAGCTGAGGCACTGCTGCCACTTGCAGAGCAAGTCTATTTCTGTGCGAGGCGG 2388
QY 1801 CAGAAAGCAAGTGAAGAGCTGATCTCGCGGAGGAGCTGAGCAATGAAGAGAGCCCTTTGAA 1860
DB 2389 CAGAAAGCAAGTGAAGAGCTGATCTCGCGGAGGAGCTGAGCAATGAAGAGAGCCCTTTGAA 2448
QY 1861 AAGCATTTAAACGACAGAGCTGACCAATGGAATTTGAGAGACATCATCTCAGAGAAC 1920
DB 2449 AAGCATTTAAACGACAGAGCTGACCAATGGAATTTGAGAGACATCATCTCAGAGAAC 2508
QY 1921 AGGTACCGGAAAGAGCTGGGAAAGTGGGAGTCACTGATCTTGTGGGAGCAGTGA 1980
DB 2509 AGGTACCGGAAAGAGCTGGGAAAGTGGGAGTCACTGATCTTGTGGGAGCAGTGA 2568
QY 1981 ATCATTTGAGTCTCC 1995
DB 2569 ATCATTTGAGTCTCC 2583

RESULT 10
US-10-425-114-26234

/ Sequence 26234, Application US/10425114

/ Publication No. US20040034888A1

/ GENERAL INFORMATION:

/ APPLICANT: Liu, Jindong

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Kovalic, David K.

/ APPLICANT: Screen, Steven E.

/ APPLICANT: Tabaska, Jack E.

/ APPLICANT: Cao, Xongwei

/ TITLE OR INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

/ TITLE OR INVENTION: Plants and Uses Thereof for Plant Improvement

/ FILE REFERENCE: 38-21 (5313)B

/ CURRENT FILING DATE: 2003-04-28

/ NUMBER OF SEQ ID NOS: 73128

/ SEQ ID NO 26234

/ LENGTH: 3625

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURES:

/ OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI

US-10-425-114-26234

Query Match 99.8%; Score 1991.8; DB 17; Length 3625;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCATGAGATGTTGGAATCTCAATTTCTTACATGAGAGTGTGGTCTGCTGAGAA 60
DB 692 ATGGCCATGAGATGTTGGAATCTCAATTTCTTACATGAGAGTGTGGTCTGCTGAGAA 751
QY 61 AGTGAACGAAAAAGTGTCTGCTAATGATAGCCGACATTTGTGGAATCAATCATCC 120
DB 752 AGTGAACGAAAAAGTGTCTGCTAATGATAGCCGACATTTGTGGAATCAATCATCC 811
QY 121 CACATTTTGAAGCCATTAATTAATCACTGCTCAAGCTTATGAAAGCGAAGTGGCAAG 180
DB 812 CACATTTTGAAGCCATTAATTAATCACTGCTCAAGCTTATGAAAGCGAAGTGGCAAG 871
QY 181 GACAAAGTGTATTAACAGAGCTCATCAGCAATTCAGGAAACATAAGTGTGACATTTGAT 240
DB 872 GACAAAGTGTATTAACAGAGCTCATCAGCAATTCAGGAAACATAAGTGTGACATTTGAT 931
QY 241 TCGAGTCAAGAGTGTGATGATGATCAAGCTCCCAAGATGTGTGCTCTCTCTTCA 300
DB 932 TCGAGTCAAGAGTGTGATGATGATCAAGCTCCCAAGATGTGTGCTCTCTCTTCA 991
QY 301 GACTGTTTTCACATGATCTTCTGAGTAACTGAGAAAGAGCTTCAACTGTTCACCTG 360
DB 992 GACTGTTTTCACATGATCTTCTGAGTAACTGAGAAAGAGCTTCAACTGTTCACCTG 1051

QY 361 CTGCGAGTGGGTTGCTGAGTTCTCTGCTGTTTCCCTGGGCTCTGTGAAGAAATCC 420
Db 1052 CTGCGAGTGGGTTGCTGAGTTCTCTGCTGTTTCCCTGGGCTCTGTGAAGAAATCC 1111
QY 421 ACTCTAGTCCCTACCTGCAATTTCTGAGCTTGTCTTACCTGTTTCCCAATTTGGGCAAC 480
Db 1112 ACTCTAGTCCCTACCTGCAATTTCTGAGCTTGTCTTACCTGTTTCCCAATTTGGGCAAC 1171
QY 481 CGAATTTCTTCCCAATTTCTTATCTTGGCTGCGCAGAGATGTCCTCAACAGAGCTGATA 540
Db 1172 CGAATTTCTTCCCAATTTCTTATCTTGGCTGCGCAGAGATGTCCTCAACAGAGCTGATA 1231
QY 541 CAGCAGATGGGATTTGTTATGTTTAAATGCGACCTTACCTGTCGCAAGCTGACTTT 600
Db 1232 CAGCAGATGGGATTTGTTATGTTTAAATGCGACCTTACCTGTCGCAAGCTGACTTT 1291
QY 601 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGAAGCTTTTGTGAAGAAATTTTG 660
Db 1292 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGAAGCTTTTGTGAAGAAATTTTG 1351
QY 661 CCGTGTGGGACAAATCAGTGAATTTCAATTGAAAGCAAAAGCTCCATGAGATGTGT 720
Db 1352 CCGTGTGGGACAAATCAGTGAATTTCAATTGAAAGCAAAAGCTCCATGAGATGTGT 1411
QY 721 CTAGTGCATGTTTGTAGTGGGATCTCCGCTCCGCAACATGCTATGCGCTACATCANG 780
Db 1412 CTAGTGCATGTTTGTAGTGGGATCTCCGCTCCGCAACATGCTATGCGCTACATCANG 1471
QY 781 AAGAGATGACATGCTTTTATGATGATGACCTTACAGATTTGTGAAGAAAGAAAGCTACT 840
Db 1472 AAGAGATGACATGCTTTTATGATGATGACCTTACAGATTTGTGAAGAAAGAAAGCTACT 1531
QY 841 ATATCTCCAAATTTCTTATGCTGGGCACTCTGTGACTATGAGAGAAATTAAGAAC 900
Db 1532 ATATCTCCAAATTTCTTATGCTGGGCACTCTGTGACTATGAGAGAAATTAAGAAC 1591
QY 901 CAGAGTGGAGATCAGGGGCAAGAGCAAACTCAAGCTGTGCACTGTGAAGAGCAAT 960
Db 1592 CAGAGTGGAGATCAGGGGCAAGAGCAAACTCAAGCTGTGCACTGTGAAGAGCAAT 1651
QY 961 GAACCTGTCCCTGTCTGTCTCAGAGGGTGAAGAGAAACGAGACGCTTCAGTCCACC 1020
Db 1652 GAACCTGTCCCTGTCTGTCTCAGAGGGTGAAGAGAAACGAGACGCTTCAGTCCACC 1711
QY 1021 TGTGCGAATCTGTCTACTCAGAGGCAAGAGCAAAAGCCCTGCTATCCGCGCAGCGTG 1080
Db 1712 TGTGCGAATCTGTCTACTCAGAGGCAAGAGCAAAAGCCCTGCTATCCGCGCAGCGTG 1771
QY 1081 CCCAGCGTCCAGAGGTGCAAGCCGTGCTGTTAAGAGCAAGCCGCTGCTCAAGCGCTC 1140
Db 1772 CCCAGCGTCCAGAGGTGCAAGCCGTGCTGTTAAGAGCAAGCCGCTGCTCAAGCGCTC 1831
QY 1141 AGTGGGCTGCACTGTCCGAGACAGGCTGAGAGCAACAATTAAGCTCAAGCGTTCCTTC 1200
Db 1832 AGTGGGCTGCACTGTCCGAGACAGGCTGAGAGCAACAATTAAGCTCAAGCGTTCCTTC 1891
QY 1201 TCTCTGATATCAATCAGTTTCATATTCAGCGACATGAGCAATCCTTACATGAGCTTC 1260
Db 1892 TCTCTGATATCAATCAGTTTCATATTCAGCGACATGAGCAATCCTTACATGAGCTTC 1951
QY 1261 TCTCTATCAAGAAAGTCTTTTGAATATCAAAACCTTCACTACTGTGATGGGCAAC 1320
Db 1952 TCTCTATCAAGAAAGTCTTTTGAATATCAAAACCTTCACTACTGTGATGGGCAAC 2011
QY 1321 AAGCTATCCAGTTCTCCCTGTCTCAGGAACTATCGAGACAGATCCCGAAACAGTCTCT 1380
Db 2012 AAGCTATCCAGTTCTCCCTGTCTCAGGAACTATCGAGACAGATCCCGAAACAGTCTCT 2071
QY 1381 GATTAAGAGAAAGCAGACATCCCAAGAGCTGACAGCCGCGCTTCAAGACAGCCAG 1440
Db 2072 GATTAAGAGAAAGCAGACATCCCAAGAGCTGACAGCCGCGCTTCAAGACAGCCAG 2131

QY 1441 AGCAAGCATATTCATTCGGTCAAGAACAGACAGAGTGCACCGCCAGAGGTCCCTTTTA 1500
Db 2132 AGCAAGCATATTCATTCGGTCAAGAACAGACAGAGTGCACCGCCAGAGGTCCCTTTTA 2191
QY 1501 TCTCCATGCAATCGAAGTGGAGAGGTGAGAGCAATTAACACACAGCTTCTTTTCGGC 1560
Db 2192 TCTCCATGCAATCGAAGTGGAGAGGTGAGAGCAATTAACACACAGCTTCTTTTCGGC 2251
QY 1561 CTTTCCACAGCAGACACCTCAAGAGTCTGTGCGCTGGGGCTTAAAGGGCTGGCAC 1620
Db 2252 CTTTCCACAGCAGACACCTCAAGAGTCTGTGCGCTGGGGCTTAAAGGGCTGGCAC 2311
QY 1621 TCGATATCTTGGGCCCCCAGACCTTACCCCTTCCCTGACACAGAGCTGATTTTGGC 1680
Db 2312 TCGATATCTTGGGCCCCCAGACCTTACCCCTTCCCTGACACAGAGCTGATTTTGGC 2371
QY 1681 ACAGATCTTCAACTTCTACTCTGTGCTGACGATCTACGAGAGAGAGGAGTCCACTCT 1740
Db 2372 ACAGATCTTCAACTTCTACTCTGTGCTGACGATCTACGAGAGAGAGGAGTCCACTCT 2431
QY 1741 GCTTACAGCTGACGACAGCTGCCACTTGGCGGAGCAAGTCTATTCTGTGGCGAGGG 1800
Db 2432 GCTTACAGCTGACGACAGCTGCCACTTGGCGGAGCAAGTCTATTCTGTGGCGAGGG 2491
QY 1801 CAGAAAGCAAGTGAACAGAGTGAATCTGCGGCGAGAGCTGGCATGAAGAGAGCCCTTTGA 1860
Db 2492 CAGAAAGCAAGTGAACAGAGTGAATCTGCGGCGAGAGCTGGCATGAAGAGAGCCCTTTGA 2551
QY 1861 AAGCATTTAAACGAGAAAGTGCCTCAATTTGAGAGAGAGCATGTCAGAGAAC 1920
Db 2552 AAGCATTTAAACGAGAAAGTGCCTCAATTTGAGAGAGAGCATGTCAGAGAAC 2611
QY 1921 AGGTCAAGGAGAAAGCTGGGAAAGTGGGCACTGACTTTTCCGCGCAGATGAA 1980
Db 2612 AGGTCAAGGAGAAAGCTGGGAAAGTGGGCACTGACTTTTCCGCGCAGATGAA 2671
QY 1981 ATCATTGAGTCTCC 1995
Db 2672 ATCATTGAGTCTCC 2686

RESULT 11
US-10-343-357-17
; Sequence 17, Application US/10343357
; Publication NO. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: ELIOTT, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HAPALIA, April J.A.
; APPLICANT: LU, Dying Aina M.; TRIBOULEY, Catherine M.
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Daniel B.; CHAMLA, Nirinder K.
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: US/10/343,357
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30

Db 2458 AGGTACCGGAAAGAGCTGGGGAAGTGGGACAGTCTAGCTTTCCGGGACAGATGAA 2517
Qy 1981 ATCATTTAGGCTCC 1995
Db 2518 ATCATTTAGGCTCC 2532

RESULT 12
US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Query Match 99.8%; Score 1991.8; DB 18; Length 4790;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCATGAGATGATTGAACTCAAAATTGTTACTGAGAGGTTGGTCTCTGTGAA 60
Db 184 ATGCCCATGAGATGATTGAACTCAAAATTGTTACTGAGAGGTTGGTCTCTGTGAA 243
Qy 61 AGTGAAGGGAAGTCTGCTAATGATGAGCGGCAATTTGGAATACAAATCACC 120
Db 244 AGTGAAGGGAAGTCTGCTAATGATGAGCGGCAATTTGGAATACAAATCACC 303
Qy 121 CACATTTTGAAGCAATTAATCACTGCTCAAGTTATGAGCAAGTTGCAAG 180
Db 304 CACATTTTGAAGCAATTAATCACTGCTCAAGTTATGAGCAAGTTGCAAG 363
Qy 181 GACAAAGTTTAATTAAGAGCTCAATCCAGCATTCAGGAAACATPAAGTTGACATTAT 240
Db 364 GACAAAGTTTAATTAAGAGCTCAATCCAGCATTCAGGAAACATPAAGTTGACATTAT 423
Qy 241 TGCAGTCAGAAAGTTGATGTTAAGATCAAAAGCTCCCAAGATTTGCTCTCTTCA 300
Db 424 TGCAGTCAGAAAGTTGATGTTAAGATCAAAAGCTCCCAAGATTTGCTCTCTTCA 483
Qy 301 GACTGTTTCTCACTGTAATCTTGGGTAACCTGAGAAAGGTTCAACTCTGTGACCTG 360
Db 484 GACTGTTTCTCACTGTAATCTTGGGTAACCTGAGAAAGGTTCAACTCTGTGACCTG 543
Qy 361 CTTCAGAGTGGATTGCTGAGTTCTCTGTTGTTCCCTGGCTCTGTGAAGAAATCC 420
Db 544 CTTCAGAGTGGATTGCTGAGTTCTCTGTTGTTCCCTGGCTCTGTGAAGAAATCC 603
Qy 421 ACTCTAGTCCCTCACTGCAATTTCTAGCCTTCTTAAGTTGCAAGTTGGGCAACC 480
Db 604 ACTCTAGTCCCTCACTGCAATTTCTAGCCTTCTTAAGTTGCAAGTTGGGCAACC 663
Qy 481 GCAATTTCTCCCAATCTTATCTTGGCTGCGAGAGATGCTCAAGAGAGCTGATA 540
Db 664 GCAATTTCTCCCAATCTTATCTTGGCTGCGAGAGATGCTCAAGAGAGCTGATA 723
Qy 541 CAGCAGAAATGGGATTTGTTATGTTAAATGCGACATTAAGTTCAAGAGCTGACTT 600
Db 724 CAGCAGAAATGGGATTTGTTATGTTAAATGCGACATTAAGTTCAAGAGCTGACTT 783

Qy 601 ATCCCGAGTCTCATTTCTGCTGCTGCTGATGACAGCTTTTGTGAGAAATTTTG 660
Db 784 ATCCCGAGTCTCATTTCTGCTGCTGCTGATGACAGCTTTTGTGAGAAATTTTG 843
Qy 661 CCGTGGTGAACAAATCAGTATGATTCAATGAAAGCAAAAGCTCCATGATGATGTT 720
Db 844 CCGTGGTGAACAAATCAGTATGATTCAATGAAAGCAAAAGCTCCATGATGATGTT 903
Qy 721 CTAGTGAATGTTTATGCTGGGATCTCCCGCTCCGACCATGCTATGCTTATCAG 780
Db 904 CTAGTGAATGTTTATGCTGGGATCTCCCGCTCCGACCATGCTATGCTTATCAG 963
Qy 781 AAGAGATGAGCATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 964 AAGAGATGAGCATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 1023
Qy 841 ATATCTCCAAATCTTCAATTTTCTGGGCAACTCTGATCTATGATGATGATGATGATG 900
Db 1024 ATATCTCCAAATCTTCAATTTTCTGGGCAACTCTGATCTATGATGATGATGATGATG 1083
Qy 901 CAGATCTGAGATCAAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGAGCAAT 960
Db 1084 CAGATCTGAGATCAAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGAGCAAT 1143
Qy 961 GAACCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 1144 GAACCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1203
Qy 1021 TGTGCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1204 TGTGCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
Qy 1081 CCCAGCTGCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1264 CCCAGCTGCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
Qy 1141 AGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1324 AGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1383
Qy 1201 TCTCTGATATCAATCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1260
Db 1384 TCTCTGATATCAATCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTA 1443
Qy 1261 TCTCTGATATCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
Db 1444 TCTCTGATATCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1503
Qy 1321 AAGCTATGCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1504 AAGCTATGCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1563
Qy 1381 GATAAG 1440
Db 1564 GATAAG 1623
Qy 1441 AGCAAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1624 AGCAAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683
Qy 1501 TCTCTGATATCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
Db 1684 TCTCTGATATCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1743
Qy 1561 CTCTTCAACCAAG 1620
Db 1744 CTCTTCAACCAAG 1803
Qy 1621 TCGAATATCTTGGCCCGCAGACCTTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1804 TCGAATATCTTGGCCCGCAGACCTTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1863

QY	1681	AAGAAGTCTCA	CACCTTTCACTTCTCTGCTTCA	GCCATCTGA	CGAGGAGCGAGTTACTT	1740
Db	1864	AAGAGTCTCA	CACCTTTCACTTCTCTGCTTCA	GCCATCTGA	CGAGGAGCGAGTTACTT	1923
QY	1741	GCTTACAGTCG	CAGCGAGCTGCCACTTGC	CGAGAGCA	CAAGTCTATTCTGTCGAGGCGG	1800
Db	1924	GCTTACAGTCG	CAGCGAGCTGCCACTTGC	CGAGAGCA	CAAGTCTATTCTGTCGAGGCGG	1983
QY	1801	CAGAAGCCAA	GTGACAGAGCTGACCTCGGGGGGAG	CTGGCATGAA	AGAGAGCCCTTTGAA	1860
Db	1984	CAGAAGCCAA	GTGACAGAGCTGACCTCGGGGGGAG	CTGGCATGAA	AGAGAGCCCTTTGAA	2043
QY	1861	AAGCAGTTTAA	ACGAGAAAGCTGCCAAATTG	GAATTGGAGAG	CATCATGTGAGAAAC	1920
Db	2044	AAGCAGTTTAA	ACGAGAAAGCTGCCAAATTG	GAATTGGAGAG	CATCATGTGAGAAAC	2103
QY	1921	AGGTCAACGG	GAAGAGCTGGGGAAAGTGGGG	CAGTCACTTACTT	TGGGGAGAGATGGAA	1980
Db	2104	AGGTCAACGG	GAAGAGCTGGGGAAAGTGGGG	CAGTCACTTACTT	TGGGGAGAGATGGAA	2163
QY	1981	ATCATTTGAG	GTCTCTC	1995		
Db	2164	ATCATTTGAG	GTCTCTC	2178		

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RESULT 13
US-10-357-930-20824
/ Sequence 20824, Application US/10357930
/ Publication No. US20040259086A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Endegeel, Wilton
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ TITLE OF INVENTION: HUMAN PROSTATE CANCER
/ FILE REFERENCE: MRI-007BCN
/ CURRENT APPLICATION NUMBER: US/10/357, 930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785, 276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183, 319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189, 862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207, 454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211, 314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219, 007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255, 281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20824
/ LENGTH: 5145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: misc feature
/ LOCATION: 1, 5144, 5145
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

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Query Match	99.8%	Score 1991.8	DB 18	Length 5145
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1993; Conservative	0	Mismatches	2	Indels 0
				Gaps 0

Qy 1 ATGGCCCATGAGATGATTGGAACTCAAAATTGTACTGAAGGTTGGTGCTCTCGA 60
| | | | |
Db 589 ATGGCCCCATGAGATGATTGGAACTCAAAATTGTACTGAAGGTTGGTGCTCTCGAA 648

QY	61	AGTGGAAAGGAAAAAGTCGTCGTAATTTGAAATGAGCGCGCATATTTGTGGAAATCAATACATCC	120
Db	649	AGTGGAAAGGAAAAAGTCGTCGTAATTTGAAATGAGCGCGCATATTTGTGGAAATCAATACATCC	708
QY	121	CACATTTTGGAAAGCCATTAAATATCAATGCTGCCAGCTTATGAGAGGAAGTTGCAACAG	180
Db	709	CACATTTTGGAAAGCCATTAAATATCAATGCTGCCAGCTTATGAGAGGAAGTTGCAACAG	768
QY	181	GACAAAGTTTAATTAACAGAGCTCAATCCAGCATTTGCGGAACATTAAGTTGACATTGAT	240
Db	769	GACAAAGTTTAATTAACAGAGCTCAATCCAGCATTTGCGGAACATTAAGTTGACATTGAT	828
QY	241	TGCAAGTCAGAAAGTTGATGATTTCAGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA	300
Db	829	TGCAAGTCAGAAAGTTGATGATTTCAGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA	888
QY	301	GACTGTTTTCTCATCTGATCTTCGGGTAAACGTGAGAAAGCTTCAACTCTGTCCCTG	360
Db	889	GACTGTTTTCTCATCTGATCTTCGGGTAAACGTGAGAAAGCTTCAACTCTGTCCCTG	948
QY	361	CTTGCAAGTGGGTTTGTAGTTCTGCTGCTGCTGTTTCCCTGGGCTCTGTGAAGAAATCC	420
Db	949	CTTGCAAGTGGGTTTGTAGTTCTGCTGCTGTTTCCCTGGGCTCTGTGAAGAAATCC	1008
QY	421	ACTTAGTCCCTAACCTGCAATTTCTCAGCCCTTGCTTAACCTGTGGCCAACTTGGGCCAAC	480
Db	1009	ACTTAGTCCCTAACCTGCAATTTCTCAGCCCTTGCTTAACCTGTGGCCAACTTGGGCCAAC	1068
QY	481	CGAATCTTCCCAATCTTTATCTTGAGCTCCGACGAGATGTCTCAACAGAGCTGATTA	540
Db	1069	CGAATCTTCCCAATCTTTATCTTGAGCTCCGACGAGATGTCTCAACAGAGCTGATTA	1128
QY	541	CAGCAGAATGGGATTTGTTATGTGTTAAATGCACTATTAACCTGTGCCAAAGCTGACCTT	600
Db	1129	CAGCAGAATGGGATTTGTTATGTGTTAAATGCACTATTAACCTGTGCCAAAGCTGACCTT	1188
QY	601	ATCCCGAGTCTCAATTTCTGCGTGTGCTGTGAATGAACGTTTGTGAAGAAATTTTG	660
Db	1189	ATCCCGAGTCTCAATTTCTGCGTGTGCTGTGAATGAACGTTTGTGAAGAAATTTTG	1248
QY	661	CCGTGGTTGGAACAATTCAGTAGATTTCAATGAGAAAGAAAGCCTCCAAATGATGTGTT	720
Db	1249	CCGTGGTTGGAACAATTCAGTAGATTTCAATGAGAAAGAAAGCCTCCAAATGATGTGTT	1308
QY	721	CTAAGTCACTGTTAAGCTGGGATCTCCCGCTCCGCAACATTCGCTATTCGCTACATCATG	780
Db	1309	CTAAGTCACTGTTAAGCTGGGATCTCCCGCTCCGCAACATTCGCTATTCGCTACATCATG	1368
QY	781	AAGAGGAATGGAACATCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT	840
Db	1369	AAGAGGAATGGAACATCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT	1428
QY	841	AATATCTCCAAACTCAATTTTCTG6GGCCAACTCTCGACATATGAGAAGATTAAGAAC	900
Db	1429	AATATCTCCAAACTCAATTTTCTG6GGCCAACTCTCGACATATGAGAAGATTAAGAAC	1488
QY	901	CAGACTGAGACATCAAGGCGCAAGAGCAAACTCAAGCTGCTGCACCTTGAGAAAGCCAAAT	960
Db	1489	CAGACTGAGACATCAAGGCGCAAGAGCAAACTCAAGCTGCTGCACCTTGAGAAAGCCAAAT	1548
QY	961	GAACCTGTGCTCTGCTGCTCAAGAGGATGGAACAGAAAGCGAGAGCGCCCTCAAGTCCACC	1020
Db	1549	GAACCTGTGCTCTGCTGCTCAAGAGGATGGAACAGAAAGCGAGAGCGCCCTCAAGTCCACC	1608
QY	1021	TGTGCGCACTCTGCTACCTCAAGAGCGACAGACAAAGGCGCTGTCAATCCCGCAGCGTG	1080
Db	1609	TGTGCGCACTCTGCTACCTCAAGAGCGACAGACAAAGGCGCTGTCAATCCCGCAGCGTG	1668
QY	1081	CCGAGCGCTGCCAGCGTGGAGCGCTGCTCTGTATAGAGACAGCCCGCTGTATCAAGGCGCTC	1140
Db	1669	CCGAGCGCTGCCAGCGTGGAGCGCTGCTCTGTATAGAGACAGCCCGCTGTATCAAGGCGCTC	1728
QY	1141	AGTGGGCTGACCTGTCTCGCAGACAGGCTGTGAAGACAGCAATTAAGCTCAAGGCTTCTTG	1200

QY	1081	1669	1141
CCAGACGTCGCCAGCGAGACCGTCGCTGTGTAGAGACAAGCCGCGTATACAGAGCGCTC	CCAGACGTCGCCAGCGAGACCGTCGCTGTGTAGAGACAAGCCGCGTGTATACAGAGCGCTC	AGTGGGCTGCACCTGTCGCGAGA CAGGCTGGAAAGACAGCATATAGCTCAAGCGCTTCCTTC	1200
Db	1728		

Db 1729 AGTGGCTGCACTCTCCGACAGAGGCTGGAAAGCAGCAATTAACCTCAAGGTTCTCTTC 1788
Qy 1201 TCTGTGATATCAATCAAGTTTCATATTCAGGCAGATGGAGCATTCCTTACATGAGCTTC 1260
Db 1789 TCTGTGATATCAATCAAGTTTCATATTCAGGCAGATGGAGCATTCCTTACATGAGCTTC 1848
Qy 1261 TCTGTGATATCAATCAAGTTTCATATTCAGGCAGATGGAGCATTCCTTACATGAGCTTC 1320
Db 1849 TCTGTGATATCAATCAAGTTTCATATTCAGGCAGATGGAGCATTCCTTACATGAGCTTC 1908
Qy 1321 AAGCTATGCGAGTTCTCCCTGTTTCAAGAACTATGAGAGCAGATTCCTGAAACCACTCT 1380
Db 1909 AAGCTATGCGAGTTCTCCCTGTTTCAAGAACTATGAGAGCAGATTCCTGAAACCACTCT 1968
Qy 1381 GATTAAGGAGAAAGCCAGATCCCAAGAAAGCTGAGACCGGCGCTTCAGAGAGCAG 1440
Db 1969 GATTAAGGAGAAAGCCAGATCCCAAGAAAGCTGAGACCGGCGCTTCAGAGAGCAG 2028
Qy 1441 AGCAAGCATTGCAATTCGGTCAAGAACAGCAGCAGATGGCAACCGCCAGAGTCCCTTTTA 1500
Db 2029 AGCAAGCATTGCAATTCGGTCAAGAACAGCAGCAGATGGCAACCGCCAGAGTCCCTTTTA 2088
Qy 1501 TCTCCATCTGATCGAAGTGGAGCGTGAAGCAATTAACCAACCAAGCTTCCTTTTCGAC 1560
Db 2089 TCTCCATCTGATCGAAGTGGAGCGTGAAGCAATTAACCAACCAAGCTTCCTTTTCGAC 2148
Qy 1561 CTTTCCACAGCAGCAGACACTCAAGAGTCTGCTGAGCTGGGCTTAAAGGCTGGAGC 1620
Db 2149 CTTTCCACAGCAGCAGACACTCAAGAGTCTGCTGAGCTGGGCTTAAAGGCTGGAGC 2208
Qy 1621 TCGGATATCTTGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGGATTTTGGC 1680
Db 2209 TCGGATATCTTGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGGATTTTGGC 2268
Qy 1681 ACAAGTCTCACTTCTACTCTGCTCAAGCATCTTACGAGAGCAGTGGCCAGTTACTCT 1740
Db 2269 ACAAGTCTCACTTCTACTCTGCTCAAGCATCTTACGAGAGCAGTGGCCAGTTACTCT 2328
Qy 1741 GCTTACAGCTGACAGCAGCTGCCCCCTTGGCGAGACCAAGTCTTATCTGTGGCGAGGG 1800
Db 2329 GCTTACAGCTGACAGCAGCTGCCCCCTTGGCGAGACCAAGTCTTATCTGTGGCGAGGG 2388
Qy 1801 CAGAAGCAGATGACAGAGCTGACTCGCGGCGAGACTGGCATGAAGAGAGCCCTTTGAA 1860
Db 2389 CAGAAGCAGATGACAGAGCTGACTCGCGGCGAGACTGGCATGAAGAGAGCCCTTTGAA 2448
Qy 1861 AAGCAGTTTAAACGAGAAAGCTGCCAAATGGAAATTGAGAGAGCATGTCAGAGAAC 1920
Db 2449 AAGCAGTTTAAACGAGAAAGCTGCCAAATGGAAATTGAGAGAGCATGTCAGAGAAC 2508
Qy 1921 AGGTCAACGAGAAAGCTGGGAAAAGTGGGAGTCAAGTCTTTCGGGCGAGCATGGA 1980
Db 2509 AGGTCAACGAGAAAGCTGGGAAAAGTGGGAGTCAAGTCTTTCGGGCGAGCATGGA 2568
Qy 1981 ATCATTGAGTCTCC 1995
Db 2569 ATCATTGAGTCTCC 2583

RESULT 14
US-10-357-930-20969
; Sequence 20969, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930

; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20969
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20969

Query Match 99.8%; Score 1991.8; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCCATGAGATGATGGAATCAATTTGATCTGAGAGTGGTGGCTCTGCTGGA 60
Db 589 ATGCCCCATGAGATGATGGAATCAATTTGATCTGAGAGTGGTGGCTCTGCTGGA 648
Qy 61 AGTGAACGAAAGTGTCTCTAATTTGATAGCCGCCATTGTTGGAATACATATCC 120
Db 649 AGTGAACGAAAGTGTCTCTAATTTGATAGCCGCCATTGTTGGAATACATATCC 708
Qy 121 CACATTTTGAAGCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAAGTTGCAACG 180
Db 709 CACATTTTGAAGCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAAGTTGCAACG 768
Qy 181 GACAAAGTGAATTAATTAAGAGCTCATCCAGCATTCAGCGAAACATPAAGTTGACATTGAT 240
Db 769 GACAAAGTGAATTAATTAAGAGCTCATCCAGCATTCAGCGAAACATPAAGTTGACATTGAT 828
Qy 241 TGCAGTCAGAAAGTGTGATTTACGATCAAGATCCCAAGATGTTGCTCTCTTCA 300
Db 829 TGCAGTCAGAAAGTGTGATTTACGATCAAGATCCCAAGATGTTGCTCTCTTCA 888
Qy 301 GACTGTTTCTCACTGATCTCTGAGTAACTGAGAAAGACTTCACTGTTCACTG 360
Db 889 GACTGTTTCTCACTGATCTCTGAGTAACTGAGAAAGACTTCACTGTTCACTG 948
Qy 361 CTTGAGGTGGGTTTGCAGATTCCTGCTGTTTCCCTGGGCTGTGAGAGAAATCC 420
Db 949 CTTGAGGTGGGTTTGCAGATTCCTGCTGTTTCCCTGGGCTGTGAGAGAAATCC 1008
Qy 421 ACTCTAGTCCCTTACCTGATTTCTCAGCTTGTCTTACCTGTTGCCAATTTGGGCAAC 480
Db 1009 ACTCTAGTCCCTTACCTGATTTCTCAGCTTGTCTTACCTGTTGCCAATTTGGGCAAC 1068
Qy 481 CGAATTTCTCCCAATCTTATCTTGCTGCGAGAGATGTCCTCAACAGAGCTGATA 540
Db 1069 CGAATTTCTCCCAATCTTATCTTGCTGCGAGAGATGTCCTCAACAGAGCTGATA 1128
Qy 541 CAGAGATGGAGTGGTATGATGTTAAATGCGAGTATTAATCTGTTCCAAAGCTGACTT 600
Db 1129 CAGAGATGGAGTGGTATGATGTTAAATGCGAGTATTAATCTGTTCCAAAGCTGACTT 1188
Qy 601 ATCCCGAGTCTCAATTCCTGCTGCTGCTGCTGATGATGACAGCTTTTGTGAGAAATTTTG 660

Db 1189 ATCCCGAGTCTCATTTCTCCGCTGCTGCTGATGACAGCTTTTGTGAGAAAATTTTG 1248
QY 661 CCGTGTGTGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCATATGATGTGT 720
Db 1249 CCGTGTGTGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCATATGATGTGT 1308
QY 721 CTAGTGCATGTTTTAGCTGGGATCTCCGCTCCGCCACATCGCTATCGCTTACATCATG 780
Db 1309 CTAGTGCATGTTTTAGCTGGGATCTCCGCTCCGCCACATCGCTATCGCTTACATCATG 1368
QY 781 AAGAGATGACATGCTTTTGAATGAGCTTACAGATTTTGTGAAAAAAGAAAGAACTTACT 840
Db 1369 AAGAGATGACATGCTTTTGAATGAGCTTACAGATTTTGTGAAAAAAGAAAGAAAGAACTTACT 1428
QY 841 ATATCTCCAAATCTCAATTTTCTGGGCCAACTCTGTGACTATGAGAAAGATTTAAGAC 900
Db 1429 ATATCTCCAAATCTCAATTTTCTGGGCCAACTCTGTGACTATGAGAAAGATTTAAGAC 1488
QY 901 CAGACTGAGACATCAGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGAGAGAGCCCAAT 960
Db 1489 CAGACTGAGACATCAGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGAGAGAGCCCAAT 1548
QY 961 GAACCTGTCCCTGCTCTCAGAGGGGTGACAGAAAAAGAGAGAGCCCTCTAGTCCACCC 1020
Db 1549 GAACCTGTCCCTGCTCTCAGAGGGGTGACAGAAAAAGAGAGAGCCCTCTAGTCCACCC 1608
QY 1021 TGTGCCGACTCTGCTACTCCTCAGAGGACAGAGCAAAAGCCCGTGATCCGCCAGCGTG 1080
Db 1609 TGTGCCGACTCTGCTACTCCTCAGAGGACAGAGCAAAAGCCCGTGATCCGCCAGCGTG 1668
QY 1081 CCCAGGTCGCCAGCGCTGACAGCCGTGCTGTTAGAGAGCAAGCCCGTGATCAGGCGCTC 1140
Db 1669 CCCAGGTCGCCAGCGCTGACAGCCGTGCTGTTAGAGAGCAAGCCCGTGATCAGGCGCTC 1728
QY 1141 AGTGCGCTCAGCTGTCCGACAGAGGCTGAGAAAGAGCAAGATTAAGCTCAAGGCTTCCCTC 1200
Db 1729 AGTGCGCTCAGCTGTCCGACAGAGGCTGAGAAAGAGCAAGATTAAGCTCAAGGCTTCCCTC 1788
QY 1201 TCTCTGAGATCAATCAGTTTCATATTCAGCCAGCATGAGCAGCATCTTTCATGAGCTTC 1260
Db 1789 TCTCTGAGATCAATCAGTTTCATATTCAGCCAGCATGAGCAGCATCTTTCATGAGCTTC 1848
QY 1261 TCCCTATCAGAAAGATGCTTTGGAATTCAGAACTTCCTTCACTCTCTGATGAGCAAC 1320
Db 1849 TCCCTATCAGAAAGATGCTTTGGAATTCAGAACTTCCTTCACTCTCTGATGAGCAAC 1908
QY 1321 AAGCTATGCGAGTTTCTCCCTGTTGAGAACTATGAGAGAGACTCCCGAAACAGATGCT 1380
Db 1909 AAGCTATGCGAGTTTCTCCCTGTTGAGAACTATGAGAGAGACTCCCGAAACAGATGCT 1968
QY 1381 GATTAAG 1440
Db 1969 GATTAAG 2028
QY 1441 AGCAAGCATGATGATTCGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 2029 AGCAAGCATGATGATTCGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2088
QY 1501 TCTTCACTGATCGAAGGTGAGAGCGTGGAGAGCAATTAACACACAGAGTTCTTTTGAGC 1560
Db 2089 TCTTCACTGATCGAAGGTGAGAGCGTGGAGAGCAATTAACACACAGAGTTCTTTTGAGC 2148
QY 1561 CTTTCCACAG 1620
Db 2149 CTTTCCACAG 2208
QY 1621 TCGGATATCTTGGCCCGCCAGAGAGCTTACACCTTCCCGTCCAGACAGAGCTGATTTTGGC 1680
Db 2209 TCGGATATCTTGGCCCGCCAGAGAGCTTACACCTTCCCGTCCAGAGAGCTGATTTTGGC 2268
QY 1681 ACGAGATCTCAGACTTCTACTCTGCTCAGAGCACTTACAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 2269 ACGAGATCTCAGACTTCTACTCTGCTCAGAGCACTTACAGAGAGAGAGAGAGAGAGAGAGAG 2328

QY 1741 GCCTACAGCTGACAGCCAGCTGCCCATCTTGCCGAGACCAAGTCTATTTCTGTGCGAGCGG 1800
Db 2329 GCCTACAGCTGACAGCCAGCTGCCCATCTTGCCGAGACCAAGTCTATTTCTGTGCGAGCGG 2388
QY 1801 CAGAAAGCAAGTGAAGAGAGCTGACCTCGCGGAGAGCTGGCATGAGAGAGAGAGAGAGAGAGAG 1860
Db 2389 CAGAAAGCAAGTGAAGAGAGCTGACCTCGCGGAGAGCTGGCATGAGAGAGAGAGAGAGAGAGAG 2448
QY 1861 AAGCAGTTTAAACGCAAGAGCTGCCAAATGGAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 2449 AAGCAGTTTAAACGCAAGAGCTGCCAAATGGAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2508
QY 1921 AGGTACGGGAAAGAGCTGGGAGAAAGTGGGAGCTGACGTTAGCTTTTGGGAGAGAGAGAG 1980
Db 2509 AGGTACGGGAAAGAGCTGGGAGAAAGTGGGAGCTGACGTTAGCTTTTGGGAGAGAGAGAGAG 2568
QY 1981 ATCATTGAGTCTCC 1995
Db 2569 ATCATTGAGTCTCC 2583
RESULT 15
US-10-357-930-21071
; Sequence 21071, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: HRI-0078CN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21071
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5145, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21071
Query Match 99.8%; Score 1991.8; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCCCATGAGATGATGGAATCTCAATTTGTTACTGAGAGGTTGCTGCTGAGAA 60
Db 589 ATGGCCCATGAGATGATGGAATCTCAATTTGTTACTGAGAGGTTGCTGCTGAGAA 648
QY 61 AGTGAAGCGAAAGAGTGTGCTAATGATGAGCCGCAATTTGTGAGATCAATATCATCC 120
Db 649 AGTGAAGCGAAAGAGTGTGCTAATGATGAGCCGCAATTTGTGAGATCAATATCATCC 708

QY 121 CACATTTTGGAGCCATTAAATCAATGCTCTCAAGCTTATGAGCGAAGTTGCAAG 180
 Db 709 CACATTTTGGAGCCATTAAATCAATGCTCTCAAGCTTATGAGCGAAGTTGCAAG 768
 QY 181 GACAAAGTTAAATTAACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 240
 Db 769 GACAAAGTTAAATTAACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 828
 QY 241 TGCAGTCAAGAGCTGTAGTTAAGATCAAGAGCTCCAAAGTTGGCTCTCTCTCA 300
 Db 829 TGCAGTCAAGAGCTGTAGTTAAGATCAAGAGCTCCAAAGTTGGCTCTCTCTCTCA 888
 QY 301 GACTGTTTCTCACTGTAATCTGAGTAACTGAGAAAGAGCTTCAACTGTTCACCTG 360
 Db 889 GACTGTTTCTCACTGTAATCTGAGTAACTGAGAAAGAGCTTCAACTGTTCACCTG 948
 QY 361 CTTCAGAGTGGGTTTGTGAGTTCTCTGTTGTTTCCCTGAGCTCTGTGAAAGAAATCC 420
 Db 949 CTTCAGAGTGGGTTTGTGAGTTCTCTGTTGTTTCCCTGAGCTCTGTGAAAGAAATCC 1008
 QY 421 ACTCAAGTCCCTCACTGATTTCTCAAGCTTGTCTTACCTGTTCAGCAATTGGGCCAAC 480
 Db 1009 ACTCAAGTCCCTCACTGATTTCTCAAGCTTGTCTTACCTGTTCAGCAATTGGGCCAAC 1068
 QY 481 GGAATTTCTCCCAATCTTATCTTGGCTGCCAGAGATGCTCTCAAGAGAGCTGADA 540
 Db 1069 GGAATTTCTCCCAATCTTATCTTGGCTGCCAGAGATGCTCTCAAGAGAGCTGADA 1128
 QY 541 CAGCAGAAATGGAGTTGTTATGTTAAATGCGACCTTACCTGTCCAAAGCTGACTTT 600
 Db 1129 CAGCAGAAATGGAGTTGTTATGTTAAATGCGACCTTACCTGTCCAAAGCTGACTTT 1188
 QY 601 ATCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTTGTGAGAAATTTTG 660
 Db 1189 ATCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTTGTGAGAAATTTTG 1248
 QY 661 CCGTGTGGAACAATCAGTAGATTTCAATTGAGAAAGAAAGCTCCAAATGATGTGT 720
 Db 1249 CCGTGTGGAACAATCAGTAGATTTCAATTGAGAAAGAAAGCTCCAAATGATGTGT 1308
 QY 721 CTAGTGAATGTTAGTGGGATCTCCGCTCCGACCATGCTTATGCTTACATCAATG 780
 Db 1309 CTAGTGAATGTTAGTGGGATCTCCGCTCCGACCATGCTTATGCTTACATCAATG 1368
 QY 781 AAGAGATGAGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGACTTACT 840
 Db 1369 AAGAGATGAGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGACTTACT 1428
 QY 841 ATATCTCAAACTTCAATTTCTGGGCCAATCCGCGAATGAGAGAAAGTTTAAGAAC 900
 Db 1429 ATATCTCAAACTTCAATTTCTGGGCCAATCCGCGAATGAGAGAAAGTTTAAGAAC 1488
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 Db 1489 CAGACTGAGCATCAGGCGCAAAAGACAACTCAAGTGTGCTGACCTGAGAGAGCAAT 1548
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 Db 1549 GAACTGTCTCTGCTGTCTCAGAGGATGAGCAAGAAAGCGAGAGCGCTTCACTACCC 1608
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 Db 1609 TGTGCGGACTGTGCTCACTCAGAGGCAAGAGCAAAAGCCGTTGCAATCCGCGCAGCTG 1668
 QY 1081 CCCAGCGTCCAGCGTCAAGCGCTGCTGTTAGAGAGCAGCCGCTGTATCAGGCGCTC 1140
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 Db 1729 AGTGGGCTGCACTGTCCGAGACAGGCTGAGAAACAGCAATTAAGCTCAAGCTTCTTC 1788

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 Db 1849 TCTCTATCAAGATGCTTTGGAAATCTTCAAACTTCCATCTACTGTGATGGAACCAAC 1908
 QY 1321 AAGCTATGCAAGTTTCCCTGTTGAGAACTATGAGAGCAGACTCCGAAACCAAGTCT 1380
 Db 1909 AAGCTATGCAAGTTTCCCTGTTGAGAACTATGAGAGCAGACTCCGAAACCAAGTCT 1968
 QY 1381 GATTAAGAGAAAGCCAGCATCCCAAGAGCTGACACCGCCAGCTTTCAGACAGCAG 1440
 Db 1969 GATTAAGAGAAAGCCAGCATCCCAAGAGCTGACACCGCCAGCTTTCAGACAGCAG 2028
 QY 1441 AGCAAGCATTTGATTCGCTGAGAAACGAGCAGAGTGCACCGCCAGAGTCCCTTTTA 1500
 Db 2029 AGCAAGCATTTGATTCGCTGAGAAACGAGCAGAGTGCACCGCCAGAGTCCCTTTTA 2088
 QY 1501 TCTCCAGTCAAGTGGGAGGAGGCTGAGAGCAATTAACAACAGCTTCCCTTTCCG 1560
 Db 2089 TCTCCAGTCAAGTGGGAGGAGGCTGAGAGCAATTAACAACAGCTTCCCTTTCCG 2148
 QY 1561 CTCTTCAACAGCCAGCAGCACTTCAAGAGTCTGCTGAGCTTGAAGGCTGAGCAG 1620
 Db 2149 CTCTTCAACAGCCAGCAGCACTTCAAGAGTCTGCTGAGCTTGAAGGCTGAGCAG 2208
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 Db 2209 TCGATATCTTGGCCCCCAAGCTTCAACCCCTTCTGACCAAGCTGTATTTTGGC 2268
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 Db 2329 GCTTACAGCTCAGCAGCACTGCCCACTTGCAGAGCAAACTTATCTGTGCGCAGGCG 2388
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 QY 1981 ATCATTTAGTCTCC 1995
 Db 2569 ATCATTTAGTCTCC 2583

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GenCore version 5.1.6
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Title: US-10-029-345A-108_COPY_538_1443

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	902.8	99.6	1998	US-09-816-494-3	Sequence 3, Appli
2	902.8	99.6	3544	US-09-816-494-1	Sequence 1, Appli
3	365.8	40.4	2377	US-09-920-668-3	Sequence 3250, Ap
4	364.2	40.2	2351	US-09-949-016-3250	Sequence 2877, Ap
5	294.6	32.5	333	US-09-513-999C-2877	Sequence 91, Appli
6	223	24.6	279	US-09-016-434-91	Sequence 3684, Ap
7	187.8	20.7	1830	US-09-513-999C-3684	Sequence 1, Appli
8	124.6	13.8	1830	US-09-557-921-1	Sequence 4617, Ap
9	106.8	11.8	2283	US-09-949-016-4617	Sequence 3, Appli
10	106.8	11.8	2303	US-09-922-146-3	Sequence 1135, Ap
11	96.2	10.6	2109	US-09-016-434-1135	Sequence 946, App
12	96.2	10.6	2109	US-09-023-655-946	Sequence 2615, App
13	96.2	10.6	2475	US-09-949-016-2615	Sequence 347, App
14	94.6	10.4	1208	US-09-023-655-347	Sequence 801, App
15	91.6	10.1	1619	US-09-702-705-801	Sequence 804, App
16	91.6	10.1	1619	US-09-736-457-801	Sequence 801, App
17	91.6	10.1	1619	US-09-614-124B-801	Sequence 801, App
18	91.6	10.1	1619	US-09-671-325-801	Sequence 801, App
19	91.6	10.1	1619	US-09-589-184-801	Sequence 801, App
20	91.6	10.1	1619	US-09-658-824-801	Sequence 804, App
21	91.6	10.1	4637	US-09-702-705-804	Sequence 804, App
22	91.6	10.1	4637	US-09-736-457-804	Sequence 804, App
23	91.6	10.1	4637	US-09-614-124B-804	Sequence 804, App
24	91.6	10.1	4637	US-09-671-325-804	Sequence 804, App
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26	91.6	10.1	4637	US-09-658-824-804	Sequence 11, Appli
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28	90	9.9	1238	US-09-702-705-803	Sequence 803, App
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36	90	9.9	2064	US-09-614-124B-825	Sequence 825, App
37	90	9.9	2064	US-09-671-325-825	Sequence 825, App
38	90	9.9	2064	US-09-589-184-825	Sequence 825, App
39	90	9.9	2064	US-09-658-824-825	Sequence 825, App
40	90	9.9	2109	US-09-702-705-826	Sequence 826, App
41	90	9.9	2109	US-09-736-457-826	Sequence 826, App
42	90	9.9	2109	US-09-614-124B-826	Sequence 826, App
43	90	9.9	2109	US-09-671-325-826	Sequence 826, App
44	90	9.9	2109	US-09-589-184-826	Sequence 826, App
45	90	9.9	2109	US-09-658-824-826	Sequence 826, App

ALIGNMENTS

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RESULT 1
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIORITY FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Query Match      99.6%; Score 902.8; DB 4; Length 1998;
Best Local Similarity 99.8%; Pred. No. 5e-308;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGCCATGAGATGATGGAACCAATTGTTACTGAGAGGTTGGTGGCTGCTGGAA 60
DB      1  ATGGCCATGAGATGATGGAACCAATTGTTACTGAGAGGTTGGTGGCTGCTGGAA 60

QY      61  AGTGAAGCAAGAAAAGTCTCTAATGATAGCCGCGCATTTGTGGAATACAAATCATCC 120
DB      61  AGTGAAGCAAGAAAAGTCTCTAATGATAGCCGCGCATTTGTGGAATACAAATCATCC 120

QY      121  CACATTTTGAAGCCATTAAATATCACTGCTCCAAAGCTTATGAGACGAAAGTTGCAACG 180
DB      121  CACATTTTGAAGCCATTAAATATCACTGCTCCAAAGCTTATGAGACGAAAGTTGCAACG 180

QY      181  GACAAAGTTAATTAACAGACTCATTCAGATTCAGGAAACATPAAGTTGACATTAT 240
DB      181  GACAAAGTTAATTAACAGACTCATTCAGATTCAGGAAACATPAAGTTGACATTAT 240

QY      241  TGCAGTCAGAGTTGTAGTTTACATCAAGACTCCAAAGTGTGCTCTCTCTTCA 300
DB      241  TGCAGTCAGAGTTGTAGTTTACATCAAGACTCCAAAGTGTGCTCTCTCTTCA 300

QY      301  GACTGTTTCTCACTGTACTTCTGGGTAACTGGAAGAGCTTCACTGTTCACCTG 360
DB      301  GACTGTTTCTCACTGTACTTCTGGGTAACTGGAAGAGCTTCACTGTTCACCTG 360

QY      361  CTTGAGAGTGGTGTTCGTAATTCTCTGTTTCCCTGGGCTCTGTGAAGAAATCC 420
DB      361  CTTGAGAGTGGTGTTCGTAATTCTCTGTTTCCCTGGGCTCTGTGAAGAAATCC 420
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Db 361 CTTCAGAGTGGGTTGCTGAGTCTCTGTTGTTTCCCTGCGCTCTGTGAGAGAAATCC 420
Qy 421 ACTCTAGTCCCTACCTGSCATTTCTCAGCCTTGCTTACTGTGCAACATTTGGGCAACC 480
Db 421 ACTCTAGTCCCTACCTGSCATTTCTCAGCCTTGCTTACTGTGCAACATTTGGGCAACC 480
Qy 481 CGAATCTTCCCAATCTTTATCTGTGCTGCGAGAGATGCTCTCAACAAGAGCTGATA 540
Db 481 CGAATCTTCCCAATCTTTATCTGTGCTGCGAGAGATGCTCTCAACAAGAGCTGATA 540
Qy 541 CAGCAGAAATGGGATTGGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTT 600
Db 541 CAGCAGAAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 600
Qy 601 ATCCCGAGTCTATTTCCGCTGCGCTGCGTGAATGAGAGAGCTTTGTGAGAAATTTTG 660
Db 601 ATCCCGAGTCTATTTCCGCTGCGCTGCGTGAATGAGAGAGCTTTGTGAGAAATTTTG 660
Qy 661 CCGTGGTTGACAAATCAGTAGATTTCATTTGAGAGAAAGCAAGCCCTCAATGGATGTT 720
Db 661 CCGTGGTTGACAAATCAGTAGATTTCATTTGAGAGAAAGCAAGCCCTCAATGGATGTT 720
Qy 721 CTAGTGCATGTTTACGTGGGATCTCCGCTCGGCCACATGCTATGCGCTACATCATG 780
Db 721 CTAGTGCATGTTTACGTGGGATCTCCGCTCGGCCACATGCTATGCGCTACATCATG 780
Qy 781 AAGAGATGAGACATGCTTTAGTAGAGCTTACAGATTGTGAGAAAGAAAGACCTACT 840
Db 781 AAGAGATGAGACATGCTTTAGTAGAGCTTACAGATTGTGAGAAAGAAAGACCTACT 840
Qy 841 AATATCCCAACTTCATTTTCTGGGCCAACTCTGAGCTATGAGAGAGATTAAAGAC 900
Db 841 AATATCCCAACTTCATTTTCTGGGCCAACTCTGAGCTATGAGAGAGATTAAAGAC 900
Qy 901 CAGACT 906
Db 901 CAGACT 906

RESULT 2
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Query Match 99.6%; Score 902.8; DB 4; Length 3544;
Best Local Similarity 99.8%; Pred. No. 7.7e-308;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCCATGAGATTTGCAATCTCAATTTGTTACTGAGAGGTTGGCTTCTGCTGAA 60
Db 589 ATGGCCCATGAGATTTGCAATCTCAATTTGTTACTGAGAGGTTGGCTTCTGCTGAA 648
Qy 61 AGTGAACGAGAAAAAGTGCTGCTAATTGATGAGCGGCAATTTTGGAATCAATATC 120

Db 649 AGTGAACGAGAAAAAGTGCTGCTAATTGATGAGCGGCAATTTTGGAATCAATATC 708
Qy 121 CACATTTTGAAGCCATTAAATATCACTGCTCAAGCTTATGAGAGCAAGGTTGCAACAG 180
Db 709 CACATTTTGAAGCCATTAAATATCACTGCTCAAGCTTATGAGAGCAAGGTTGCAACAG 768
Qy 181 GACAAAGTTAATTTACAGAGCTCATCCAGATTCAGGAAACATTAAGTTGACATTGAT 240
Db 769 GACAAAGTTAATTTACAGAGCTCATCCAGATTCAGGAAACATTAAGTTGACATTGAT 828
Qy 241 TGCACTCAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 829 TGCACTCAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 888
Qy 301 GACTGTTTCTCAGTATCTTCTGAGTAACTGAGAGAGAGCTTCAACTGTTCACCTG 360
Db 889 GACTGTTTCTCAGTATCTTCTGAGTAACTGAGAGAGAGCTTCAACTGTTCACCTG 948
Qy 361 CTTCAGAGTGGGTTTGTGAGTCTCTGTTGTTTCCCTGGCTCTGTGAGAGAAATCC 420
Db 949 CTTCAGAGTGGGTTTGTGAGTCTCTGTTGTTTCCCTGGCTCTGTGAGAGAAATCC 1008
Qy 421 ACTCTAGTCCCTACCTGATTTCTCAGCCTTGCTTACTGTTGCAACATTTGGGCAACC 480
Db 1009 ACTCTAGTCCCTACCTGATTTCTCAGCCTTGCTTACTGTTGCAACATTTGGGCAACC 1068
Qy 481 CGAATCTTCCCAATCTTTATCTTGCTGCGAGAGAGTCTCTCAACAAGAGCTGATG 540
Db 1069 CGAATCTTCCCAATCTTTATCTTGCTGCGAGAGAGTCTCTCAACAAGAGCTGATG 1128
Qy 541 CAGCAGAAATGGGATTGGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCCTGACT 600
Db 1129 CAGCAGAAATGGGATTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACT 1188
Qy 601 ATCCCGAGTCTATTTCCGCTGCGCTGCGTGAATGAGAGCTTTGTGAGAAATTTTG 660
Db 1189 ATCCCGAGTCTATTTCCGCTGCGCTGCGTGAATGAGAGAGCTTTGTGAGAAATTTTG 1248
Qy 661 CCGTGGTTGACAAATCAGTAGATTTCATTTGAGAGAAAGCAAGCCCTCAATGGATGTT 720
Db 1249 CCGTGGTTGACAAATCAGTAGATTTCATTTGAGAGAAAGCAAGCCCTCAATGGATGTT 1308
Qy 721 CTAGTGCATGTTTACGTGGGATCTCCGCTCGGCCACATGCTATGCGCTACATCATG 780
Db 1309 CTAGTGCATGTTTACGTGGGATCTCCGCTCGGCCACATGCTATGCGCTACATCATG 1368
Qy 781 AAGAGATGAGACATGCTTTAGTAGAGCTTACAGATTGTGAGAAAGAAAGACCTACT 840
Db 1369 AAGAGATGAGACATGCTTTAGTAGAGCTTACAGATTGTGAGAAAGAAAGACCTACT 1428
Qy 841 AATATCCCAACTTCATTTTCTGGGCCAACTCTGAGCTATGAGAGAGATTAAAGAC 900
Db 1429 AATATCCCAACTTCATTTTCTGGGCCAACTCTGAGCTATGAGAGAGATTAAAGAC 1488
Qy 901 CAGACT 906
Db 1489 CAGACT 1494

RESULT 3
US-09-920-668-3
; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Coweert
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RTS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3

LENGTH: 2377
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (135)...(2012)
US-09-920-668-3

Query Match 40.4% Score 365.8; DB 4; Length 2377;
Best Local Similarity 64.5%; Pred. No. 6.1e-118;
Matches 563; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

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225 GACAGCGGCTCTCTGCTGATACAAACAGCTGCGATGCTCAGCTCCGCAACATCTGC 284
148 TGCTCCAGCTTTGAAGCGAAGTTGCAAGAGCAAGGTTAATTAACAGCTCATC 207
285 TGCTCCAGCTGTGAGAGCGGCGCTGCAAGGCAAGTGAACCATTCGAGCTATC 344
208 CAGCATTCAGCGAACAATAAGTTGACATTTGACAGTCAAGAGTTGTATTCGAT 267
345 CAGCGGCTGACACGACGAGCTGAGAGCTACAGAGCAAGACGTGTGTATAC 404
268 CAAGCTCCCAAGATGTTGCTCTCTCTTCAAGCTGTTTCTCATCTAATTCTGGGT 327
405 CAGAGCAGCGGAGACGCGAGGCTGCGCGCAGACAGCTTCTCTCATCTGAGC 464
328 AAATGGAAGAGACTTCAATCTGTTCACCTGCTGAGAGTGGTGTGTGAGTCTCT 387
465 AAGCTGACGCGCTCTTGAAGAGGCTGACAGGCTGCTCACTGAGGCTTGCACCTTCTCC 524
388 CGTGTGTCCCTGCTCTGTGAGAGAAATCCACT---CTAGTCCCTACCTGATTTCT 444
525 TCCTGCTTCCCGGCTCTGTGAGAGGCAAGCTGTGCTGCTGCTACCATAGCTCTCC 584
445 CAGCTTGTCTTACCTGTGCAAGATGGGCAACCCGAAATCTTCCCAATCTTATCTT 504
585 CAGCGCTGCTGCTGTGAGCGAGGCTGAGCGGCTGACCGGCTGCTCATCTGCTACCTG 644
505 GCGCTGCAAGAGATGTCTCAACAAGAGCTGATACAGCAAGTGGATGGTGTATG 564
645 GCGCTGCAAGAGAGCTCTTAAACAAGATCTGATGACGCAAAATGGAATAGCTACGTC 704
565 TTAAATGCAAGCTTACCTGTGCAAGAGCTGATTTATCCCGAGTCTCATTTCTGCGT 624
705 CTCAAGCGCAAGACTCTGCTCCCAAGCTTCACTTCTGAGAGCGCTTCAATGCGG 764
625 GTGCTGTGATGACAGCTTTTGTGAGAAATTTTGCCTGTGTCACAAATCAATAGAT 684
765 GTCCCATCAACGACACTACTGTGAGAAATCTGCTGCGCTGTGAGCAATGATGAG 824
685 TTCAATTGAGAAAGCAAGCTCTCAATGATGTGTTCTAGTCACTGTTTACTGGGATC 744
825 TTCAATCAATAAAGCAAGCTCTCAAGCTGCAAGCTGATCTGCTGCTGCTGCTGCTC 884
745 TCCGCTGCGGCAAGCTGCTGATGCGCTGATCAATCAATGAAGAGATGAGATCTTTGAT 804
885 TCCGCTGCTGCAACATGCGCTGCTGATCAATCAATGAAGACCAATGAGGATGCTTCCGAC 944
805 GAACTTACAGATTTGTGAGAAAGAAAGAACTTATATCTCAAACTTCAATTTCTG 864
945 GAGCGCTACAGATTTGTGAGAGAGAGAGCGCGCTGCTCAATCTGCGCAACTTCACTCTG 1004
865 GCGCACTCTGAGCTATGAGAGAGATTAAG 897
1005 GCGCAGCTGTGAGTACGAGCGCAGCTGAAG 1037

RESULT 4

US-09-949-016-3250
Sequence 3250, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3250
LENGTH: 2351
TYPE: DNA
ORGANISM: Human
US-09-949-016-3250

Query Match 40.2% Score 364.2; DB 4; Length 2351;
Best Local Similarity 64.4%; Pred. No. 2.2e-117;
Matches 562; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

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139 ATGATGCAAGAGTGTGCTGCTGCGGGGCGGCGCTGGGGGCGCTGCTATC 198
88 GATAGCGGCGCATTTGTGGAATACATATCCACATTTTGAAGCCATTAAATCAAC 147
199 GACAGCGGCTCTCTGCTGATACAAACAGCTGAGATGCTCAGCTCCGCAACATCTGC 258
148 TGCTCCAGCTTTGAAGCGAAGTTGCAAGAGCAAGGTTAATTAACAGCTCATC 207
259 TGCTCCAGCTGTGAGAGCGGCGCTGCAAGGCAAGTGAACATTCGAGCTATC 318
208 CAGCATTCAGCGAACAATAAGTTGACATTTGACAGTCAAGAGTTGTATTCGAT 267
319 CAGCGGCTGACACGACGAGCTGAGAGCTGAGAGCAAGACGTGTGTATAC 378
268 CAAGCTCCCAAGATGTTGCTCTCTCTTCAAGCTGTTTCTCATCTGATCTTGGGT 327
379 CAGAGCAGCGGAGACGCGAGGCTGCGCGCAGACAGCTTCTCTCATCTGCTGAGC 438
328 AAATGGAAGAGACTTCAATCTGTTCACCTGCTGAGAGTGGTGTGTGAGTCTCT 387
439 AAGCTGACGCGCTCTTGAAGAGGCTGACAGGCTGCTCACTGAGGCTTGCACCTTCTCC 498
388 CGTGTGTCCCTGCTCTGTGAGAGAAATCCACT---CTAGTCCCTACCTGATTTCT 444
499 TCCTGCTTCCCGGCTCTGTGAGAGGCAAGCTGTGCTGCTGCTACCATAGCTCTCC 558
445 CAGCTTGTCTTACCTGTGCAAGATGGGCAACCCGAAATCTTCCCAATCTTATCTT 504
559 CAGCGCTGCTGCTGTGAGCGAGGCTGAGCGGCTGACCGGCTGCTGCTCATCTGCTG 618
505 GCGCTGCAAGAGATGTCTCAACAAGAGCTGATACAGCAAGTGGATGGTGTATG 564
619 GCGCTGCAAGAGAGCTCTTAAACAAGATCTGATGACGCAAAATGGAATAGCTACGTC 678
565 TTAAATGCAAGCTTACCTGTGCAAGAGCTGATTTATCCCGAGTCTCATTTCTGCGT 624
679 CTCAAGCGCAAGACTCTGCTGCGCAAGCTTCACTTCTGAGAGCGGCTTCAATGCGG 738
625 GTGCTGTGATGACAGCTTTTGTGAGAAATTTTGCCTGTGTCACAAATCAATAGAT 684
739 GTCCCATCAACGACACTACTGTGAGAAATCTGCTGCGCTGTGAGCAATGCTCATGAG 798

QY 685 TTCAATGAGAAAGCAAAAGCCTCCATGATGATGTCTAGTGCACCTGTTAGTGGATC 744
Db 799 TTCAATGAGTAAAGCCAAAGCTCTCCAGCTGCAAGTCACTGCTGCTGGCATC 858
QY 745 TCCGCTCCGCGACCATGCTATGCTCTACATCAATGAGAGATGACATGCTTTAGAT 804
Db 859 TCCGCTCCGCGACCATGCTATGCTCTACATCAATGAGAGATGACATGCTTTAGAT 804
QY 805 GAACTTACAGATTTGTAAGAAAGAAAGCCTTATCTCCAACTTCAATTTCTG 864
Db 919 GAGCCTTACAGATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
QY 865 GGCCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
Db 979 GGCCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011

RESULT 5
US-09-513-999C-2877

/ Sequence 2877, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59.US2.REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 2877
/ LENGTH: 333
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 127..333
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 17
/ OTHER INFORMATION: h=a or c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: y=c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 19
/ OTHER INFORMATION: k=g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 36
/ OTHER INFORMATION: n=a, g, c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 58
/ OTHER INFORMATION: r=a or g
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 237
/ OTHER INFORMATION: w=a or t
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 37
/ OTHER INFORMATION: Xaa=His or Gln
/ US-09-513-999C-2877

Query Match 32.5%; Score 294.6; DB 4; Length 333;
Best Local Similarity 97.3%; Pred. No. 2,2e-93;

Matches 326; Conservative 5; Mismatches 0; Indels 4; Gaps 3;
QY 34 ACTGAGAGGTGGTGGCTCTGCTGGAAGAGTGAACGG-AAAAGGCTGCTTAATTGATG 92
Db 1 ACTGAGAGGTGGTGGH--KCTGAAAGTGAACGAAAGAGTGGCTGCTTAATTGATG 58
QY 93 CCGGCTATTTGGTAAT-CAATACATCCCATTTTGAAGCCATTAAATACATGCT 151
Db 59 CCGGCTATTTGGTAATCAATACATCCCATTTTGAAGCCATTAAATACATGCT 118
QY 152 CCAAGCTTATGAAGAGAGTGAACAGAGCAAGAGTAAATATACAGAGCTCATCCAGC 211
Db 119 CCAAGCTTATGAAGAGAGTGAACAGAGCAAGAGTAAATATACAGAGCTCATCCAGC 178
QY 212 ATTACGCAAAATTAAGGTGACATTAATGACAGTGAAGAGTGTGATTAGATCAAA 271
Db 179 ATTACGCAAAATTAAGGTGACATTAATGACAGTGAAGAGTGTGATTAGATCAAA 238
QY 272 GCTCCCAAGAGTGGCTCTCTCTCTTCAAGCTGTTTCTCACTGTACTTGGGTAAC 331
Db 239 GCTCCCAAGAGTGGCTCTCTCTCTTCAAGCTGTTTCTCACTGTACTTGGGTAAC 298
QY 332 TGAAGAAAGCTTCAACTGTTTCACTGTTCACTGTTCA 366
Db 299 TGAAGAAAGCTTCAACTGTTTCACTGTTCACTGTTCA 333

RESULT 6
US-09-016-434-91

/ Sequence 91, Application US/09016434
/ Patent No. 6500938
/ GENERAL INFORMATION:
/ APPLICANT: Janice Au-Young
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
/ TITLE OF INVENTION: PATHWAY GENE EXPRESSION
/ NUMBER OF SEQUENCES: 1490
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,434
/ FILING DATE: HERewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0002 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 845-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 91:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 279 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: LUNGHE103
/ CLONE: 1234795

US-09-016-434-91

Query Match	24.6%	Score 223;	DB 4;	Length 279;
Best Local Similarity	100.0%	Pred. No. 4.1e-68;		
Matches 223;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	181	GACAAAGTGAATTAATACAGAGCTCATCCAGCATTCAGCGAAAC	223
QY	205	GACAAAGTGAATTAATACAGAGCTCATCCAGCATTCAGCGAAAC	247
Db	25	ATGGCCCATGATGATGTGGAACTCAAAATGTTACTGAGAGGGTGTGGCTCTGCGAA	84
QY	61	AGTGGAAACGGAAAAAGTGCCTGCTAAATGTAATAGCCGCGCATTTGTGGAATACAAATACATCC	120
Db	85	AGTGGAAACGGAAAAAGTGCCTGCTAAATGTAATAGCCGCGCATTTGTGGAATACAAATACATCC	144
QY	121	CACATTTGGAGACCCATTAATATCAACATGCTCCAAAGCTTAATGAAAGCGAAGGTTCGAACAG	180
Db	145	CACATTTGGAGACCCATTAATATCAACATGCTCCAAAGCTTAATGAAAGCGAAGGTTCGAACAG	204

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RESULT 7
US-09-513-999C-3684/c
: Sequence 3684, Application US/09513999C
: Patent No. 6783961
: GENERAL INFORMATION:
: APPLICANT: Dumais Mline Edwards, J.B.
: APPLICANT: Ducleit, A.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
: Patent No. 6783961
: FILE REFERENCE: 59.US2.REG
: CURRENT APPLICATION NUMBER: US/09/513.999C
: CURRENT FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/122,487
: PRIOR FILING DATE: 1999-02-26
: NUMBER OF SEQ ID NOS: 36681
: SOFTWARE: Patent.pm
: SEQ ID NO 3684
: LENGTH: 378
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 216..377
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 164
: OTHER INFORMATION: k=g or t
: US-09-513-999C-3684

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Query Match	20.7%	Score 187.8;	DB 4;	Length 378;
Best Local Similarity	99.0%	Pred. No. 1.5e-55;		
Matches 189; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 4 TGGTGGCTGCTGCGAAATGGAAACGAAAAAGTCTCTTAATGATATGCGGACATTTG 103

Db 378 TGGTGGCTGCTGCGAAAGTGAACGAAAAAGTCTCTTAATGATATGCGGACATTTG 319

QY 104 TGGAAATACAAATACATCCCAATTTTGGAAAGCCATTAAATATCAATGCTCCAAAGTTATGA 163

Db 318 TGGAAATACAAATACATCCCAATTTTGGAAAGCCATTAAATCACTGCTCCAAAGTTATGA 259

QY 164 AGCGAAAGTTCGAACAGACGAAAGTTTAATTACAGAGCTCATCCAGCATTCAGCGAAAC 223

Db 258 AGCGAAAGTTCGAACAGACGAAAGTTTAATTACAGAGCTCATCCAGCATTCAGCGAAAC 199

QY 224 ATAAAGTTGAC 234

Db 198 ATAAAGTTAAAC 188

RESULT 8
US-09-557-921-1

Sequence 1, Application US/09557921

PATENT NO. 6551810

APPLICANT: Luche, Ralf M.

APPLICANT: Wei, Bo

TITLE OF INVENTION: DSP-1

FILE REFERENCE: 200125.416
CIBRENT APPLICATION NIMRR: IIS/09/557 921

CURRENT FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSeq for Windows Version 4.0.0

SEQ ID NO 1
LENGTH: 1830

TYPE: DNA

ORGANISM: Hc

S-09-557-921-1

Query Match

Best Local Site

Matches 251; Conservative 0; Mismatches 189; Indels 3;

Qy	461	TTGCAACATTTGGGCGCAACCGAATCTTCCCAATCTTTACTTTCGTGGCCAGCGAGATG	520
Db	1036	TCGAGAACGCTGAAGCTACACCCCACTCTTGCCCTTCCTGTTCCCTTGCAATAGCAGATG	1099
Qy	521	TCCTCAACAGAGACTGATACAGCAAGATGGATTTGGTTATGTGTAAATGCCACTATA	580
Db	1096	CTCAGAGACTGACACCATGACGGCGGTGAACATCGGCTACGTATCAACGTCACTC	1158
Qy	581	CTGTCCAAAGCGTGACTTT--ATGCCAGTCTCATTTCCGCGTGGCTGTGATG	637
Db	1156	ATCTTCCCTTACCACTATGAGAAAGCCCTGTTCAACTACAGCGGCTGCGACGACTG	1215
Qy	638	ACAGCTTTTGTGAGAAATTTTGGCGTGTGCAAAATCAGTAGATTTCATTGAGAAAG	697
Db	1216	ACAGCAACAGAGAACCTGGCGAGTACTTTGAAAGAGGCTTTGAGTTCAATTGAGAAAG	1275
Qy	698	CAAAAGCTCCCAATGATGTGTTTACTGACACTGTTTACGTGGGATCTCCGCTCCGCA	757
Db	1276	CTACCAAGTGTGGAGAGGGGCTTCTCATCACTCCAGGCTGGGGTGTCCGCTCCGCA	1335
Qy	758	CCATCGCTATCGCTTACATCATGAGAGAGATGACATGTCTTTAGATGAACCTTACAGAT	817
Db	1336	CCATCGCTATCGCTTACTTGAATGAGACACTCGGATGACCATGACTGATCTTATTAAT	1395
Qy	818	TTGTGAAGAAAAAGACTACTATATCTCCAACTTCAATTTTCTGGGCCAACTCCTGG	877
Db	1396	TTGTCAAAAGCAACGACCAATATCTCCCAACTTAACTTATGAGGGGAGTTGCTAG	1455
Qy	878	ACTATGAGAAAGATTAAAGC 900	
Db	1456	AGTTGAGAGACTTAAACAC 1478	

```

RESULT 9
US-09-949-016-4617
; Sequence 4617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

```

;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4617
;; LENGTH: 2283
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-4617

Query Match 11.8%; Score 106.8; DB 4; Length 2283;
Best Local Similarity 55.3%; Pred. No. 2,7e-26;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTTCTTCCCAATCTTTATCTTGGCTGCGAGGAGATGCTCAACAAGAG 534
Db CCGTCCAGATCTGCGCAACTCTATCTGGGAGTCCCGGATTCGGCAATTTGGAG 782
Qy 535 CTGATACAGAGATGAGATGTTGTTATGTTTAAATGCCAGCTATACCTGTCCAA--G 591
Db AGCCTGCGCAAACTGGGCACTCGCTACATCTCAATGTCAACCCCAACTCCCAACTTC 842
Qy 592 CCGACTTTATCCCGAGTCTCATTTCCGCGTGTGAGATGAGAGAGCTTTGTGAG 651
Db TTGAGAGAGATGATGATCTTCACTACAGAGATCCCATCTCCGACCACTGGAGCCG 902
Qy 652 AAAATTTTGGCGTGTGAGCAAAATCAGTATTTGATGAGAAAGCAAAAGCTTCCAT 711
Db AACCTGTGCGGCTTCTTTCGAGGCGCATTTGATGAGAGGCTTGTCCAGAAC 962
Qy 712 GATGTTCTAGTGAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 771
Db TGGGGGTGCTGCTCCAGCTGCTGGGGGTGAGGCGTGTGATGATGATGATGATGATG 1022
Qy 772 TACATCATGAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 831
Db TACCTATGCAAGAGCTTCACTCTCTCAACGATGCTATGACTGTGCAAGAGAG 1082
Qy 832 AGACCTACTATATCTCCAACTTCAATTTTCTGGGCAACTCTGACTATGAG 885
Db AAGCTAACATCTCCCACTTCACTTCAATGAGGAGGAGTGTGACTTTGAG 1136

RESULT 10
US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowbert
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RTS-0252
; CURRENT APPLICATION NUMBER: US/09/922.146
; FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 2303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114) ... (1268)
US-09-922-146-3

Query Match 11.8%; Score 106.8; DB 4; Length 2303;
Best Local Similarity 55.3%; Pred. No. 2,7e-26;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTTCTTCCCAATCTTTATCTTGGCTGCGAGGAGATGCTCAACAAGAG 534
Db CCGTCCAGATCTGCGCAACTCTATCTGGGAGTCCCGGATTCGGCAATTTGGAG 782
Qy 535 CTGATACAGAGATGAGATGTTGTTATGTTTAAATGCCAGCTATACCTGTCCAA--G 591

Db 783 AGCCTGCGCAAACTGGGCACTCGCTACATCTCAATGTCAACCCCAACTCCCAACTTC 842
Qy 592 CCGACTTTATCCCGAGTCTCATTTCTGGGTGCGCTGAGATGAGAGCTTTGTGAG 651
Db TTGAGAGAGATGATGATCTTCACTACAGAGATCCCATCTCCGACCACTGGAGCCG 902
Qy 652 AAAATTTTGGCGTGTGAGCAAAATCAGTATTTGATGAGAAAGCAAAAGCTTCCAT 711
Db AACCTGTGCGGCTTCTTTCGAGGCGCATTTGATGAGAGGCTTGTCCAGAAC 962
Qy 712 GATGTTCTAGTGAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 771
Db TGGGGGTGCTGCTCCAGCTGCTGGGGGTGAGGCGTGTGATGATGATGATGATGATG 1022
Qy 772 TACATCATGAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 831
Db TACCTATGCAAGAGCTTCACTCTCTCAACGATGCTATGACCTGTGCAAGAGAG 1082
Qy 832 AGACCTACTATATCTCCAACTTCAATTTTCTGGGCAACTCTGACTATGAG 885
Db AAGCTAACATCTCCCACTTCACTTCAATGAGGAGGAGTGTGACTTTGAG 1136

RESULT 11
US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1418933
US-09-016-434-1135

Query Match 10.6%; Score 96.2; DB 4; Length 2109;
Best Local Similarity 53.8%; Pred. No. 1,4e-22;

Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

Qy 484 ATCTTCCCAATCTTATCTTGTGCTGCCAGGAGATGCTCTCAACAGAGAGCTGATACAG 543
Db 979 ATCTTCCCTTCTCTACTTGGGCTGTGCGCAAGACTCTCACCACTTGAGCTGTGGAG 1038

Qy 544 CAGAAATGGATGGTATATGTGTAAATGACAGACTATACCTGTCCAAAGC---CTGACTTT 600
Db 1039 GAATTCGGCATCAAGTACATCTTGAAGCTCAACCCCAATTTGGCAATCTCTTGAGAAC 1098

Qy 601 ATCCCCAGTCTCATTTCTGCTGCTGTGCTGTGAATGACAGCTTTTGTGAAGAAATTTTG 660
Db 1099 GCAGAGAGTTTAAATACAGCAAAATCCCATCTGATCTGAGAGCCAAATCTGTGCC 1158

Qy 661 CCGGTGTGACAAATGATGATTTTCAATGAGAAAGCAAAAGCCTCAATGATGTGT 720
Db 1159 CAGTTTTCCTGAGGCGCATTTCTTCAATGAGAGCCCGGGGCAAGACTGTGTGTCTC 1218

Qy 721 CTAGTGCATGTTTATGCTGGGATCTCCGCTCCGCAACATGCTATGCTCAATCATG 780
Db 1219 TTGGTACATTTGCTGGCTGGCATTAAGCGCTCAATGCTGATGCTGTGCTTACTTATG 1278

Qy 781 AAGAGATGACATGCTTTTATGATGAGAGCTTACAGATTTGTGAAGAAAAAGACTTACT 840
Db 1279 CAGAGCTCAATCTGTGATGAGAGATGCTATGACATTTGCAAAATGAAAAATCCAAC 1338

Qy 841 ATATCTCCAACTTCAATTTCTGTGGCCCACTCTGAGCTATGAGAAAGAT 893
Db 1339 ATATCCCTTAATCTCAATCTGATGAGCTGTGAGCTTGTGAGAGAGCCT 1391

RESULT 12

US-09-023-655-946

Sequence 946, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 946:
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1418933
US-09-023-655-946

Query Match 10.6%; Score 96.2; DB 4; Length 2109;
Best Local Similarity 53.8%; Pred. No. 1.4e-22;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

Qy 484 ATCTTCCCAATCTTATCTTGTGCTGCCAGGAGATGCTCTCAACAGAGAGCTGATACAG 543
Db 979 ATCTTCCCTTCTCTACTTGGGCTGTGCGCAAGACTCTCACCACTTGAGCTGTGGAG 1038

Qy 544 CAGAAATGGATGGTATATGTGTAAATGACAGACTATACCTGTCCAAAGC---CTGACTTT 600
Db 1039 GAATTCGGCATCAAGTACATCTTGAAGCTCAACCCCAATTTGGCAATCTCTTGAGAAC 1098

Qy 601 ATCCCCAGTCTCATTTCTGCTGCTGTGCTGTGAATGACAGCTTTTGTGAAGAAATTTTG 660
Db 1099 GCAGAGAGTTTAAATACAGCAAAATCCCATCTGATCTGAGAGCCAAATCTGTGCC 1158

Qy 661 CCGGTGTGACAAATGATGATTTTCAATGAGAAAGCAAAAGCCTCAATGATGTGT 720
Db 1159 CAGTTTTCCTGAGGCGCATTTCTTCAATGAGAGCCCGGGGCAAGACTGTGTGTCTC 1218

Qy 721 CTAGTGCATGTTTATGCTGGGATCTCCGCTCCGCAACATGCTATGCTCAATCATG 780
Db 1219 TTGGTACATTTGCTGGCTGGCATTAAGCGCTCAATGCTGATGCTGTGCTTACTTATG 1278

Qy 781 AAGAGATGACATGCTTTTATGATGAGAGCTTACAGATTTGTGAAGAAAAAGACTTACT 840
Db 1279 CAGAGCTCAATCTGTGATGAGAGATGCTATGACATTTGCAAAATGAAAAATCCAAC 1338

Qy 841 ATATCTCCAACTTCAATTTCTGTGGCCCACTCTGAGCTATGAGAAAGAT 893
Db 1339 ATATCCCTTAATCTCAATCTGATGAGCTGTGAGCTTGTGAGAGAGCCT 1391

RESULT 13

US-09-949-016-2615

Sequence 2615, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2615
LENGTH: 2475
TYPE: DNA
ORGANISM: Human
US-09-949-016-2615

Query Match 10.6%; Score 96.2; DB 4; Length 2475;
Best Local Similarity 53.8%; Pred. No. 1.6e-22;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

Qy 484 ATCTTCCCAATCTTATCTTGTGCTGCCAGGAGATGCTCTCAACAGAGAGCTGATACAG 543
Db 1068 ATCTTCCCTTCTCTACTTGGGCTGTGCGCAAGACTCTCACCACTTGAGCTGTGGAG 1127

QY 544 CAGATGGGATGGTAAATGTTAAATGCCAGCTATACCTGTCACAAAGC---CTGACTTT 600
Db 1128 GAATTCGGCATCAAGTACATCTTGAAGTACACCCCAATTTGCCAATCTTTTGAAGAC 1187
QY 601 ATCCCGAGCTCATTTCTCGCGTGCCTGTGTGAATGACAGCTTTGTGAGAAATTTTG 660
Db 1188 GCAGAGAGTTTAAATACAGCAAAATCCCATCTCGATCATCTGAGACAAACCTGTTC 1247
QY 661 CCGTGTGGAGCAATCAGTATGATTTGATGAGAAACAAACCTCCATGATGTGTT 720
Db 1248 CAGTTTTTCCCTGAGGCAATTTCTTTATAGATGAGACCCGGGAGAAACTGTGTGTC 1307
QY 721 CTAGTGCAGTGTTAGTGGATCTCCGCTCCGCCACCATCCCTATCCCTACATCATG 780
Db 1308 TTGTTACATTGCTGTGGCTGAGCATTAAGCCGCTCAGTCACTGTGACTGTGCTTACCTTATG 1367
QY 781 AAGAGATGACATGCTTTAGATGAGAGCTTACAGATTTGTGAGAAAAAGAAAGACTTACT 840
Db 1368 CAGAGCTCATCTGTGATGAGAGAGATCCCTATGACATGTCTCAAAATGAAAAATCTCAAC 1427
QY 841 ATATCTCCAACTTCATTTTCTGGGCCAACTCCTGGAATGAGAGAAAGAT 893
Db 1428 ATATCCCTTAATCTCAACTTCATGGGTCACTGACTTGAGAGAGAGCT 1480

RESULT 14
US-09-023-655-347
; Sequence 347, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF INVENTIONS: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYNOT03
; CLONE: 1444245
US-09-023-655-347

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Best Local Similarity 64.3%; Pred. No. 3,4e-22;
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Db 124 TGACTGATGCTTATTAATTTGTCAAAAGGCAAAAGCAACCAATATCTCCCAAGCTTAAT 183
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; Sequence 801, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Derrick
; APPLICANT: Reiter, Marc
; APPLICANT: Mannon, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121,478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; NUMBER OF SEQ ID NOS: 2000-10-30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-801

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Db 320 ATCTCTCCCTTCTCTACTCTCGCAGTGCCTACATGCTGCGGAGAGACATGTGAC 379
QY 544 CAGAATGGAGTTGTTATGTGTTAATGCCAGCTTACTCTGCCAAAGCTGACTTATC 603
Db 380 GCCCTGGGATCAGGGCTGTGTGATGTCTCTGAGCTGCCAACC---ACTTTGAA 436
QY 604 CCGAGTCTATTTCTCGTGTGCTGTGATGACAGCTTTTGTGAGAAATTTTGGCG 663
Db 437 GGACACTATCAGTACAGATGATCCCATGTGAAGATTAACCAAGGCCGATCAGCTCC 496
QY 664 TGGTTGAGAAATCAGTATGATTTATTGAGAAAGCAAAAGCTCCAAATGATGTGTTCTA 723
Db 497 TGGTTTCATGAGAGCCATGAGATCATGATCCGTGAAGAGACTGCGGTGGCGGTGCTG 556
QY 724 GTGACATGTTAGCTGGGATCTCCGCGCTCGGCCACCATCGCTATCTGCTTATATATGAG 783
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Job time : 164.961 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

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(without alignments)
9670.754 Million cell updates/sec

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Gapop 10.0, Gapept 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	902.8	99.6	1998	18	US-10-377-072-27
4	902.8	99.6	2071	17	US-10-072-012-257
5	902.8	99.6	2732	17	US-10-168-506-2
6	902.8	99.6	3059	17	US-10-257-026-1
7	902.8	99.6	3496	9	US-09-964-227-1
8	902.8	99.6	3521	18	US-10-370-715B-261
9	902.8	99.6	3544	17	US-09-816-494-1
10	902.8	99.6	3544	17	US-10-377-072-25
11	902.8	99.6	3544	18	US-10-377-072-25

12	902.8	99.6	3625	17	US-10-425-114-26234	Sequence 26234, A
13	902.8	99.6	3766	17	US-10-343-357-17	Sequence 17, Appl
14	902.8	99.6	4790	18	US-10-648-593-115	Sequence 115, Appl
15	902.8	99.6	5145	18	US-10-357-930-20824	Sequence 20824, A
16	902.8	99.6	5145	18	US-10-357-930-20969	Sequence 20969, A
17	902.8	99.6	5145	18	US-10-357-930-21071	Sequence 21071, A
18	902.8	99.6	5145	18	US-10-357-930-21083	Sequence 21083, A
19	902.8	99.6	5145	18	US-10-357-930-21307	Sequence 21307, A
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24	902.8	99.6	5145	18	US-10-357-930-26912	Sequence 26912, A
25	902.8	99.6	5145	18	US-10-357-930-26923	Sequence 26923, A
26	902.8	99.6	5145	18	US-10-357-930-27145	Sequence 27145, A
27	902.8	99.6	5145	18	US-10-357-930-27149	Sequence 27149, A
28	902.8	99.6	5145	18	US-10-357-930-28675	Sequence 28675, A
29	901.2	99.5	2102	17	US-10-094-749-673	Sequence 673, App
30	899.6	99.3	2966	17	US-10-296-115-520	Sequence 520, App
31	817.8	90.3	2200	17	US-10-072-012-255	Sequence 255, App
32	564.8	62.3	3332	9	US-09-964-277-20	Sequence 20, Appl
33	411.2	45.4	418	18	US-10-357-930-11243	Sequence 11243, A
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35	410.2	45.3	461	18	US-10-357-930-41000	Sequence 41000, A
36	410.2	45.3	461	18	US-10-357-930-41346	Sequence 41346, A
37	395.4	43.6	427	18	US-10-357-930-10878	Sequence 10878, A
38	363.6	40.1	2453	13	US-10-005-658-1	Sequence 1, Appl
39	359.8	39.7	419	18	US-10-357-930-32060	Sequence 32060, A
40	349	38.5	422	18	US-10-357-930-2074	Sequence 2074, App
41	340.8	37.6	346	18	US-10-357-930-11236	Sequence 11236, A
42	339.8	37.5	345	18	US-10-357-930-2067	Sequence 2067, App
43	338.8	37.4	377	18	US-10-357-930-32409	Sequence 32409, A
44	338.8	37.4	377	18	US-10-357-930-11339	Sequence 11339, A
45	335.8	37.1	2476	17	US-10-220-120-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Query Match 99.6%; Score 902.8; DB 9; Length 1998;
Best Local Similarity 99.8%; Pred. No. 3,4e+280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 ATGGCCATGAGATGATGGAATCAATTTCTACTGAGAGTGTGGCTCTCTGGAA 60
QY 61 AGTGAAGCAAAAAGTCTCTAATGATGAGCCGCAATTTGGGAAATACATCAATCC 120
DB 61 AGTGAAGCAAAAAGTCTCTAATGATGAGCCGCAATTTGGGAAATACATCAATCC 120
QY 121 CACATTTTGAAGCATTAATATCACTGCTCAAGCTTATGAAGCAAGTTGCAACAG 180

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Db 241 TGCAGTCAGAAAGTTAGTTTACGATCAAAAGCTCCCAAGATTTCTCTCTCTTA 300
Qy 301 GACTGTTTCTCACTGTACTTCTGGGTAACTGGAAGAAAGCTTCAACTCTGTCCTG 360
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US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.U.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williams, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USUS THEREFOR
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FILE REFERENCE: MP103-0180NM1M
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
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; LOCATION: (1) ... (1998)
US-10-377-072-27
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Query Match 99.6%; Score 902.8; DB 17; Length 1998;
Best Local Similarity 99.8%; Pred. No. 3.4e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 121 CACATTTGGAAGCCATTAATATCACTGCTCCAGCTTATGAGGAAAGTTGCAACG 180
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Db      901 CAGACT 906

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: Sequence 27, Application US/10377072
: Publication No. US20040157221A9
GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals Inc.
: APPLICANT: Cutlis, Roy A.J.
: APPLICANT: Logan, Thomas Joseph
: APPLICANT: Glucksmann, Maria A.
: APPLICANT: Meyers, Rachel E.
: APPLICANT: Williamson, Mark J.
: APPLICANT: Rudolph-Owen, Laura A.
: APPLICANT: Tsai, Fong-Ying
: TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117.
: TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
: TITLE OF INVENTION: AND USES THEREFOR
: FILE REFERENCE: MPI03-0180XNIM
: CURRENT APPLICATION NUMBER: US/10/377,072
: CURRENT FILING DATE: 2003-02-27
: PRIOR APPLICATION NUMBER: US 09/895,860
: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: US 60/215,370
: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: US 09/723,806
: PRIOR FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: US 60/187,455
: PRIOR FILING DATE: 2000-03-07
: PRIOR APPLICATION NUMBER: US 09/843,297
: PRIOR FILING DATE: 2001-04-25
: PRIOR APPLICATION NUMBER: US 60/199,801
: PRIOR FILING DATE: 2000-04-26
: PRIOR APPLICATION NUMBER: US 09/861,801
: PRIOR FILING DATE: 2001-05-21
: PRIOR APPLICATION NUMBER: US 60/205,508
: PRIOR FILING DATE: 2000-05-19
: PRIOR APPLICATION NUMBER: US 09/816,494
: PRIOR FILING DATE: 2001-03-23
: PRIOR APPLICATION NUMBER: US 09/815,419
: PRIOR FILING DATE: 2001-03-22
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 114

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SOFTWARE:FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1998)
; US-10-377-072-27

Query Match      99.6%; Score 902.8; DB 18; Length 1998;
Best Local Similarity 99.8%; Pred. No. 3.4e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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DB      1 ATGCCCCATGAGATGATGTTGAACTCAATTGTTACTGAGAGGTGGTGGCTCTGCTGAA 60
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DB      301 GACGTTTTCTCACTGTACTCTGGGTAACTGGAAGAGCTTCAACTCTGTCACTG 360
QY      361 CTTCAGGTGGGTTTGTCTGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC 420
DB      361 CTTCAGGTGGGTTTGTCTGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC 420
QY      421 ACTCTAGTCCCTACCTGCAATTCACAGCCTTGCTTACCTGTGTCCAAACTTTGGGCCAAC 480
DB      421 ACTCTAGTCCCTACCTGCAATTCACAGCCTTGCTTACCTGTGTCCAAACTTTGGGCCAAC 480
QY      481 CGAATTTCTCCCAATCTTTATCTTGCTGCGCAGCGAAGTTCCTCAACAAGAGCTGATA 540
DB      481 CGAATTTCTCCCAATCTTTATCTTGCTGCGCAGCGAAGTTCCTCAACAAGAGCTGATA 540
QY      541 CAGCAGAAATGGGAATGGTATGTGTAAATGCAAGCTTAATCTGTCCAAAGCCTGACTT 600
DB      541 CAGCAGAAATGGGAATGGTATGTGTAAATGCAAGCTTAATCTGTGTCCAAAGCCTGACTT 600
QY      601 ATCCCGAGTCTCAATTCCTGCGGTGTGCTGTAATGACAGCTTTTGTGAAAAATTTTG 660
DB      601 ATCCCGAGTCTCAATTCCTGCGGTGTGCTGTAATGACAGCTTTTGTGAAAAATTTTG 660
QY      661 CCGTGTGTGCAAAATCAATGATGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGATGTGTT 720
DB      661 CCGTGTGTGCAAAATCAATGATGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGATGTGTT 720
QY      721 CTAGTGCACGTGTATAGCTGGAGATCTCCGCGTCCGCGCACATGCGTATGCGCTCAATCATG 780
DB      721 CTAGTGCACGTGTATAGCTGGAGATCTCCGCGTCCGCGCACATGCGTATGCGCTCAATCATG 780
QY      781 AAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACT 840
DB      781 AAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACT 840
QY      841 ATATCTCCAAATCTCAATTTCTGGGCCCACTCTCGACATATGAGAAAGATTAAAGAC 900
DB      841 ATATCTCCAAATCTCAATTTCTGGGCCCACTCTCGACATATGAGAAAGATTAAAGAC 900

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QY	901	CAGACT	906
Db	901	CAGACT	906

RESULT 4

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US-10-0-2-012-257
1 Sequence 257, Application US/10072012
2 Publication No. US20040033493A1
3 GENERAL INFORMATION:
4 APPLICANT: Tchernev, Velizar
5 APPLICANT: Spyrek, Kimberly
6 APPLICANT: Zernusen, Bryan
7 APPLICANT: Patcurajan, Meera
8 APPLICANT: Shimkets, Richard
9 APPLICANT: Li, Li
10 APPLICANT: Gangolli, Esha
11 APPLICANT: Padigaru, Muralidhara
12 APPLICANT: Anderson, David W.
13 APPLICANT: Rastelli, Luca
14 APPLICANT: Miller, Charles E.
15 APPLICANT: Gerlach, Valerie
16 APPLICANT: Taudier Jr, Raymond J.
17 APPLICANT: Guev, Vladimir Y.
18 APPLICANT: Colman, Steven D.
19 APPLICANT: Wolenc, Adam R.
20 APPLICANT: Pena, Carol E. A.
21 APPLICANT: Putrak, Katarzyna
22 APPLICANT: Grosse, William M.
23 APPLICANT: Alsbrook II, John P.
24 APPLICANT: Lepley, Denise M.
25 APPLICANT: Rieger, Daniel K.
26 APPLICANT: Burgess, Catherine E.
27 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
28 FILE REFERENCE: 21402-258
29 CURRENT APPLICATION NUMBER: US/10/072.012
30 CURRENT FILING DATE: 2002-01-31
31 PRIOR APPLICATION NUMBER: 60/265,102
32 PRIOR FILING DATE: 2001-01-30
33 PRIOR APPLICATION NUMBER: 60/265,514
34 PRIOR FILING DATE: 2001-01-31
35 PRIOR APPLICATION NUMBER: 60/265,517
36 PRIOR FILING DATE: 2001-01-31
37 PRIOR APPLICATION NUMBER: 60/265,412
38 PRIOR FILING DATE: 2001-01-31
39 PRIOR APPLICATION NUMBER: 60/265,395
40 PRIOR FILING DATE: 2001-01-31
41 PRIOR APPLICATION NUMBER: 60/266,406
42 PRIOR FILING DATE: 2001-02-02
43 PRIOR APPLICATION NUMBER: 60/266,767
44 PRIOR FILING DATE: 2001-02-05
45 PRIOR APPLICATION NUMBER: 60/267,057
46 PRIOR FILING DATE: 2001-02-07
47 PRIOR APPLICATION NUMBER: 60/266,975
48 PRIOR FILING DATE: 2001-02-07
49 PRIOR APPLICATION NUMBER: 60/267,459
50 PRIOR FILING DATE: 2001-02-08
51 Remaining Prior Application data removed - See File Wrapper or PALM.
52 NUMBER OF SEQ ID NOS: 1391
53 SOFTWARE: PatentIn Ver. 2.1
54 SEQ ID NO 257
55 LENGTH: 2071
56 TYPE: DNA
57 ORGANISM: Homo sapiens
58 IS-10-072-012-257

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Query Match	99.6%	Score 902.8,	DB 17,	Length 2071,
Best Local Similarity	99.8%	Pred. No. 3.4e-280,		
Matches 904,	Conservative	2,	Indels	0, Gaps 0,

QY	1	ATGCCCTCATGATGATTCGAACTCAATTGTTACTGAGAGTTGCTGCTGCTGCA	60

Db	61	ATGGCCCATGATGATGTGGAACTCAAAATTGTTACTGAGAGTTGGTGCTCTGCTGGAA	120
Qy	61	AGTGGAAACGGAAAAGTGGCTGTAATTGATAGCCGGCCATTGTGGAAATCAATACATCC	120
Db	121	AGTGGAAACGGAAAAGTGGCTGTAATTGATAGCCGGCCATTGTGGAAATCAATACATCC	180
Qy	121	CACATTTTGGAAAGCCATTAAATATCACTGCTCCAGCTTATGAAAGGAAGTTGAAACG	180
Db	181	CACATTTTGGAAAGCCATTAAATATCACTGCTCCAGCTTATGAAAGGAAGTTGAAACG	240
Qy	181	GACAAAGTGTAAATTAACAAGCTCATCCAGCATTCACGAAAATTAAGTTGACATTGAT	240
Db	241	GACAAAGTGTAAATTAACAAGCTCATCCAGCATTCACGAAAATTAAGTTGACATTGAT	300
Qy	241	TGCAGTCAGAAAGTTGATGTTTAACGATTCAAAGCTCCAGAAATGTTGCCCTCTCTCTTA	300
Db	301	TGCAGTCAGAAAGTTGATGTTTAACGATTCAAAGCTCCAGAAATGTTGCCCTCTCTCTTA	360
Qy	301	GACTGTTTTCTCACTGACTCTTGAGGTAACTGSAAGAGCTTCAACTCTTACCTG	360
Db	361	GACTGTTTTCTCACTGACTCTTGAGGTAACTGSAAGAGCTTCAACTCTTACCTG	420
Qy	361	CTTGCAGAGTGGGTTTGGCTGATGTTCTCGTGTGTTCCCTGGCCTCTGTGAAGAAAATCC	420
Db	421	CTTGCAGAGTGGGTTTGGCTGATGTTCTCGTGTGTTCCCTGGCCTCTGTGAAGAAAATCC	480
Qy	421	ACTCTAGTCCCACTGACATTTCTCAGCCTTCTTACCTGTTGACCAATTTGGGCCAAC	480
Db	481	ACTCTAGTCCCACTGACATTTCTCAGCCTTCTTACCTGTTGACCAATTTGGGCCAAC	540
Qy	481	CGAATTTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGAGCTGATA	540
Db	541	CGAATTTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGAGCTGATA	600
Qy	541	CAGCAGAAATGGATTTGGTTATGTTGTTAATGCAAGCTATACTGTCCAAAGCTGACATT	600
Db	601	CAGCAGAAATGGATTTGGTTATGTTGTTAATGCAAGCTATACTGTCCAAAGCTGACATT	660
Qy	601	ATCCCGAGTCTCAATTCCTGCGGTGTGCTGTGATGACAGCTTTTGTGAGAAAATTTTG	660
Db	661	ATCCCGAGTCTCAATTCCTGCGGTGTGCTGTGATGACAGCTTTTGTGAGAAAATTTTG	720
Qy	661	CGTGGTTGGACAATCACTGATGATTTTCAATGAGAAAGAAAAGCTCCAAATGATGTGTT	720
Db	721	CGTGGTTGGACAATCACTGATGATTTTCAATGAGAAAGAAAAGCTCCAAATGATGTGTT	780
Qy	721	CTAAGTGACTGTTTAGCTGGAGATCTCCGCGCTCGCGACACATCGCTATCGCTACATG	780
Db	781	CTAAGTGACTGTTTAGCTGGAGATCTCCGCGCTCGCGACACATCGCTATCGCTACATG	840
Qy	781	AAGAGGATGACATGCTCTTATGATGAAGCTTACAGATTTGTGAAAAGAAAAGCTTACT	840
Db	841	AAGAGGATGACATGCTCTTATGATGAAGCTTACAGATTTGTGAAAAGAAAAGCTTACT	900
Qy	841	ATATCTCCAAACTCAATTTTCTGGGCGCAACTCTGACATATGAGAGGAATTAAGAAC	900
Db	901	ATATCTCCAAACTCAATTTTCTGGGCGCAACTCTGACATATGAGAGGAATTAAGAAC	960
Qy	901	CAGACT 906	
Db	961	CAGACT 966	

RESULT 5

US-10-168-506-2
Sequence 2, Application US/10168506
Publication No. US20040053229A1
GENERAL INFORMATION:
APPLICANT: PLOMAN, GREGORY D.
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WYTHE, DAVID
APPLICANT: MANNING, GERRARD
APPLICANT: SUDASANAM, SUCHA

APPLICANT: HILL, RON
APPLICANT: FLANAGAN, PETER
TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
FILE REFERENCE: 038602/1351
CURRENT APPLICATION NUMBER: US/10/168,506
CURRENT FILING DATE: 2002-06-21
PRIORITY APPLICATION NUMBER: PCT/US00/34736
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 2732
TYPE: DNA
ORGANISM: Homo sapiens
US-10-168-506-2

Query Match 99.6%; Score 902.8; DB 17; Length 2732;
Best Local Similarity 99.8%; Pred. No. 4.1e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGCCCATGAGATGATTTGAACCTCAATTGTTACTGAGAGGTTGGTGGCTGTGCGAA 60
538 ATGGCCCATGAGATGATTTGAACCTCAATTGTTACTGAGAGGTTGGTGGCTGTGCGAA 597
61 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGCGCATTTGTGGAATACATATCACC 120
598 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGCGCATTTGTGGAATACATATCACC 657
121 CACATTTTGAAGCCATTATATCACTGCTCCAAAGCTTTATGAGCGAAGTTGCAACAG 180
658 CACATTTTGAAGCCATTATATCACTGCTCCAAAGCTTTATGAGCGAAGTTGCAACAG 717
181 GACAAAGTTAATTATGAGAGCTCATCCAGATTCAGGGAACATTAAGTTGACATTGAT 240
718 GACAAAGTTAATTATGAGAGCTCATCCAGATTCAGGGAACATTAAGTTGACATTGAT 777
241 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
778 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 837
301 GACTGTTTCTCACTGATCTTCTGGGTAACCTGGAAGAGCTTCACTGTTCACTG 360
838 GACTGTTTCTCACTGATCTTCTGGGTAACCTGGAAGAGCTTCACTGTTCACTG 897
361 CTTCGAGTGGGTTTGTGCTGATTTCTCTGTTGTTCCCTGGCCCTGTGGAAGAAATCC 420
898 CTTCGAGTGGGTTTGTGCTGATTTCTCTGTTGTTCCCTGGCCCTGTGGAAGAAATCC 957
421 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTTGGGCCAAC 480
958 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTTGGGCCAAC 1017
481 CGAATTTCTTCCCAATCTTTATCTTGGCTGCCAGGAGATGTCCTCAACAGAGCTGATA 540
1018 CGAATTTCTTCCCAATCTTTATCTTGGCTGCCAGGAGATGTCCTCAACAGAGCTGATA 1077
541 CAGAGAAATGGGATTTGTTAGTGTAAATGCCAGCTATACCTGTCCAAAGCTTACCTT 600
1078 CAGAGAAATGGGATTTGTTAGTGTAAATGCCAGCTATACCTGTCCAAAGCTTACCTT 1137
601 ATCCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
1138 ATCCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
661 CCGTGTGTGAACAATCAGTATGATTTCAATGAAAGCAAAAGCTTCAATGATGTGT 720
1198 CCGTGTGTGAACAATCAGTATGATTTCAATGAAAGCAAAAGCTTCAATGATGTGT 1257
721 CTAATGCACTGTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
1258 CTAATGCACTGTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
781 AAGAGATGATGATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

1318 AAGAGATGATGATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
841 ATATCTCCAACTCAATTTTCTGGGCGCACTCCGAGCTATGAGAGATTAAGAAC 900
1378 ATATCTCCAACTCAATTTTCTGGGCGCACTCCGAGCTATGAGAGATTAAGAAC 1437
901 CAGACT 906
1438 CAGACT 1443

RESULT 6
US-10-257-026-1
Sequence 1, Application US/10257026
Publication No. US2004008659A1

GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
TITLE OF INVENTION: New dual specificity phosphatase
FILE REFERENCE: DUSP10XDS
CURRENT APPLICATION NUMBER: US/10/257,026
CURRENT FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 3059
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (127)..(2121)
US-10-257-026-1

Query Match 99.6%; Score 902.8; DB 17; Length 3059;
Best Local Similarity 99.8%; Pred. No. 4.3e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGCCCATGAGATGATTTGAACCTCAATTGTTACTGAGAGGTTGGTGGCTGTGCGAA 60
127 ATGGCCCATGAGATGATTTGAACCTCAATTGTTACTGAGAGGTTGGTGGCTGTGCGAA 186
61 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGCGCATTTGTGGAATACATATCACC 120
187 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGCGCATTTGTGGAATACATATCACC 246
121 CACATTTTGAAGCCATTATATCACTGCTCCAAAGCTTTATGAGCGAAGTTGCAACAG 180
247 CACATTTTGAAGCCATTATATCACTGCTCCAAAGCTTTATGAGCGAAGTTGCAACAG 306
181 GACAAAGTTAATTATGAGAGCTCATCCAGATTCAGGGAACATTAAGTTGACATTGAT 240
307 GACAAAGTTAATTATGAGAGCTCATCCAGATTCAGGGAACATTAAGTTGACATTGAT 366
241 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
367 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 426
301 GACTGTTTCTCACTGATCTTCTGGGTAACCTGGAAGAGCTTCACTGTTCACTG 360
427 GACTGTTTCTCACTGATCTTCTGGGTAACCTGGAAGAGAGCTTCACTGTTCACTG 486
361 CTTCGAGTGGGTTTGTGCTGATTTCTCTGTTGTTCCCTGGCCCTGTGGAAGAAATCC 420
487 CTTCGAGTGGGTTTGTGCTGATTTCTCTGTTGTTCCCTGGCCCTGTGGAAGAAATCC 546
421 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTTGGGCCAAC 480
547 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTTGGGCCAAC 606
481 CGAATTTCTTCCCAATCTTTATCTTGGCTGCCAGGAGATGTCCTCAACAGAGCTGATA 540
607 CGAATTTCTTCCCAATCTTTATCTTGGCTGCCAGGAGATGTCCTCAACAGAGCTGATA 666

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QY 541 CAGCAGATGGGATGGTATGTTAAATGCCAGTATACCTGTCCAAAGCCGACTTT 600
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|
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Db 667 CAGCAGATGGGATGGTATGTTAAATGCCAGCATACTGTCCAAAGCCGACTTT 726
|
|
|
QY 601 ATCCCGAGTCTCATTTCTGCGCTGCTGTGATGACAGCTTTGTGAAAAATTTTG 660
|
|
|
Db 727 ATCCCGAGTCTCATTTCTGCGCTGCTGTGATGACAGCTTTGTGAAAAATTTTG 786
|
|
|
QY 661 CCGTGTGGCAAAATCAGATGATTTATGAGAAAGCAAAAGCTCCCAATGGAATGTT 720
|
|
|
Db 787 CCGTGTGGCAAAATCAGATGATTTATGAGAAAGCAAAAGCTCCCAATGGAATGTT 846
|
|
|
QY 721 CTAGTGCATGTTTAACTGGGATCTCCGCTCCGCCAACATGCTATCGCTACATCATG 780
|
|
|
Db 847 CTAGTGCATGTTTAACTGGGATCTCCGCTCCGCCAACATGCTATCGCTACATCATG 906
|
|
|
QY 781 AAGAGATGAGCATGCTTTAGATGAGCTTACAGATTTGTGAAAAAGAAAGCTTACT 840
|
|
|
Db 907 AAGAGATGAGCATGCTTTAGATGAGCTTACAGATTTGTGAAAAAGAAAGCTTACT 966
|
|
|
QY 841 ATATCTCCAAACTTCATTTTCTGGGCCAACTCTGCACTATGAGAAAGATTTAAGAC 900
|
|
|
Db 967 ATATCTCCAAACTTCATTTTCTGGGCCAACTCTGCACTATGAGAAAGATTTAAGAC 1026
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|
QY 901 CAGACT 906
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Db 1027 CAGACT 1032
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RESULT 7

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US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1
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Query Match 99.6%; Score 902.8; DB 9; Length 3496;

Best Local Similarity 99.8%; Pred. No. 4,7e-280;

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Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCATGAGATGATGAACTCAATTGTTACTGAGAGTTGGTCTGTCTGAA 60
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|
|
Db 562 ATGGCCATGAGATGATGAACTCAATTGTTACTGAGAGTTGGTCTGTCTGAA 621
|
|
|
QY 61 AGTGAAGGAAAAAGTCTGCTAATTGATAGCCGCCATTGTGGAATACATACATCC 120
|
|
|
Db 622 AGTGAAGGAAAAAGTCTGCTAATTGATAGCCGCCATTGTGGAATACATACATCC 681
|
|
|
QY 121 CACATTTTGAAGCATTATATCAACGCTCCAAAGCTTAAGAACGGAAGTTGCAACAG 180
|
|
|
Db 682 CACATTTTGAAGCATTATATCAACGCTCCAAAGCTTAAGAACGGAAGTTGCAACAG 741
|
|
|
QY 181 GACAAAGTGTATTAACAGAGCTCATCCAGCATTCAGGAAACATAAGTTGACATTGAT 240
|
|
|
Db 742 GACAAAGTGTATTAACAGAGCTCATCCAGCATTCAGGAAACATAAGTTGACATTGAT 801
|
|
|
QY 241 TGCAGTCAGAGGTTTGAATGTTAAGATCAAGGCTCCAGAGTTGCTCTCTCTTCA 300
|
|
|
Db 802 TGCAGTCAGAGGTTTGAATGTTAAGATCAAGGCTCCAGAGTTGCTCTCTCTTCA 861
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|
|
QY 301 GACTGTTTCTCACTGTACTTCTGGGTAACTGGAAGAGCTTCAACTGTCTCACTG 360
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Db 862 GACTGTTTCTCACTGTACTTCTGGGTAACTGGAAGAGCTTCAACTGTCTCACTG 921
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|
QY 361 CTTCGAGGTTGGTTTGTGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAGAGAAATCC 420
|
|
|
Db 922 CTTCGAGGTTGGTTTGTGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAGAGAAATCC 981
|
|
|
QY 421 ACTTAATGCTTACTGATTTTCTCAGCTTGTCTTACTCTGTGCAACATTGGGCCAAC 480
|
|
|
Db 982 ACTTAATGCTTACTGATTTTCTCAGCTTGTCTTACTCTGTGCAACATTGGGCCAAC 1041
|
|
|
QY 481 CGAATTCCTCCCAATCTTTATCTTGGCTGCGCAGCGAGATGCTCCAAAGAGCTGATA 540
|
|
|
Db 1042 CGAATTCCTCCCAATCTTTATCTTGGCTGCGCAGCGAGATGCTCCAAAGAGCTGATA 1101
|
|
|
QY 541 CAGCAGATGGGATGGTATGTTAAATGCCAGTATACCTGTCCAAAGCCGACTTT 600
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|
|
Db 1102 CAGCAGATGGGATGGTATGTTAAATGCCAGCATACTGTCCAAAGCCGACTTT 1161
|
|
|
QY 601 ATCCCGAGTCTCATTTCTGCGCTGCTGTGATGACAGCTTTGTGAAAAATTTTG 660
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|
|
Db 1162 ATCCCGAGTCTCATTTCTGCGCTGCTGTGATGACAGCTTTGTGAAAAATTTTG 1221
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|
|
QY 661 CCGTGTGGCAAAATCAGATGATTTATGAGAAAGCAAAAGCTCCCAATGGAATGTT 720
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|
Db 1222 CCGTGTGGCAAAATCAGATGATTTATGAGAAAGCAAAAGCTCCCAATGGAATGTT 1281
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|
QY 721 CTAGTGCATGTTTAACTGGGATCTCCGCTCCGCCAACATGCTATCGCTACATCATG 780
|
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|
Db 1282 CTAGTGCATGTTTAACTGGGATCTCCGCTCCGCCAACATGCTATCGCTACATCATG 1341
|
|
|
QY 781 AAGAGATGAGCATGCTTTAGATGAGCTTACAGATTTGTGAAAAAGAAAGCTTACT 840
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|
Db 1342 AAGAGATGAGCATGCTTTAGATGAGCTTACAGATTTGTGAAAAAGAAAGCTTACT 1401
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|
|
QY 841 ATATCTCCAAACTTCATTTTCTGGGCCAACTCTGCACTATGAGAAAGATTTAAGAC 900
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|
Db 1402 ATATCTCCAAACTTCATTTTCTGGGCCAACTCTGCACTATGAGAAAGATTTAAGAC 1461
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|
QY 901 CAGACT 906
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Db 1462 CAGACT 1467
|
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RESULT 8

US-10-370-715B-261

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; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
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; APPLICANT: Bodary, Sarah C.
; APPLICANT: Clark, Hillary
; APPLICANT: BRISBELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 261
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-261
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Query Match 99.6%; Score 902.8; DB 18; Length 3521;

Best Local Similarity 99.8%; Pred. No. 4,7e-280;

Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAATCAATTTGTACTGAGAGTTGGTCTCTGCTGGA 60
Db 564 ATGGCCCATGAGATGATGGAATCAATTTGTACTGAGAGTTGGTCTCTGCTGGA 623
QY 61 AGTGAACGGAAAAAGTCTCTAATTTGATGACCGCCCATTTTGTGAATACATATCC 120
Db 624 AGTGAACGGAAAAAGTCTCTAATTTGATGACCGCCCATTTTGTGAATACATATCC 683
QY 121 CACATTTTGGAAAGCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAAGTTGGAACAG 180
Db 684 CACATTTTGGAAAGCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAAGTTGGAACAG 743
QY 181 GACAAAGTTAATTTACAGAGCTCATCCAGATTCAAGGAAACATPAAGTTGACATTGAT 240
Db 744 GACAAAGTTAATTTACAGAGCTCATCCAGATTCAAGGAAACATPAAGTTGACATTGAT 803
QY 241 TGCAGTCGAAAGTTGATGATTAAGATCAAAAGCTCCAAAGTGTTCCTCTCTCTCA 300
Db 804 TGCAGTCGAAAGTTGATGATTAAGATCAAAAGCTCCAAAGTGTTCCTCTCTCTCA 863
QY 301 GACTGTTTCTCACTGTAATCTTGTGGTAACTGGAAGAAAGCTTCAATCTGTTCACCTG 360
Db 864 GACTGTTTCTCACTGTAATCTTGTGGTAACTGGAAGAAAGCTTCAATCTGTTCACCTG 923
QY 361 CTTCAGAGTGGGTTTGTGAGTCTCTGCTGTTTCCCTGGCTCTGTGAAGAAATCC 420
Db 924 CTTCAGAGTGGGTTTGTGAGTCTCTGCTGTTTCCCTGGCTCTGTGAAGAAATCC 983
QY 421 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTGGCAACATTTGGCCAAAC 480
Db 984 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTGGCAACATTTGGCCAAAC 1043
QY 481 CGAATTTCTTCCCAATCTTTATCTTGGCTGCGAGGAGATGCTTCAACAGAGCTGATA 540
Db 1044 CGAATTTCTTCCCAATCTTTATCTTGGCTGCGAGGAGATGCTTCAACAGAGCTGATA 1103
QY 541 CAGAGAAATGGGATTTGTTATGTTAAATGCGAGCTATACCTGTCCAAAGCTGACTT 600
Db 1104 CAGAGAAATGGGATTTGTTATGTTAAATGCGAGCTATACCTGTCCAAAGCTGACTT 1163
QY 601 ATCCCGAGTCTCAATTTCTGCTGCTGCTGCTGTAATGACAGCTTTTGTGAAGAAATTTTG 660
Db 1164 ATCCCGAGTCTCAATTTCTGCTGCTGCTGCTGTAATGACAGCTTTTGTGAAGAAATTTTG 1223
QY 661 CCGTGTGGACAATCAATCAATGATTTCAATGAGAAAGCAAAAGCTTCCATGATGTGT 720
Db 1224 CCGTGTGGACAATCAATCAATGATTTCAATGAGAAAGCAAAAGCTTCCATGATGTGT 1283
QY 721 CTAGTGAATGTTAGTGGGATCTCCCGCTCCGCAACATGCTATGAGCTTACATCATG 780
Db 1284 CTAGTGAATGTTAGTGGGATCTCCCGCTCCGCAACATGCTATGAGCTTACATCATG 1343
QY 781 AAGAGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAGAAAGAAAGACTTACT 840
Db 1344 AAGAGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAGAAAGAAAGACTTACT 1403
QY 841 ATATCTCCAAATTTCTGAGGCAACTCTCTGACATATGAGAAAGATTTAAGAAC 900
Db 1404 ATATCTCCAAATTTCTGAGGCAACTCTCTGACATATGAGAAAGATTTAAGAAC 1463
QY 901 CAGACT 906
Db 1464 CAGACT 1469

RESULT 9
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY

; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2583)
US-09-816-494-1

Query Match 99.6%; Score 902.8; DB 9; Length 3544;
Best Local Similarity 99.8%; Pred. No. 4.7e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAATCAATTTGTACTGAGAGTTGGTCTCTGCTGGA 60
Db 589 ATGGCCCATGAGATGATGGAATCAATTTGTACTGAGAGTTGGTCTCTGCTGGA 648
QY 61 AGTGAACGGAAAAAGTCTCTAATTTGATGACCGCCCATTTTGTGAATACATATCC 120
Db 649 AGTGAACGGAAAAAGTCTCTAATTTGATGACCGCCCATTTTGTGAATACATATCC 708
QY 121 CACATTTTGGAAAGCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAAGTTGGAACAG 180
Db 709 CACATTTTGGAAAGCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAAGTTGGAACAG 768
QY 181 GACAAAGTTAATTTACAGAGCTCATCCAGATTCAAGGAAACATPAAGTTGACATTGAT 240
Db 769 GACAAAGTTAATTTACAGAGCTCATCCAGATTCAAGGAAACATPAAGTTGACATTGAT 828
QY 241 TGCAGTCGAAAGTTGATGATTAAGATCAAAAGCTCCAAAGTGTTCCTCTCTCTCA 300
Db 829 TGCAGTCGAAAGTTGATGATTAAGATCAAAAGCTCCAAAGTGTTCCTCTCTCTCA 888
QY 301 GACTGTTTCTCACTGTAATCTTGTGGTAACTGGAAGAAAGCTTCAATCTGTTCACCTG 360
Db 889 GACTGTTTCTCACTGTAATCTTGTGGTAACTGGAAGAAAGCTTCAATCTGTTCACCTG 948
QY 361 CTTCAGAGTGGGTTTGTGAGTCTCTGCTGTTTCCCTGGCTCTGTGAAGAAATCC 420
Db 949 CTTCAGAGTGGGTTTGTGAGTCTCTGCTGTTTCCCTGGCTCTGTGAAGAAATCC 1008
QY 421 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTGGCAACATTTGGCCAAAC 480
Db 1009 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTGGCAACATTTGGCCAAAC 1068
QY 481 CGAATTTCTTCCCAATCTTTATCTTGGCTGCGAGGAGATGCTTCAACAGAGCTGATA 540
Db 1069 CGAATTTCTTCCCAATCTTTATCTTGGCTGCGAGGAGATGCTTCAACAGAGCTGATA 1128
QY 541 CAGAGAAATGGGATTTGTTATGTTAAATGCGAGCTATACCTGTCCAAAGCTGACTT 600
Db 1129 CAGAGAAATGGGATTTGTTATGTTAAATGCGAGCTATACCTGTCCAAAGCTGACTT 1188
QY 601 ATCCCGAGTCTCAATTTCTGCTGCTGCTGCTGTAATGACAGCTTTTGTGAAGAAATTTTG 660
Db 1189 ATCCCGAGTCTCAATTTCTGCTGCTGCTGCTGTAATGACAGCTTTTGTGAAGAAATTTTG 1248
QY 661 CCGTGTGGACAATCAATCAATGATTTCAATGAGAAAGCAAAAGCTTCCATGATGTGT 720
Db 1249 CCGTGTGGACAATCAATCAATGATTTCAATGAGAAAGCAAAAGCTTCCATGATGTGT 1308
QY 721 CTAGTGAATGTTAGTGGGATCTCCCGCTCCGCAACATGCTATGAGCTTACATCATG 780
Db 1309 CTAGTGAATGTTAGTGGGATCTCCCGCTCCGCAACATGCTATGAGCTTACATCATG 1368

QY 781 AAGAGATGACATGCTTTAGATGAGCTTACATGTTGTGAAGAAAAAGACCTACT 840
Db 1369 AAGGAGATGACATGCTTTAGATGAGCTTACATGTTGTGAAGAAAAAGACCTACT 1428
QY 841 ATATCTCCAAACTTCAATTTTCTGGGCAACTCTCTGACTATGAGAAGATTAAAGAC 900
Db 1429 ATATCTCCAAACTTCAATTTTCTGGGCAACTCTCTGACTATGAGAAGATTAAAGAC 1488
QY 901 CAGACT 906
Db 1489 CAGACT 1494

RESULT 10
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Teal, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MP103-0180NM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895, 860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Query Match 99.6%; Score 902.8; DB 17; Length 3544;
Best Local Similarity 99.8%; Pred. No. 4,76-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCCCCATGATGATTTGCAACTCAATTTTATCTGAGAGCTTGAGCTTGCTGGAA 60
Db 589 ATGCCCCATGATGATTTGCAACTCAATTTTATCTGAGAGCTTGAGCTTGCTGGAA 648

QY 61 AGTGAACGGAAAAAGTCTGTCTAATTGATAGCCGGCACTTTTGGAAATACATATCCTC 120
Db 649 AGTGAACGGAAAAAGTCTGTCTAATTGATAGCCGGCACTTTTGGAAATACATATCCTC 708
QY 121 CACATTTTGGAAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAAGCGAAGTTGCAACAG 180
Db 709 CACATTTTGGAAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAAGCGAAGTTGCAACAG 768
QY 181 GACAAAGTTTAATTACAGAGCTCATCCAGATTTCAGGAAACAATAAGTTGACATTGAT 240
Db 769 GACAAAGTTTAATTACAGAGCTCATCCAGATTTCAGGAAACAATAAGTTGACATTGAT 828
QY 241 TGCAAGTCAGAAAGTTTGAAGTTTAAAGTCAAGCTCCCAAGATTTGGCTCTCTCTTCA 300
Db 829 TGCAAGTCAGAAAGTTTGAAGTTTAAAGTCAAGCTCCCAAGATTTGGCTCTCTCTTCA 888
QY 301 GACTGTTTCTCACTGATCTTCTGGTAAACTGGAAGAAGCTTCAACTCTGTTCACTG 360
Db 889 GACTGTTTCTCACTGATCTTCTGGTAAACTGGAAGAAGCTTCAACTCTGTTCACTG 948
QY 361 CTTCGAGGTGGGTTTCTGAGTTCTCTGTTGTTTCCCTGAGCTCTGTAAGAAAAATCC 420
Db 949 CTTCGAGGTGGGTTTCTGAGTTCTCTGTTGTTTCCCTGAGCTCTGTAAGAAAAATCC 1008
QY 421 ACTCTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTGCAACATTTGGGCCAAC 480
Db 1009 ACTCTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTGCAACATTTGGGCCAAC 1068
QY 481 CGAATTTTCCCAATCTTATCTTGGCTGCGAGAGATGCTTCAACAAGAGCTGATA 540
Db 1069 CGAATTTTCCCAATCTTATCTTGGCTGCGAGAGATGCTTCAACAAGAGCTGATA 1128
QY 541 CAGCAGATGGGATGGTTATGTTTAAATCCAGCTATACCTGTCCAAAGCTGACTT 600
Db 1129 CAGCAGATGGGATGGTTATGTTTAAATCCAGAGTAACCTGTCCAAAGCTGACTT 1188
QY 601 ATCCCCGAGTCTCATTTTCTGCTGCTGCTGCTGATGACAGCTTTGTGGAATAATTTTG 660
Db 1189 ATCCCCGAGTCTCATTTTCTGCTGCTGCTGCTGATGACAGCTTTGTGGAATAATTTTG 1248
QY 661 CCGTGTGGACAATATCATGATTTTCAATTGAGAAAGCAAAAGCTTCAATGATGTGT 720
Db 1249 CCGTGTGGACAATATCATGATTTTCAATTGAGAAAGCAAAAGCTTCAATGATGTGT 1308
QY 721 CTAGTGACGTGTAGCTGGGATCTCCGCTCGGCAACATGCTATCCGCTTACATCATG 780
Db 1309 CTAGTGACGTGTAGCTGGGATCTCCGCTCGGCAACATGCTATCCGCTTACATCATG 1368
QY 781 AAGAGATGACATGCTTTAGATGAGCTTACAGATTTGTGAAGAAAAAGACCTACT 840
Db 1369 AAGAGATGACATGCTTTAGATGAGCTTACAGATTTGTGAAGAAAAAGACCTACT 1428
QY 841 ATATCTCCAAACTTCAATTTTCTGGGCAACTCTCTGACTATGAGAAGATTAAAGAC 900
Db 1429 ATATCTCCAAACTTCAATTTTCTGGGCAACTCTCTGACTATGAGAAGATTAAAGAC 1488
QY 901 CAGACT 906
Db 1489 CAGACT 1494

RESULT 11
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.


```

APPLICANT: Chun, Myoung
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: MP103-0180NM1H
CURRENT APPLICATION NUMBER: US/10/377,072
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589)...(2586)
US-10-377-072-25

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Query Match 99.6%; Score 902.8; DB 18; Length 3544;
Best Local Similarity 99.8%; Pred. No. 4.7e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAACCAATTTGTAAGAGAGTGTGCTGCTGGA 60
DB 589 ATGGCCCATGAGATGATGGAACCAATTTGTAAGAGAGTGTGCTGCTGGA 648
QY 61 AGTGAACGAAAAAGTCTGCTAATTTGATAGCCGCGCATTTTGGAAATACATATCC 120
DB 649 AGTGAACGAAAAAGTCTGCTAATTTGATAGCCGCGCATTTTGGAAATACATATCC 708
QY 121 CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAAAGGTTGCAACG 180
DB 709 CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAAAGGTTGCAACG 768
QY 181 GACAAAGTTAATTAACAGACTCATCCAGCATTCAGGAAACATTAAGTGAATAT 240
DB 769 GACAAAGTTAATTAACAGACTCATCCAGCATTCAGGAAACATTAAGTGAATAT 828
QY 241 TGCAGTCGAGAGTTGATGATTAAGCAAGCTCCCAAGATGTTGCTCTCTCTCA 300
DB 829 TGCAGTCGAGAGTTGATGATTAAGCAAGCTCCCAAGATGTTGCTCTCTCTCA 888
QY 301 GACTGTTTCTCACTGATCTTCTGGGTAACGTGAAAGACCTTCAACTCTGTTCACTG 360
DB 889 GACTGTTTCTCACTGATCTTCTGGGTAACGTGAAAGACCTTCAACTCTGTTCACTG 948
QY 361 CTTCGAGGTGGGTTGCTGAGATCTCTGCTGTTTCCCTGCGCTCTGGAAGAAATCC 420
DB 949 CTTCGAGGTGGGTTGCTGAGATCTCTGCTGTTTCCCTGCGCTCTGGAAGAAATCC 1008
QY 421 ACTCTAGTCCTACCTGATTTCTAGGCTTGCTTACTGTTGCCAATTTGGGCAATCC 480

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DB 1009 ACTCTAGTCCTACCTGATTTCTAGGCTTGCTTACTGTTGCCAATTTGGGCAATCC 1068
QY 481 CGAATCTTCCCAATCTTATCTTGGCGGCAAGAGATGCTCAACAAGAGCTGATA 540
DB 1069 CGAATCTTCCCAATCTTATCTTGGCGGCAAGAGATGCTCAACAAGAGCTGATA 1128
QY 541 CAGCAGAAATGGATGTTATGTTAATGCAAGCTATACCTGTCCAAGCTGACTTT 600
DB 1129 CAGCAGAAATGGATGTTATGTTAATGCAAGCTATACCTGTCCAAGCTGACTTT 1188
QY 601 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGAGAAATTTTG 660
DB 1189 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGAGAAATTTTG 1248
QY 661 CCGTGTGGAACAATCACTGATTTCAATGAGAAAGAAAGCCTCCAAATGAGATGT 720
DB 1249 CCGTGTGGAACAATCACTGATTTCAATGAGAAAGAAAGCCTCCAAATGAGATGT 1308
QY 721 CTAGTCAGCTGTTTATGCTGGGATCTCCGCTCCGCAACATGCTATGCTCATCATG 780
DB 1309 CTAGTCAGCTGTTTATGCTGGGATCTCCGCTCCGCAACATGCTATGCTCATCATG 1368
QY 781 AAGAGATGACATGCTTTAGATGAACTTACAGATTTTGAAAGAAAGAAAGCTACT 840
DB 1369 AAGAGATGACATGCTTTAGATGAACTTACAGATTTTGAAAGAAAGAAAGCTACT 1428
QY 841 ATATCTCCAACTCAATTTTCTGGGCAACTCTCCGCACTATGAGAAAGATTAAGAC 900
DB 1429 ATATCTCCAACTCAATTTTCTGGGCAACTCTCCGCACTATGAGAAAGATTAAGAC 1488
QY 901 CAGACT 906
DB 1489 CAGACT 1494

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RESULT 12
US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

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Query Match 99.6%; Score 902.8; DB 17; Length 3625;
Best Local Similarity 99.8%; Pred. No. 4.8e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAACCAATTTGTAAGAGAGTGTGCTGCTGGA 60
DB 692 ATGGCCCATGAGATGATGGAACCAATTTGTAAGAGAGTGTGCTGCTGGA 751
QY 61 AGTGAACGAAAAAGTCTGCTAATTTGATAGCCGCGCATTTTGGAAATACATATCC 120
DB 752 AGTGAACGAAAAAGTCTGCTAATTTGATAGCCGCGCATTTTGGAAATACATATCC 811

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QY 121 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCGAAGTTGCAACG 180
Db 812 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCGAAGTTGCAACG 871
QY 181 GACAAATGTTAATTAAGAGCTCATCAGCATTCAGCGAACAATAAGTTGACATTGAT 240
Db 872 GACAAATGTTAATTAAGAGCTCATCAGCATTCAGCGAACAATAAGTTGACATTGAT 931
QY 241 TGCAGTCAGAAAGTTAGTTTACGATCAAAAGCTCCAGATGTTGTCCTCTCTCTCA 300
Db 932 TGCAGTCAGAAAGTTAGTTTACGATCAAAAGCTCCAGATGTTGTCCTCTCTCTCA 991
QY 301 GACTGTTTCTCATCTGACTCTTGCGGTAACTGAGAAAGCTTCAACTCTGTTCACTG 360
Db 992 GACTGTTTCTCATCTGACTCTTGCGGTAACTGAGAAAGCTTCAACTCTGTTCACTG 1051
QY 361 CTGCAAGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCGCGCTCTGTGAAGAAATTC 420
Db 1052 CTGCAAGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCGCGCTCTGTGAAGAAATTC 1111
QY 421 ACTTAGTCCCTAAGCTGATTTCTCAGCTTGTCTTACTGTTGCCAAATGGGCGCAAC 480
Db 1112 ACTTAGTCCCTAAGCTGATTTCTCAGCTTGTCTTACTGTTGCCAAATGGGCGCAAC 1171
QY 481 CGAATTTCTCCCAATCTTTATCTTGCGCTGCGCAGCGAGATGTCCTCAACAGAGCTGATA 540
Db 1172 CGAATTTCTCCCAATCTTTATCTTGCGCTGCGCAGCGAGATGTCCTCAACAGAGCTGATA 1231
QY 541 CAGCAGAAATGGGATTGTTATGTTAATGCAAGTATACCTGTCCAAAGCTGACTT 600
Db 1232 CAGCAGAAATGGGATTGTTATGTTAATGCAAGTATACCTGTCCAAAGCTGACTT 1291
QY 601 ATCCCGAGTCTCATTTCTGCGGTGCTGCTGGAATGACAGCTTTTGTGAAGAAATTTTG 660
Db 1292 ATCCCGAGTCTCATTTCTGCGGTGCTGCTGGAATGACAGCTTTTGTGAAGAAATTTTG 1351
QY 661 CGTGGTTGGAACAATCACTAGATTTTCACTGAGAAAGCAAAAGCTCCAAATGATGTGT 720
Db 1352 CGTGGTTGGAACAATCACTAGATTTTCACTGAGAAAGCAAAAGCTCCAAATGATGTGT 1411
QY 721 CTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCGCACCATGCTATGCGCTCACTCATG 780
Db 1412 CTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCGCACCATGCTATGCGCTCACTCATG 1471
QY 781 AAGAGATGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTTACT 840
Db 1472 AAGAGATGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTTACT 1531
QY 841 ATATCTCCAAATCTCAATTTTCTGGGCGCACTCCGCGACTATGAGAAAGATTTAAGAAC 900
Db 1532 ATATCTCCAAATCTCAATTTTCTGGGCGCACTCCGCGACTATGAGAAAGATTTAAGAAC 951
QY 901 CAGACT 906
Db 1592 CAGACT 1597

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RESULT 13
US-10-343-357-17
; Sequence 17, Application US/10343357
; Publication No. US20040058341A1

GENERAL INFORMATION:

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; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. TOM
; APPLICANT: ELIOTT, Vicki S.; RAMKUMAR, Jayalakmi
; APPLICANT: YAO, Monique G.; BUREFORD, Neil
; APPLICANT: WANG, Yumei B.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; TRIBOULEY, April J.A.
; APPLICANT: LU, Dying Aina M.; TRIBOULEY, Catherine M.
; APPLICANT: GRIFPIN, Jennifer A.; BAUGHN, Mariah R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Daniel B.; CHAWLA, Nandinder K.
; APPLICANT: KEARNEY, Liam

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; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: PERL Program
; SEQ ID NO: 17
; LENGTH: 3766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CB1
US-10-343-357-17

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Query Match 99.6%; Score 902.8; DB 17; Length 3766;
Best Local Similarity 99.8%; Pred. No. 4.9e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGCCCATGATGATGATGGAACCTCAATTTGTTATCGAAGGTTGGCTGCTGGAA 60
Db 538 ATGCCCATGATGATGATGGAACCTCAATTTGTTATCGAAGGTTGGCTGCTGGAA 597
QY 61 AGTGAACGAAAAAGTGTCTAATGATAGCCGCGCATTTGTGAATCAATATC 120
Db 598 AGTGAACGAAAAAGTGTCTAATGATAGCCGCGCATTTGTGAATCAATATC 657
QY 121 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCAAGTTGCAACG 180
Db 658 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCAAGTTGCAACG 717
QY 181 GACAAATGTTAATTAAGAGCTCATCAGCTTACCGAGAAACATAAGTTGACATTGAT 240
Db 718 GACAAATGTTAATTAAGAGCTCATCAGCTTACCGAGAAACATAAGTTGACATTGAT 777
QY 241 TGCAGTCAGAAAGTTAGTTTACGATCAAAAGCTCCAGATGTTGCTCTCTCTCA 300
Db 778 TGCAGTCAGAAAGTTAGTTTACGATCAAAAGCTCCAGATGTTGCTCTCTCTCA 837
QY 301 GACTGTTTCTCATCTGACTCTTGCGGTAACTGAGAAAGCTTCAACTCTGTTCACTG 360
Db 838 GACTGTTTCTCATCTGACTCTTGCGGTAACTGAGAAAGCTTCAACTCTGTTCACTG 897
QY 361 CTGCAAGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCGCGCTCTGTGAAGAAATTC 420
Db 898 CTGCAAGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCGCGCTCTGTGAAGAAATTC 957
QY 421 ACTTAGTCCCTAAGCTGATTTCTCAGCTTGTCTTACTGTTGCCAAATGGGCGCAAC 480
Db 958 ACTTAGTCCCTAAGCTGATTTCTCAGCTTGTCTTACTGTTGCCAAATGGGCGCAAC 1017
QY 481 CGAATTTCTCCCAATCTTTATCTTGCGCTGCGCAGCGAGATGTCCTCAACAGAGCTGATA 540
Db 1018 CGAATTTCTCCCAATCTTTATCTTGCGCTGCGCAGCGAGATGTCCTCAACAGAGCTGATA 1077
QY 541 CAGCAGAAATGGGATTGTTATGTTAATGCAAGTATACCTGTCCAAAGCTGACTT 600
Db 1078 CAGCAGAAATGGGATTGTTATGTTAATGCAAGTATACCTGTCCAAAGCTGACTT 1137

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Qy 601 ATCCCCGAGTCTCATTTCTGCGTGTGCGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660
Db 1138 ATCCCCGAGTCTCATTTCTGCGTGTGCGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 1197
Qy 661 CCGTGGTTGACAAATCGATGATTTTCATTTGAGAAAGCAAAAGCTTCCAAATGAGATGTT 720
Db 1198 CCGTGGTTGACAAATCGATGATTTTCATTTGAGAAAGCAAAAGCTTCCAAATGAGATGTT 1257
Qy 721 CTAGTGCATGTTTGTAGTGGATCTCCGCGTCCGCGACCATGCTATGCGCTACATCANG 780
Db 1258 CTAGTGCATGTTTGTAGTGGATCTCCGCGTCCGCGACCATGCTATGCGCTACATCANG 1317
Qy 781 AAGAGATGACATGCTTTTGTAGTGAATGACATTTGTGAGAAAGCAAAAGCTTACT 840
Db 1318 AAGAGATGACATGCTTTTGTAGTGAATGACATTTGTGAGAAAGCAAAAGCTTACT 1377
Qy 841 ATATCTCCAAATCTCAATTTTCTGGGCCAATCTCTGACATATGAGAAAGATTAAAGAC 900
Db 1378 ATATCTCCAAATCTCAATTTTCTGGGCCAATCTCTGACATATGAGAAAGATTAAAGAC 1437
Qy 901 CAGACT 906
Db 1438 CAGACT 1443

RESULT 14

US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Query Match 99.6%; Score 902.8; DB 18; Length 4790;
Best Local Similarity 99.8%; Pred. No. 5,6e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 184 ATGCCCCATGATGATGATGGAATCAAAATGTTACTGAGAGGTTGGGCTCTGCTGGA 243
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Db 244 AGTGAAGCGAAAAGTCTGTAATTTAGTCGGCGCATTTGGGATTAACAATCATCC 303
Qy 121 CACATTTTGAAGCAATTAATCAACTGCTCAAGCTTAAGAAGCGAAGTTGCAAG 180
Db 304 CACATTTTGAAGCAATTAATCAACTGCTCAAGCTTAAGAAGCGAAGTTGCAAG 363
Qy 181 GACAAAGTGTATTAATCAAGCTCATCAAGCATTCAGCGAAACATTAAGTTGACATTGAT 240
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Qy 241 TGCAGTCGAAGTGTGTAGTTAGATCAAGGCTCCGAAGTGTGCTCTCTCTCA 300
Db 424 TGCAGTCGAAGTGTGTAGTTAGATCAAGGCTCCGAAGTGTGCTCTCTCTCA 483
Qy 301 GACTGTTTCTCACTGATCTTCTGGGTTAACTGAGAGAGCTTCAACTGTTCACTG 360

Db 484 GACTGTTTCTCACTGATCTTCTGGGTTAACTGAGAGAGCTTCAACTGTTCACTG 543
Qy 361 CTGAGAGTGGGTTTGTGATGTTCTCTGTTGTTTCCCTGGGCTCTGTGAAGAAATCC 420
Db 544 CTGAGAGTGGGTTTGTGATGTTCTCTGTTGTTTCCCTGGGCTCTGTGAAGAAATCC 603
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Db 604 ACTGATGCTCCCTACCTGATTTCTCAGCTTCTTACCTGTTGGCCAAATGGGCAAC 663
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Db 664 GCAATTTCTCCCAATCTTATCTTGTGCTGCCAGGAGATGCTCTAACAAGAGCTGATA 723
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Db 724 CAGAGAAATGGGATTTGTTATGTTTAAATGCGAGCTTACTGTCCAAAGCTGACTT 783
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Db 1084 CAGACT 1089

RESULT 15

US-10-357-930-20824
; Sequence 20824, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6232
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 20824
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824
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Query Match          99.6%; Score 902.8; DB 18; Length 5145;
Best Local Similarity 99.8%; Pred. No. 5,9e-280;
Matches 904; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Job time : 553.782 secs
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RESULT 2
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Query Match 34.8%; Score 1896; DB 4; Length 1998;
Basic Local Similarity 99.9%; Pred. No. 0;
Matches 1996; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1858 AAGCTATGCAATTTCTCCCTGTTCAAGAACTATCGAGCACTCCGAAACAGATCTT 1917
1321 AAGCTATGCAATTTCTCCCTGTTCAAGAACTATCGAGCACTCCGAAACAGATCTT 1380
1918 GATTAAGAGAGAGGCAATCCCAAGAGCTGAGAGCCGCAAGCTTGAAGAGCAG 1977
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2038 TCTCTCACTGATCGAAGTGGAGGCTGAGAGCAATTAACACACACCTTCTTTTGGC 2097
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QY	2098	CTTTCCACGACGACAGACCTCAGAAAGTGTGGCTGAGGCTTAAAGGCTGGAC	2157
Db	1561	CTTTCCACGACGACAGACCTCAGAAAGTGTGTGGCTTAAAGGCTGGAC	1620
QY	2158	TCGGATATCTTGGCCCCCGAAGCTTAAACCTTCCCTGACGACGTGGTATTTTGC	2217
Db	1621	TCGGATATCTTGGCCCCCGAAGCTTAAACCTTCCCTGACGACGTGGTATTTTGC	1680
QY	2218	ACAGAGTCTCACTTTCTACTCTGGCTCAAGCATCTACGAGGAGAGTGGCCAGTTACT	2277
Db	1681	ACAGAGTCTCACTTTCTACTCTGGCTCAAGCATCTACGAGGAGAGTGGCCAGTTACT	1740
QY	2278	GCTTACAGCTGACGACGACGTGCCACTTTCGGGAGACAAAGTCTATTCTGTGCGAGGCG	2337
Db	1741	GCTTACAGCTGACGACGACGTGCCACTTTCGGGAGACAAAGTCTATTCTGTGCGAGGCG	1800
QY	2338	CAGAAAGCCAAATGACAGACTGACTTCGCGCGGAGAGCTGGCATGAAAGAGCCCTTTGAA	2397
Db	1801	CAGAAAGCCAAATGACAGACTGACTTCGCGCGGAGAGCTGGCATGAAAGAGCCCTTTGAA	1860
QY	2398	AAGCAGTTTAAACGAGAAAGCTGCCAAATTGGAAATTGGAGAGACATCATGTCAAGAAC	2457
Db	1861	AAGCAGTTTAAACGAGAAAGCTGCCAAATTGGAAATTGGAGAGACATCATGTCAAGAAC	1920
QY	2458	AGGTCACGGAGAAAGCTGGGAAAATGGGCGAGTCAAGTCTAGCTTTTGGGCGACATGAA	2517
Db	1921	AGGTCACGGAGAAAGCTGGGAAAATGGGCGAGTCAAGTCTAGCTTTTGGGCGACATGAA	1980
QY	2518	ATCATTTGAGCTCTCTGA	2535
Db	1981	ATCATTTGAGCTCTCTGA	1998

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1      RESULT 3
2      US-09-016-434-91
3      ; Sequence 91, Application US/09016434
4      ; Patent No. 6500938
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Janice Au-Young
7      ; APPLICANT: Jeffrey J. Sellmeier
8      ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
9      ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
10     ; NUMBER OF SEQUENCES: 1490
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
13     ; STREET: 3174 PORTER DRIVE
14     ; CITY: PALO ALTO
15     ; STATE: CALIFORNIA
16     ; COUNTRY: USA
17     ; ZIP: 94304
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/09/016,434
25     ; FILING DATE: HERETWITH
26     ; CLASSIFICATION:
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER:
29     ; FILING DATE:
30     ; CLASSIFICATION:
31     ; ATTORNEY/AGENT INFORMATION:
32     ; NAME: Zeller, Karen J.
33     ; REGISTRATION NUMBER: 37,071
34     ; REFERENCE/DOCKET NUMBER: PA-0002 US
35     ; TELECOMMUNICATION INFORMATION:
36     ; TELEPHONE: (650) 855-0555
37     ; TELEFAX: (650) 845-4166
38     ; INFORMATION FOR SEQ ID NO: 91:
39     ; SEQUENCE CHARACTERISTICS:

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; LENGTH: 279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGEF03
; CLONE: 1234795
US-09-016-434-91

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Query Match	4.5%;	Score 247;	DB 4;	Length 279;
Best Local Similarity	100.0%;	Pred. No. 7.2e-113;		
Matches 247;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	514	GGGAAAAGAGCACTTATTGTTGTCAATGSCCATAGATGATTGGAATCAATTTGTA	CT	573
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QY	574	GAGAGTTGTGTGCTCTGCTGAAAAGTGGAAAGGAAAAAGTGCTGTAATTGATAGCCG		633
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QY	634	CCATTGTGGAATCAATATCATCCCAATTTGGAGCCATTAATATCAATGCTCTCAAG		693
Db	121	CCATTGTGGAATCAATATCATCCCAATTTGGAGCCATTAATATCAATGCTCTCAAG		180
QY	694	CTTATGAACGAGAGTTGCCAACAGAGCAAAAGTGTAAATTACAGAGCTCATCCAGATTCA		753
Db	181	CTTATGAACGAGAGTTGCCAACAGAGCAAAAGTGTAAATTACAGAGCTCATCCAGATTCA		240
QY	754	GGGAAAC	760	
Db	241	GGGAAAC	247	

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RESULT 4
US-09-513-999C-2877
Sequence 2877, Application US/0951399C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2877
LENGTH: 333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 127..333
FEATURE:
NAME/KEY: misc_feature
LOCATION: 17
OTHER INFORMATION: h=a or c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: y=c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19
OTHER INFORMATION: k=g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 36

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OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 58
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 237
OTHER INFORMATION: w=a or t
FEATURE:
NAME/KEY: UNSURE
LOCATION: 37
OTHER INFORMATION: xaa=His or Gin
US-09-513-999C-2877

Query Match 3.8%; Score 205; DB 4; Length 333;
Best Local Similarity 99.6%; Pred. No. 8e-92;
Matches 255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 708 GTTGCACAGGACAAAGTTTATTAATACAGAGCTCATCCAGATTGAGGAAACATTAAGT 767
DB 138 GTTGCACAGGACAAAGTTTATTAATACAGAGCTCATCCAGATTGAGGAAACATTAAGT 197
QY 768 TGACATTATGTCAGTCAAGAGTTGTATGATTAATCAATCAAGCTCCCAAGATGTTGCTTC 827
DB 198 TGACATTATGTCAGTCAAGAGTTGTATGATTAATCAATCAAGCTCCCAAGATGTTGCTTC 257
QY 828 TCTCTCTCAGAGCTTTTCTCACTGTACTTCTGGGTAACGAGAAAGCTTCAAGTC 887
DB 258 TCTCTCTCAGAGCTTTTCTCACTGTACTTCTGGGTAACGAGAAAGCTTCAAGTC 317
QY 888 TGTTCACCTGCTTGCA 903
DB 318 TGTTCACCTGCTTGCA 333

RESULT 5
US-09-513-999C-3684/C
Sequence 3684, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ductert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3684
LENGTH: 378
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 216..377
FEATURE:
NAME/KEY: misc_feature
LOCATION: 164
OTHER INFORMATION: k=g or t
US-09-513-999C-3684

Query Match 3.4%; Score 187; DB 4; Length 378;
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QY 641 TGAATACATATCATCCCAATTTTGAAGCCATTATATCAAGCTCTCAAGCTTATGA 700
DB 318 TGAATACATATCATCCCAATTTTGAAGCCATTATATCAAGCTCTCAAGCTTATGA 259
QY 701 AGCGAAGTTGCAACAGGAAAGTTAATTAATCAAGAGCTCATCCAGATTGAGGAAAC 760
DB 258 AGCGAAGTTGCAACAGGAAAGTTAATTAATCAAGAGCTCATCCAGATTGAGGAAAC 199
QY 761 ATTAAGT 767
DB 198 ATTAAGT 192

RESULT 6
US-09-513-999C-24342
Sequence 24342, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ductert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 24342
LENGTH: 259
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 230
OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-24342

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Best Local Similarity 100.0%; Pred. No. 2.9e-53;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4978 GTGTAAGTTAGTGAAGAAAGCTGTAATGTTAATATGAATATGATGCTTTGAAGT 5037
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QY 5038 AAGCCAGCTGTTGAACGTTAACTGATGCTATTTCTCATTTGATGATGATGTTA 5097
DB 162 AAGCCAGCTGTTGAACGTTAACTGATGCTATTTCTCATTTGATGATGATGTTA 221
QY 5098 ATGTATGA 5105
DB 222 ATGTATGA 229

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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(without alignments)
11613.401 Million cell updates/sec

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Perfect score: 5450
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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 5378673 seqs, 2950229984 residues

Word size : 100

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Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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10	4413	81.0	5145	18	US-10-357-930-26815
11	4413	81.0	5145	18	US-10-357-930-26912
					Sequence 26923, A

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14	4413	81.0	5145	18	US-10-357-930-28675	Sequence 28675, A
15	4262	78.2	4790	18	US-10-648-593-115	Sequence 115, App
16	3482	63.9	3766	17	US-10-343-357-117	Sequence 17, Appl
17	3238	59.4	3625	17	US-10-425-114-26234	Sequence 26234, A
18	3118	57.2	3496	9	US-09-964-277-1	Sequence 1, Appl1
19	3079	56.5	3544	9	US-09-816-494-1	Sequence 1, Appl1
20	3079	56.5	3544	17	US-10-377-072-25	Sequence 25, Appl
21	3079	56.5	3544	18	US-10-377-072-25	Sequence 25, Appl
22	3069	56.3	3521	18	US-10-370-715B-261	Sequence 261, App
23	2837	52.1	3059	17	US-10-257-026-1	Sequence 1, Appl1
24	2624	48.1	2966	17	US-10-296-115-520	Sequence 520, App
25	2459	45.1	2732	9	US-10-168-506-2	Sequence 2, Appl1
26	2117	38.8	2332	9	US-09-964-277-20	Sequence 20, Appl
27	2098	38.5	2558	17	US-10-104-047-1750	Sequence 1750, App
28	1896	34.8	1998	9	US-09-816-494-3	Sequence 3, Appl1
29	1896	34.8	1998	17	US-10-377-072-27	Sequence 27, Appl
30	1896	34.8	1998	18	US-10-377-072-27	Sequence 27, Appl
31	1889	34.7	2102	17	US-10-094-749-673	Sequence 673, App
32	1889	27.3	1916	17	US-10-108-260A-2429	Sequence 2429, App
33	1318	24.2	2071	17	US-10-072-012-257	Sequence 257, App
34	1225	22.5	2200	17	US-10-072-012-255	Sequence 255, App
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ALIGNMENTS

RESULT 1

US-10-357-930-20824
Sequence 20824, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: KRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357, 930
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20824
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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284 CGCTGGCTGTCGAAGCATCTTTGTTGTGAAATGTTATCCAGTCATCTCTTATGA 343
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RESULT 2
US-10-357-930-20969
; Sequence 20969, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BON
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/189,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20969
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20969

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Dh 3703 GGTACAAATTCCTGAGAGAGAAAGACAGAAACCTGTTTCTTATAGTGGCTTTATCCCTCG 3762
Qy 3713 CATGCGATGGGGGAGATTTCTATGATGCTCAGACTTTACATTTACTAGTGGGCT 3772
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Dh 3823 GAGAGAGCTTTAGTGAAGAAAGAAATATTCAGAAATAAAGGTTGAGAAAGCTGAGAGA 3882
Qy 3833 CCATTGAGTTTGTATCAGTTGTGAATAGAGTCAAAAGCCATGGCCAGAGCTGTTTGGAA 3892
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Dh 4063 AGGTCACTGAAACAAGTATAGTCAATTTGGCTTTTCAACATCTCTGGCTGAGTTT 4122
Qy 4073 TATCAGCTACATGTGGGCTCTTTTGAAGCTTAAATTCACAAACAGACGTTTGGGG 4132
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Qy 4313 CCGACTGTGTTATGGGGATGATGAGCCGACAGACCTCACTAGTGTGACAAATATATG 4372
Dh 4363 CCGACTGTGTTATGGGGATGATGAGCCGACAGACCTCACTAGTGTGACAAATATATG 4422
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Qy 4433 AAGGTGCTGTCACAGATTTGAGTGTGTTTAAATATACATTTAAATCTTTATATAGAC 4492
Dh 4483 AAGGTGCTGTCACAGATTTGAGTGTGTTTAAATATACATTTAAATCTTTATATAGAC 4542
Qy 4493 ATTCTCAGTTTCAACAGATGTTTGTATGATGTATGATACACACCAAAATGTGTAACA 4552
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Dh 4663 TCCCTGCTAACAGATGTTTCAAGAGGTTTGGGCACTGGGTTTAAAGGCTTCTGCAAT 4722
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Dh 4723 TAGGGCTTCTTGGCCATGTGCCCTTCTCTGGAACGTGATGATGATGATGATGATG 4782
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Dh 4903 TGGCTGG 4909

RESULT 3
US-10-357-930-21071
; Sequence 21071, Application US/10357930

Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 21071
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21071

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 704 CATCCACATTTTGGAAAGCCATTAATATCAATGCTCCAAAGCTTATGAAAGGAGTTGC 763
QY 713 AACGAGCAAAAGTGTATTAACAGAGCTCATCCAGCATTTGAGCCGAAACATAAGTTGACA 772
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QY 773 TTGATGAGTCAAGAGGTTAGTTATGATCAATCAAGCTCCCAAGATGTGGCTCTCT 832
DB 824 TTGATGAGTCAAGAGGTTAGTTATGATCAATCAAGCTCCCAAGATGTGGCTCTCT 883
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DB 884 CTTCAGACTGTTTTCTACAGTACTTCTGGGTAAACGTGAGAGAGCTTCAACTGTTC 943
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DB 944 ACTGCTTGACAGGTGGTTTCTGAGTTCCTGTTTCCCTGGCTCTGTGAGGAA 1003
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DB 1064 CAACCCGAATTCCTCCAAATCTTATCTTGGCTGCAAGAGATGCTCTCAACAGAGAGC 1123
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DB 1304 GTGTTTATGAGCACTGTTTATGCTGGGATCTCCGCTCGGCAACATGCTTATGCTTACA 1363
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DB 1484 AGAACCAAGCTGAGCATCAAGGGCCAAAGAGCAAACTCAAGCTGTGCACTGAGAAAGC 1543
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2983 TAGGCTGAGATGAGCTGAGCTTGGGGCTCAAGTATGAGACCTCTTTAGGAGCAGAGCC 3042
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3763 CATGCAATGGGCTGATGTTTCTATGATGCTTCACTGACATTTCAATTAAGAGGCT 3822
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3943 AGGCTGGCCGCGCTCTTCACTGAGAAAGCAATCAAAATGAGAGAGCAAGGGG 4002

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Db 4303 ACTTCATGTTTCTTATGTTGACTTTTAAACAGACAGATGATATGATCAACACAGA 4362
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Db 4423 GCTATGATGAGGAGTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4482
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Db 4543 ATTCTCAGTTTCAACAGTATGTTTGAATGATGATGATGATGATGATGATGATGATG 4602
QY 4553 GTTCAACCACTTCAAGATGAGTGTGATGAGCCAAACATGTTTGAAGAAAGAGAGTAC 4612
Db 4603 GTTCAACCACTTCAAGATGAGTGTGATGAGCCAAACATGTTTGAAGAAAGAGAGTAC 4662
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QY 4793 GCGAAGGGGTGCTCGAGAGGCAAGGCTGAGAGTGTGATGATGATGATGATGATG 4852
Db 4843 GCGAAGGGGTGCTCGAGAGGCAAGGCTGAGAGTGTGATGATGATGATGATGATG 4902
QY 4853 TGGCTGG 4859
Db 4903 TGGCTGG 4909

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RESULT 4
 US-10-357-930-21083
 ; Sequence 21083, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson

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; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
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; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
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; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21083
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21083

Query Match      81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY 713 AACAGCAAAAGTGAATTATACAGAGCTCATCCAGATTCAAGCAAAATAAGTTGACA 772
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RESULT 5
US-10-357-930-21303
; Sequence 21303, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilbert
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER


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/ FILE REFERENCE: MRI-007BCN
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
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/ SOFTWARE: PASCSeq for Windows Version 4.0
/ SEQ ID NO 21303
/ LENGTH: 5145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1, 5144, 5145
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21303
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Matches 4663; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Db 3283 CCAATTCAACTGTCTATGCACAAAATTCGCGGGGCTAGATGGAAGATTAATTTTTTTT 3342
Qy 3293 CTCTCAGCTTTATGAAGAGAGGAACTGTCTAGATTCAGCTGAACCAACAGAAACC 3352
Db 3343 CTCTCAGCTTTATGAAGAGAGGAACTGTCTAGATTCAGCTGAACCAACAGAAACC 3402
Qy 3353 TGGCAATCAAGATTTTAAAGTTAGTGGAGGCTAACAGTCTACCTCCCTTTGTA 3412
Db 3403 TGGCAATCAAGATTTTAAAGTTAGTGGAGGCTAACAGTCTACCTCCCTTTGTA 3462
Qy 3413 AATCAAGAAATTTGTTAAATAGGAAATGTCAATCCTTAAATTAAGATGAATTTGTTTC 3472
Db 3463 AATCAAGAAATTTGTTAAATAGGAAATGTCAATCCTTAAATTAAGATGAATTTGTTTC 3522
Qy 3473 AAGCAAAATGTAAATTAATTTGGTGTGTAGACAGACAGACCTTCAATTCAGC 3532
Db 3523 AAGCAAAATGTAAATTAATTTGGTGTGTAGACAGACAGACCTTCAATTCAGC 3582
Qy 3533 CAAAGCAGATTTTTTGGCTTTTCTGCTTCACTGATGATACAGTGTGTAAATGTAAAT 3592
Db 3583 CAAAGCAGATTTTTTGGCTTTTCTGCTTCACTGATGATACAGTGTGTAAATGTAAAT 3642
Qy 3593 AATATGGAGAAATTTTATAGAAACCTCTAGGGAGGTAAATTTAGGAAGTTAAGAA 3652
Db 3643 AATATGGAGAAATTTTATAGAAACCTCTAGGGAGGTAAATTTAGGAAGTTAAGAA 3702
Qy 3653 GGTACAAATTCCTAGAGAGAGAGCAAGAACTGTTCCTTAGTGCTTTTATCCCTCGG 3712
Db 3703 GGTACAAATTCCTAGAGAGAGAGCAAGAACTGTTCCTTAGTGCTTTTATCCCTCGG 3762
Qy 3713 CATGCGATGGGCTGATGTTTCTATGATGCTCAGACTTTCACATTTACTATAGTGGCT 3772
Db 3763 CATGCGATGGGCTGATGTTTCTATGATGCTCAGACTTTCACATTTACTATAGTGGCT 3822
Qy 3773 GAGAGAGGCTTTAGTGAAGAGAAATTTCAAGATTAAGCGTTGAGAAAGCTGAGAA 3832
Db 3823 GAGAGAGGCTTTAGTGAAGAGAAATTTCAAGATTAAGCGTTGAGAAAGCTGAGAA 3882
Qy 3833 CCATTTAGTTTGTATGATTCAGTTGTGAATAGAGTGAAGCAAGCCATGCGCAACTGTTTGA 3892
Db 3883 CCATTTAGTTTGTATGATTCAGTTGTGAATAGAGTGAAGCAAGCCATGCGCAACTGTTTGA 3942
Qy 3893 ACGCTGGCGGCGTGTCTTCACTGAGAAAGCAAAATGGAAGCAAGCAAGGCGG 3952
Db 3943 ACGCTGGCGGCGTGTCTTCACTGAGAAAGCAAAATGGAAGCAAGCAAGGCGG 4002
Qy 3953 CGTCTCAGTCTCAACTCAATCAATCACTGTATGGAATGGGCTGGGAGCTGAACATAGG 4012
Db 4003 CGTCTCAGTCTCAACTCAATCAATCACTGTATGGAATGGGCTGGGAGCTGAACATAGG 4062
Qy 4013 AGTCACTGAACAAGTATAGTCAAGATTGGCTTTCAAACATCTCTGCTGAGATT 4072
Db 4063 AGTCACTGAACAAGTATAGTCAAGATTGGCTTTCAAACATCTCTGCTGAGATT 4122

QY 4073 TATAGCTACATATGAGGCTCTCTTTGAGCCCTATATTCAGAACAGAGCTTTTGGGG 4132
DB 4123 TATAGCTACATATGAGGCTCTCTTTGAGCCCTATATTCAGAACAGAGCTTTTGGGG 4182
QY 4133 GTGGGGCTGGGGCGGGGTGTCTATGTTCTTTCTCTTCTGTAAGTGTGCTAGTTCG 4192
DB 4183 GTGGGGCTGGGGCGGGGTGTCTATGTTCTTTCTCTTCTGTAAGTGTGCTAGTTCG 4242
QY 4193 CCTGATCTCAGATTTTCTGTTTGTAGAAATGAGCAGTTTGTGACAGAGATG 4252
DB 4243 CCTGATCTCAGATTTTCTGTTTGTAGAAATGAGCAGTTTGTGACAGAGATG 4302
QY 4253 ACTTCATGTTTCTTATGTAAGTCTTAAACAGCAGAGATGATGATGATGATGATG 4312
DB 4303 ACTTCATGTTTCTTATGTAAGTCTTAAACAGCAGAGATGATGATGATGATGATG 4362
QY 4313 CCGATCTGTTATGAGGATGATGAGCCGACAGACTCTCATGTTGTGACAAATATGT 4372
DB 4363 CCGATCTGTTATGAGGATGATGAGCCGACAGACTCTCATGTTGTGACAAATATGT 4422
QY 4373 GCTATGATGAGGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 4432
DB 4423 GCTATGATGAGGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 4482
QY 4433 AAAAGTCTGTCACAGATTTGATGATTTTATATATATATATATATATATATATAT 4492
DB 4483 AAAAGTCTGTCACAGATTTGATGATTTTATATATATATATATATATATATATAT 4542
QY 4493 ATTTCAGATTTTACAGATTTTATGATTTTATATATATATATATATATATATAT 4552
DB 4543 ATTTCAGATTTTACAGATTTTATGATTTTATATATATATATATATATATATATAT 4602
QY 4553 GTTCAACATTTTACAGATTTTATGATTTTATATATATATATATATATATATATAT 4612
DB 4603 GTTCAACATTTTACAGATTTTATGATTTTATATATATATATATATATATATATAT 4662
QY 4613 TCTTCTGTAACATTTTACAGATTTTATGATTTTATATATATATATATATATATAT 4672
DB 4663 TCTTCTGTAACATTTTACAGATTTTATGATTTTATATATATATATATATATATAT 4722
QY 4673 TAGGCTCTCTTGGCAGATTTTCTCTTCTGTAAGTGTGATGATGATGATGATG 4732
DB 4723 TAGGCTCTCTTGGCAGATTTTCTCTTCTGTAAGTGTGATGATGATGATGATG 4782
QY 4733 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4792
DB 4783 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4842
QY 4793 GCGAAGGGGTGCGCTCGAAGGAGGCTCTGAGAGCTGCTGATGATGATGATGATG 4852
DB 4843 GCGAAGGGGTGCGCTCGAAGGAGGCTCTGAGAGCTGCTGATGATGATGATGATG 4902
QY 4853 TGGCTGG 4859
DB 4903 TGGCTGG 4909

RESULT 6
US-10-357-930-21307
Sequence 21307, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21307
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 514, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21307

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 173 GCTTTCAGTCCAGTGTAAAGCTGTGAGCGCGGAGCAAGGTAAAGATGATGATG 232
DB 224 GCTTTCAGTCCAGTGTAAAGCTGTGAGCGCGGAGCAAGGTAAAGATGATGATG 283
QY 233 CGCTGCTGCTCCAAAGCATTTTGTGTGATGTTATTCAGTCACTCTTTATGA 292
DB 284 CGCTGCTGCTCCAAAGCATTTTGTGTGATGTTATTCAGTCACTCTTTATGA 343
QY 293 ATCAATGTAGAGGCGCTGTGTGAGCGGAGCTTTGCAAGAGCATCAACGGGAAA 352
DB 344 ATCAATGTAGAGGCGCTGTGTGAGCGGAGCTTTGCAAGAGCATCAACGGGAAA 403
QY 353 GAGAAAGACATTCATCTTGAGAGGCTCTTGCTGAATAATGGTTAACTCTCTTTG 412
DB 404 GAGAAAGACATTCATCTTGAGAGGCTCTTGCTGAATAATGGTTAACTCTCTTTG 463
QY 413 AGTACACAGCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATG 472
DB 464 AGTACACAGCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATG 523
QY 473 ACAACACATTCATCTTGAGAGGCTCTTGCTGAATAATGGTTAACTCTCTTTG 532
DB 524 ACAACACATTCATCTTGAGAGGCTCTTGCTGAATAATGGTTAACTCTCTTTG 583
QY 533 TTGTCAATGCGCCATGATGATGATGATGATGATGATGATGATGATGATGATG 592
DB 584 TTGTCAATGCGCCATGATGATGATGATGATGATGATGATGATGATGATGATG 643
QY 593 TGGAAAGTGAACGGAAGAAAGTGTCTAATGATGATGATGATGATGATGATGATG 652
DB 644 TGGAAAGTGAACGGAAGAAAGTGTCTAATGATGATGATGATGATGATGATGATG 703
QY 653 CATCCACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAGCAAGGTTGC 712
DB 704 CATCCACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAGCAAGGTTGC 763
QY 713 AACAGACAAAGTGTAAATTAAGAGCTCATCAGCATTCAGCGAAACATAAGTTGACA 772
DB 764 AACAGACAAAGTGTAAATTAAGAGCTCATCAGCATTCAGCGAAACATAAGTTGACA 823
QY 773 TTGATTCAGTCAAGAGGTGTGATGATGATGATGATGATGATGATGATGATGATG 832
DB 824 TTGATTCAGTCAAGAGGTGTGATGATGATGATGATGATGATGATGATGATGATG 883

Qy 833 CTTCAGACTGTTTCTCACTGTACTTGTGGGTAACTGAGAGAGAGCTTCACTGTTC 892
Db 884 CTTCAGACTGTTTCTCACTGTACTTGTGGGTAACTGAGAGAGAGCTTCACTGTTC 943
Qy 893 AACTGCTTGGCAGAGTGGGTTTGTGTGTTCTCTGTGTGTTTCCCTGTGTGAGGAA 952
Db 944 AACTGCTTGGCAGAGTGGGTTTGTGTGTTCTCTGTGTGTTTCCCTGTGTGAGGAA 1003
Qy 953 AATCACTCTAGTCCCTCACTGTCACTTTCAGAGCTTGTGTACCTGTGTGCAACATTTGGGC 1012
Db 1004 AATCACTCTAGTCCCTCACTGTCACTTTCAGAGCTTGTGTACCTGTGTGCAACATTTGGGC 1063
Qy 1013 CAACCCGAATTCCTCCAACTCTTATCTGTGTGTCAGAGAGAGTGTCTCAACAAGAGC 1072
Db 1064 CAACCCGAATTCCTCCAACTCTTATCTGTGTGTCAGAGAGAGTGTCTCAACAAGAGC 1123
Qy 1073 TGAATACAGAGAAATGGGATTTGGTTATGTGTTAAATGCGAGCTAATCTGTCCAAAGCCTG 1132
Db 1124 TGAATACAGAGAAATGGGATTTGGTTATGTGTTAAATGCGAGCAATCTGTCCAAAGCCTG 1183
Qy 1133 ACTTTATCCCGAGTCTCAATTTCCGTGGTGTGCTGTGAATGACAGCTTTGTGAGAAA 1192
Db 1184 ACTTTATCCCGAGTCTCAATTTCCGTGGTGTGCTGTGAATGACAGCTTTGTGAGAAA 1243
Qy 1193 TTTTGCCTGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCCTCAATGGAT 1252
Db 1244 TTTTGCCTGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCCTCAATGGAT 1303
Qy 1253 GTGTTCTAGTCACTGTTTAACTGGGATCTCCCGCTCCGCAACATGCTTATGCGCTTACA 1312
Db 1304 GTGTTCTAGTCACTGTTTAACTGGGATCTCCCGCTCCGCAACATGCTTATGCGCTTACA 1363
Qy 1313 TCATGAGAGAGATGGACAATGCTTTAGATGAAAGCTTAAAGATTTGTGAAAAGAAAAGAC 1372
Db 1364 TCATGAGAGAGATGGACAATGCTTTAGATGAAAGCTTAAAGATTTGTGAAAAGAAAAGAC 1423
Qy 1373 CTACTATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTGGAATAGAGAAAGATTA 1432
Db 1424 CTACTATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTGGAATAGAGAAAGATTA 1483
Qy 1433 AGAATCAGAGCTGAGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTGTGACCTGAGAGC 1492
Db 1484 AGAATCAGAGCTGAGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTGTGACCTGAGAGC 1543
Qy 1493 CAATGAGAACTGTCCCTGTGTCTCAAGAGGTGAGCAAAAAGAGAGCCCTCTCACTC 1552
Db 1544 CAATGAGAACTGTCCCTGTGTCTCAAGAGGTGAGCAAAAAGAGAGCCCTCTCACTC 1603
Qy 1553 CAACCTGTGCGGACTGTGTCTCAAGAGAGAGCAAAAGCCGTGTGATCCGCGCA 1612
Db 1604 CAACCTGTGCGGACTGTGTCTCAAGAGAGAGCAAAAGCCGTGTGATCCGCGCA 1663
Qy 1613 GCGGTGCCAGGCGTCCAGCGGTGACGCCGTGTGTAGAGAGAGCCCGCTGTGTACAG 1672
Db 1664 GCGGTGCCAGGCGTCCAGCGGTGACGCCGTGTGTAGAGAGAGCCCGCTGTGTACAG 1723
Qy 1673 GCGTCAAGTGGGCTGCACTGTGTCCGAGACAGGCTGTGAAAGACAGCAATAGCTCAAGCTT 1732
Db 1724 GCGTCAAGTGGGCTGCACTGTGTCCGAGACAGGCTGTGAAAGACAGCAATAGCTCAAGCTT 1783
Qy 1733 CCTTCTCTGTGATATCAAAATCAGTTTCAATTAATGAGCAGAGATGGCAGCATCTTACATG 1792
Db 1784 CCTTCTCTGTGATATCAAAATCAGTTTCAATTAATGAGCAGAGATGGCAGCATCTTACATG 1843
Qy 1793 GCTTCTCTCATAGAAAGATCTTTGAAATACTAACAACCTTCACTTCTGTGATGGGA 1852
Db 1844 GCTTCTCTCATAGAAAGATCTTTGAAATACTAACAACCTTCACTTCTGTGATGGGA 1903
Qy 1853 CCAACAAAGCTATGCAAGTCTTCCCTGTGTGAGAAAGCTATGAGAGAGACTCCGAGAACCA 1912
Db 1904 CCAACAAAGCTATGCAAGTCTTCCCTGTGTGAGAAAGCTATGAGAGAGACTCCGAGAACCA 1963
Qy 1913 GTCTGTATAGAGAGAGCAGCATCCCAAGAAAGCTGACAGACCGGCGCTTCAAGCA 1972

Db 1964 GTCCGTATAGAGAGAGACAGCATCCCAAGAAAGCTCAAGACCCGACAGGCTTACAGCA 2023
Qy 1973 GCGAGAGAGAGATTTGATTTCCGTGAGAACAGAGAGAGTGGCAACCCCGAGAGTCCC 2032
Db 2024 GCGAGAGAGAGATTTGATTTCCGTGAGAACAGAGAGAGTGGCAACCCCGAGAGTCCC 2083
Qy 2033 TTTTATCTCCATCTGATGGAAGTGGAGCGGTGAGAGCAATTTACACACAGCTTCTT 2092
Db 2084 TTTTATCTCCATCTGATGGAAGTGGAGCGGTGAGAGCAATTTACACACAGCTTCTT 2143
Qy 2093 TCGGCTTTTCCAGCAGCAGAGCACTTACAGAAATCTGTGGCTGTGGCTTTAAGGCT 2152
Db 2144 TCGGCTTTTCCAGCAGCAGAGCACTTACAGAAATCTGTGGCTGTGGCTTTAAGGCT 2203
Qy 2153 GGCACCTGGATATCTTGGCCCCCAGAGCTTACCCCTTCCCTGACACAGAGCTGTATT 2212
Db 2204 GGCACCTGGATATCTTGGCCCCCAGAGCTTACCCCTTCCCTGACACAGAGCTGTATT 2263
Qy 2213 TTGCAACAGAGTCCCTCACTTCTACTGTGCTGAGCATCTAAGAGAGAGTGCAGTT 2272
Db 2264 TTGCAACAGAGTCCCTCACTTCTACTGTGCTGAGCATCTAAGAGAGAGTGCAGTT 2323
Qy 2273 ACTGTGCTTACAGCTGACAGCAGCTGCCCACTTGTGGAGACCAAGTCTATTCTGTGCGCA 2332
Db 2324 ACTGTGCTTACAGCTGACAGCAGCTGCCCACTTGTGGAGACCAAGTCTATTCTGTGCGCA 2383
Qy 2333 GCGCGCAGAGACCAAGTGAACAGAGCTGACTGCGCGCGGAGCTGGGATGAGAGAGCCCT 2392
Db 2384 GCGCGCAGAGACCAAGTGAACAGAGCTGACTGCGCGCGGAGCTGGGATGAGAGAGCCCT 2443
Qy 2393 TTGAAAGCAGTTTAAACGAGAAAGCTGCGCAATGGAATTTGAGAGAGCATCATGTGAG 2452
Db 2444 TTGAAAGCAGTTTAAACGAGAAAGCTGCGCAATGGAATTTGAGAGAGCATCATGTGAG 2503
Qy 2453 AGAACAAGTCAACGAGAAAGCTGCGGAAAGTGGGCACTGACTTGTGCGGAGAGCA 2512
Db 2504 AGAACAAGTCAACGAGAAAGCTGCGGAAAGTGGGCACTGACTTGTGCGGAGAGCA 2563
Qy 2513 TGAATATCATTTGAGTCTCTGAGAGAAAGACCTTGTGACTTCTATAGACAAATTTT 2572
Db 2564 TGAATATCATTTGAGTCTCTGAGAGAAAGACCTTGTGACTTCTATAGACAAATTTT 2622
Qy 2573 TTTTCTGTGCAAAAATAATCCCTGTAAATCTGAAATATATATAGTATACATATTA 2632
Db 2623 TTTTCTGTGCAAAAATAATCCCTGTAAATCTGAAATATATATAGTATACATATTA 2682
Qy 2633 TATTTTGGAAAAATGAGACTTGTGTAAAGCAACAGTGGATCAACCCAGTTGTACT 2692
Db 2683 TATTTTGGAAAAATGAGACTTGTGTAAAGCAACAGTGGATCAACCCAGTTGTACT 2742
Qy 2693 CTCTTAACATCTGCAATTTGAGAGATCAGCTAATATCTTCTCAACAAAAATGAGAGGCA 2752
Db 2743 CTCTTAACATCTGCAATTTGAGAGATCAGCTAATATCTTCTCAACAAAAATGAGAGGCA 2802
Qy 2753 GATGCTAAGATTCCTCCCTTGAACGAGAGAAAAATTTTATTCAGTGAATTAACATCTCT 2812
Db 2803 GATGCTAAGATTCCTCCCTTGAACGAGAGAAAAATTTTATTCAGTGAATTAACATCTCT 2862
Qy 2813 TTTGTTCTTAAAAAGCAAGTGTCTTGTGTGTGAGAGCAAAATCCCTTACATTTTAC 2872
Db 2863 TTTGTTCTTAAAAAGCAAGTGTCTTGTGTGTGAGAGCAAAATCCCTTACATTTTAC 2922
Qy 2873 GTTGTGCTACTAAGAGATCTCAAAATATATAGTCTTGTGTGCGGACCTTTCATAGTACCT 2932
Db 2923 GTTGTGCTACTAAGAGATCTCAAAATATATAGTCTTGTGTGCGGACCTTTCATAGTACCT 2982
Qy 2933 TAGGCTGAGACTGAGCAGCTTGGGGGTCAAGTATGAGACCTGTTAAGGAGAGAGCC 2992
Db 2983 TAGGCTGAGACTGAGCAGCTTGGGGGTCAAGTATGAGACCTGTTAAGGAGAGAGCC 3042
Qy 2993 TAGTGTAAATCCAAAGAAATGATCTTATCCAAAGCTGATTTCAAAACCAACGCTCAC 3052

Db 3043 TAGGTGAATTCAGAGAAATGATCTATCCAAAGCTGATTCACAAACCCAGCTCACC 3102
QY 3053 TGACAGCCGAGGACACAGACATCACTCTGAGAGGACATTTAGGGGCTTGCCAAAG 3112
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Db 3163 TCTACCTTAGAGCAAAACCCAGTACTCAGACAGAAAGTCGGGGCTTTGACCACTACAT 3222
QY 3173 ATCTGGTAGCCCATTTTCTAGGCACTTGGAATGATAGTATGATCTACATTTTGCA 3232
Db 3223 ATCTGGTAGCCCATTTTCTAGGCACTTGGAATGATAGTATGATCTACATTTTGCA 3282
QY 3233 CCAATTCAACTGTCTATGACCAAAATCCCGTGGGCTAGATGAGATTAATTTTTTT 3292
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QY 3353 TGGCAATCAGATTTAAGCTAAGGTGGGAGGCTAAGAGCTACCTCCCTTTGTA 3412
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QY 3413 AATCAAGAATTTGTTAAATGGGATTTGCAATCTTTAAATGAAGTAAGTGTTC 3472
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QY 3473 AAGCCAAATGTAATTTATTTGGGTTGTGACAGACAGACACCTTCAATTTCTCAGC 3532
Db 3523 AAGCCAAATGTAATTTATTTGGGTTGTGACAGACAGACACCTTCAATTTCTCAGC 3582
QY 3533 CAAAGCAGATTTTTCCTTTCTGCTTCACTGATGATACAGTGGTAAATATAT 3592
Db 3583 CAAAGCAGATTTTTCCTTTCTGCTTCACTGATGATACAGTGGTAAATATAT 3642
QY 3593 AATATGCGCAATTTTATATGAAACTTCTAGGAGGTAAATATATGGAAGTTAAGAA 3652
Db 3643 AATATGCGCAATTTTATATGAAACTTCTAGGAGGTAAATATATGGAAGTTAAGAA 3702
QY 3653 GGTACAAATGCTGAGAGAGAGCAAGAACTGTTTCTTATGAGCTTTATCCCTGCG 3712
Db 3703 GGTACAAATGCTGAGAGAGAGCAAGAACTGTTTCTTATGAGCTTTATCCCTGCG 3762
QY 3713 CATGCGATGGGCTGATGTTTCTATGATGCTCAGACTTCACTTACTAGTGGCT 3772
Db 3763 CATGCGATGGGCTGATGTTTCTATGATGCTCAGACTTCACTTACTAGTGGCT 3822
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Db 3823 GAGAGAGCTTTATGAGAGAGAAATATTCAGAAATAAACGTTGAGAACTGAGAA 3882
QY 3833 CCATTTAGTTTGTATCAGTTGATGATGAGAGCAAGCAAGGCAAGCTGTTTGGAA 3892
Db 3883 CCATTTAGTTTGTATCAGTTGATGATGAGAGCAAGCAAGGCAAGCTGTTTGGAA 3942
QY 3893 ACGCTGCGCGGCTGTCTTCACTAGTGAAGAAACCAATCAAAATGAGAGCAAGCAAGG 3952
Db 3943 ACGCTGCGCGGCTGTCTTCACTAGTGAAGAAACCAATCAAAATGAGAGCAAGCAAGG 4002
QY 3953 CGTCTCAGTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4012
Db 4003 CGTCTCAGTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4062
QY 4013 AGGTCACTGAAACAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 4072
Db 4063 AGGTCACTGAAACAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 4122
QY 4073 TATAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4132
Db 4123 TATAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4182

QY 4133 GTGGGCTGGGCGGGTGTTCATTTGTTTCCCTTCTGTAAAGTGTCTAGTGTG 4192
Db 4183 GTGGGCTGGGCGGGTGTTCATTTGTTTCCCTTCTGTAAAGTGTCTAGTGTG 4242
QY 4193 CCTGATCTCAGGTTTTCTCTGTTTTGAGAAATGAGCAGTTTTTTTGAACAGATGTG 4252
Db 4243 CCTGATCTCAGGTTTTCTCTGTTTTGAGAAATGAGCAGTTTTTTTGAACAGATGTG 4302
QY 4253 ACTTCATTTTCTATGTTGATCTTCTAAACCAAGCAAGATGATGATGATGATGATGAT 4312
Db 4303 ACTTCATTTTCTATGTTGATCTTCTAAACCAAGCAAGATGATGATGATGATGATGAT 4362
QY 4313 CGGACTGGTTATGAGGAGATGATGAGCGGACAGACCTCAGTATGTTGCAAAATATGT 4372
Db 4363 CGGACTGGTTATGAGGAGATGATGAGCGGACAGACCTCAGTATGTTGCAAAATATGT 4422
QY 4373 GCTATGATGGGTTTAAAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4432
Db 4423 GCTATGATGGGTTTAAAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4482
QY 4433 AAAGTGTGTGCAAGATTTGATGATTTTATGATATATGATTAATGATGATGATGAT 4492
Db 4483 AAAGTGTGTGCAAGATTTGATGATTTTATGATATATGATTAATGATGATGATGAT 4542
QY 4493 ATTCTCAAGTTTCAAGATGATTTTATGATGATGATGATGATGATGATGATGATGATG 4552
Db 4543 ATTCTCAAGTTTCAAGATGATTTTATGATGATGATGATGATGATGATGATGATGATG 4602
QY 4553 GTTCACCACTTCCAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 4612
Db 4603 GTTCACCACTTCCAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 4662
QY 4613 TCCCTGCTAAGATTTTCAAGATTTTGGGAGGTTGGGAGGAGGAGGAGGAGGAGGAGG 4672
Db 4663 TCCCTGCTAAGATTTTCAAGATTTTGGGAGGTTGGGAGGAGGAGGAGGAGGAGGAGG 4722
QY 4673 TAGGGCTTCTCTTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 4732
Db 4723 TAGGGCTTCTCTTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 4782
QY 4733 AGCTTTAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4792
Db 4783 AGCTTTAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4842
QY 4793 GCGAGAGGAGGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4852
Db 4843 GCGAGAGGAGGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4902
QY 4853 TGGCTGG 4859
Db 4903 TGGCTGG 4909

RESULT 7
US-10-357-930-22820
; Sequence 22820, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862

;; PRIOR FILING DATE: 2000-03-16
;; PRIOR APPLICATION NUMBER: 60/207,454
;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: 60/211,314
;; PRIOR FILING DATE: 2000-06-09
;; PRIOR APPLICATION NUMBER: 60/219,007
;; PRIOR FILING DATE: 2000-07-18
;; PRIOR APPLICATION NUMBER: 60/255,281
;; PRIOR FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 62232
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 22820
;; LENGTH: 5145
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1, 5144, 5145
;; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-22820

Query Match 81.0%; Score 4413; DB 18; Length 5145;

Beet Local Similarity 99.9%; Pred. No. 0;

Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 173 GCTTCAGTCCAGTGAAGCTGTGAGCGCGGAGCAAGGTAAAGATGATGTAATG 232
DB 224 GCTTCAGTCCAGTGAAGCTGTGAGCGCGGAGCAAGGTAAAGATGATGTAATG 283
QY 233 CGCTGCTGCTCCAAAGCATCTTTTGTGTGGAATGTTATTCAGTCATCTTTATGA 292
DB 284 CGCTGCTGCTCCAAAGCATCTTTTGTGTGGAATGTTATTCAGTCATCTTTATGA 343
QY 293 ATCAATGTGAGGGCTGCTTTGTGTGAGAGAGTCTTTGCAAGACATCAAGGAAA 352
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QY 533 TTGTGATGCGCCATGAGATGATTTGGAATCAAAATTTGTTAATGAGAGTGGTGGCTGCG 592
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DB 644 TGAAGAGTGAACGAAAAAGTGTCTTAATGATAGCGGCAATTTGTGAAATACAATA 703
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DB 704 CATCCACATTTTGGAGCCATTAATATCACTGCTCAAGCTTATGAAAGCAAGGTTGC 763
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DB 824 TTGATTCAGTCAGAGGTTGATTAAGATCAAGCTCCCAAGATGTTGGCTCTCTCTCT 883
QY 833 CTTCAGACTGTTTCTCACTGTATCTTGTGGTAACTGAGAGAGCTTCAACTCTGTTC 892
DB 884 CTTCAGACTGTTTCTCACTGTATCTTGTGGTAACTGAGAGAGCTTCAACTCTGTTC 943

QY 893 ACTGCTTGACAGTGGGTTTGTGAGTTCCTGTTGTTTCCGTGGCTCTGTGAAGAA 952
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DB 1004 AATCCACTCTAGTCCCTACCTGACATTTCTCAGCTTGTGCTTACTGTGTCACATTTGGGC 1063
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DB 1424 CTACATATATCTCCAAATCTTCAATTTCTGGGCGCACTCTGACATATGAGAAAGATTA 1483
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DB 1904 CCAACAAAGCTATGCAAGTTCTCCCTGTTCAGAACTATCGAGAGCAGCTCCGAAACA 1963
QY 1913 GTCTGATTAAGAGAGAGCCAGCATCCCAAGAAAGCTGCAACCCGAGGCTTTAGACA 1972
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QY 1973 GCAAGAGCAAGGATGTCATTGCGTCAAGAACAGAGAGTGGCACCCGCAAGAGTCCC 2032

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Qy      2093 TCGGCTTTTCCACGAGCAGCAGCACTTCAGAAAGTCTGCTGGGCTGGGCTTAAGGGCT 2152
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Qy      2153 GGCACCTCGAATATCTTGGCCCCCAGACCTTAACCCCTTCCCTGACAGAGCTGGTAT 2212
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Qy      2753 GATGCTAAGATCCCCCTAGACGAGGAAAAACATTTTATTCAGTAAATTCACATCTC 2812
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Qy      2813 TTGTTCTTAAAAAAGCAAGTGTCTTTGTGTGAGAGCAAAATCCCTTCCATTTTAC 2872
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Qy      3773 GAGAGAGGCTTTAGTGAAGAGAAATATTCAGAAATTAACGTTGAGAAAGCTGAGAGA 3832
Db      3823 GAGAGAGGCTTTAGTGAAGAGAAATATTCAGAAATTAACGTTGAGAAAGCTGAGAGA 3882
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Qy      3893 AGCTGGCGGGCGTGTCTTCAGTGAAAAAGCAATCAAAATGAGAGCGAGCAAGGGG 3952
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Qy      4133 GTGGGGCTGGGGGGGGGTGATGATGTTCTTCCCTCTGTAATGTGCTAGTGTCTG 4192
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 RESULT 8
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 ; Sequence 26669, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endegge, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; PRIOR APPLICATION NUMBER: 2003-02-04
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/189,319
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 ; PRIOR APPLICATION NUMBER: 60/189,862
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 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314

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 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26669
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-26669
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 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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 Db 284 CGTGGGCTGCTCAAGCATCTTTGTTGGAAATGTTTCAAGTATGATGATGATGATGATG 343
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 Db 524 ACACCAACATTCATCACTGCTGAGCAATTAAGAAAGAGTGGGAAAGAGACTTATG 583
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Db	1004	AATCACTCTAAGTCCCACTCGATTCTCAGCCTTGCTTAACTGTGGCAACATTGGGC	1063
Qy	1013	CAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCGACGAGGATGCTCCAAACAGAGC	1072
Db	1064	CAACCCGAATTCTTCCCAATCTTTATCTTGGCTGCGACGAGGATGCTCCAAACAGAGC	1123
Qy	1073	TGATAGAGGAGATGGGATTTGGTTATGTGTAAATGCCAGCTATACTGTCCAAAGCTG	1132
Db	1124	TGATAGAGGAGATGGGATTTGGTTATGTGTAAATGCCAGCTATACTGTCCAAAGCTG	1183
Qy	1133	ACTTTATCCCGCAGTCTCAATTTCTCGCGGTGCTGCTGTAAATGACAGCTTTTGTAGAAA	1192
Db	1184	ACTTTATCCCGCAGTCTCAATTTCTCGCGGTGCTGCTGTAAATGACAGCTTTTGTAGAAA	1243
Qy	1193	TTTTGGCCGTGGTTGGCAAAATGATGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGAT	1252
Db	1244	TTTTGGCCGTGGTTGGCAAAATGATGATTTCAATTGAGAAAGCAAAAGCCTCCAAATGAT	1303
Qy	1253	GTGTCTTAGTGCACGTATTAGGCGGGGATCTCCCGCTCGCCACATGCTATGCCCTTACA	1312
Db	1304	GTGTCTTAGTGCACGTATTAGGCGGGGATCTCCCGCTCGCCACATGCTATGCCCTTACA	1363
Qy	1313	TCATGAAAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC	1372
Db	1364	TCATGAAAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC	1423
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Db	1424	CTACTATCTATCCAAACTTCAATTTCTGGGCGCAACTCCGTGACATATGAGAAAGATT	1483
Qy	1433	AGAACCAAGCTGAGACATCAAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGAGC	1492
Db	1484	AGAACCAAGCTGAGACATCAAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGAGC	1543
Qy	1493	CAAAATGAACCTGCTCCCTGCTGTCTCAGAGGGTGTGACAGAAAAGGACAGCCCTTCAATC	1552
Db	1544	CAAAATGAACCTGCTCCCTGCTGTCTCAGAGGGTGTGACAGAAAAGGACAGCCCTTCAATC	1603
Qy	1553	CACCTGTGCGCAGCTCTGCTCACTTCAAGAGGACAGAGCAAAAGGCGCTGCTATCCCGCA	1612
Db	1604	CACCTGTGCGCAGCTCTGCTCACTTCAAGAGGACAGAGCAAAAGGCGCTGCTATCCCGCA	1663
Qy	1613	GGTGGCCAGGCTGCGCCAGCGGTGACAGCGCTGTGTAGAGACAGCGCGCTGTACAGG	1672
Db	1664	GGTGGCCAGGCTGCGCCAGCGGTGACAGCGCTGTGTAGAGACAGCGCGCTGTGTACAGG	1723
Qy	1673	CGCTCAGTGGGCTGACCTGTCCGACAGACAGGCTGGAAGACAGCAATTAAGCTCAAGCTT	1732
Db	1724	CGCTCAGTGGGCTGACCTGTCCGACAGACAGGCTGGAAGACAGCAATTAAGCTCAAGCTT	1783
Qy	1733	CCCTTCTCTGCGGATATCAAAATCACTTTCATATTCAGCGAGCATGCGAGATCCTTACATG	1792
Db	1784	CCCTTCTCTGCGGATATCAAAATCACTTTCATATTCAGCGAGCATGCGAGATCCTTACATG	1843
Qy	1793	GCTTCTCCTCATCAGAGATGCTTTGGAAATCTACAAACCTTCACTACCTGAGATGGGA	1852
Db	1844	GCTTCTCCTCATCAGAGATGCTTTGGAAATCTACAAACCTTCACTACCTGAGATGGGA	1903
Qy	1853	CCAAACAAGCTATGCGCACTTCCCTGTGTCAAGAACTATCGAGACGACTTCCGAAACCA	1912
Db	1904	CCAAACAAGCTATGCGCACTTCCCTGTGTCAAGAACTATCGAGACGACTTCCGAAACCA	1963
Qy	1913	GTCTCTGATTAAGAGAGAGCGAGCATCCCCAAGAAAGCTGAGACCGCAGAGCTTTAGACA	1972
Db	1964	GTCTCTGATTAAGAGAGAGCGAGCATCCCCAAGAAAGCTGAGACCGCAGAGCTTTAGACA	2023
Qy	1973	GCCAGAGCAAGCGATTGCAATTCGCTGAGAAACCAAGCAGAGTGGCAACCGCCAGAGCTCC	2032
Db	2024	GCCAGAGCAAGCGATTGCAATTCGCTGAGAAACCAAGCAGAGTGGCAACCGCCAGAGCTCC	2083
Qy	2033	TTTTATCTCACTGATCGAAGTGGGAGGCTGAGAGCAATTACACACACAGCTTCCCTTT	2092

Db	2084	TTTTATCTCAGTCGATCGAAGTGGGAGGCTGAGGACATTTACACACAGCTTCTCTTT	2143
QY	2093	TCGGCCCTTTCCACACAGCCAGACAGACCTTACAGAACTCTGCTGGCTTGAGGAGGCT	2152
Db	2144	TCGGCCCTTTCCACACAGCCAGACAGACCTTACAGAACTCTGCTGGCTTGAGGAGGCT	2203
QY	2153	GGCAGCTCGAATATCTTGGCCCCCAGACCTTCAACCCCTTCCCTGACAGACGCTGGATT	2212
Db	2204	GGCAGCTCGAATATCTTGGCCCCCAGACCTTCAACCCCTTCCCTGACAGACGCTGGATT	2263
QY	2213	TTGCGCACAGAGTCTTCAACCTTCTACTCTGCTCAGCCATCTTACGAGGAGCTGCCAGTT	2272
Db	2264	TTGCGCACAGAGTCTTCAACCTTCTACTCTGCTCAGCCATCTTACGAGGAGCTGCCAGTT	2323
QY	2273	ACTCTCCCTTACAGCTGACAGCTGACAGCTGCCCACTTGGGAGAGCAAGTCTATCTGTTGGCA	2332
Db	2324	ACTCTCCCTTACAGCTGACAGCTGACAGCTGCCCACTTGGGAGAGCAAGTCTATCTGTTGGCA	2383
QY	2333	GCGCGCAGAAAGCCCAAGTGAAGAGCTGACAGCTGACTCGCGCGAGAGCTGACATGAAGAGCCCT	2392
Db	2384	GCGCGCAGAAAGCCCAAGTGAAGAGCTGACAGCTGACTCGCGCGAGAGCTGACATGAAGAGCCCT	2443
QY	2393	TTGAAAAGAGAGTTTAAAGCGAGAAAGCTGCCAAATGAGAAATTTGGAGAGAGCATCTGTCCAG	2452
Db	2444	TTGAAAAGAGAGTTTAAAGCGAGAAAGCTGCCAAATGAGAAATTTGGAGAGAGCATCTGTCCAG	2503
QY	2453	AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGCAGTCAAGTCTTACGCTTTTCGGGACGCA	2512
Db	2504	AGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGCAGTCAAGTCTTTCGGGACGCA	2563
QY	2513	TGGAATATCTTGAAGGTCCTCGAGAGAAAGAACCTTGTACCTTCTATACAAATTTTTT	2572
Db	2564	TGGAATATCTTGAAGGTCCTCGAGAGAAAGAACCTTGTACCTTCTATACAAATTTTTT	2622
QY	2573	TTTTCTTGTCACAAAAAAATTCCTGTAAATCTGAATATATATATGTACATACATATA	2632
Db	2623	TTTTCTTGTCACAAAAAAATTCCTGTAAATCTGAATATATATATGTACATACATATA	2682
QY	2633	TATTTTGGAAAAATGAGAGCTATGGTGTAAAGCAACAGGTGATTCAAACCAAGTTGTACT	2692
Db	2683	TATTTTGGAAAAATGAGAGCTATGGTGTAAAGCAACAGGTGATTCAAACCAAGTTGTACT	2742
QY	2693	CTCTTAAACATCTGCAATTTGAGAGATCAGCTAATATCTCTCAACAAAAATGGAAGGGA	2752
Db	2743	CTCTTAAACATCTGCAATTTGAGAGATCAGCTAATATCTCTCAACAAAAATGGAAGGGA	2802
QY	2753	GATGCTAAATACCCCCCTTACACGGAAGAAAACAATTTATCTCAGTAATTAACAATCTTC	2812
Db	2803	GATGCTAAATACCCCCCTTACACGGAAGAAAACAATTTATCTCAGTAATTAACAATCTTC	2862
QY	2813	TTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTGGAAGAACAAATCCCTACCAATTTTCA	2872
Db	2863	TTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTGGAAGAACAAATCCCTACCAATTTTCA	2922
QY	2873	GTGTGTCTTAAAGAGATCTCAAAATATTAAGTCTTGTCCGACCCCTTCATAGTACACT	2932
Db	2923	GTGTGTCTTAAAGAGATCTCAAAATATTAAGTCTTGTCCGACCCCTTCATAGTACACT	2982
QY	2933	TAGGCTGAGACTGAGCAGCTCTTGGGGGTCAAGGTAGTGAACCTGTTAAGGACAGAGCC	2992
Db	2983	TAGGCTGAGACTGAGCAGCTCTTGGGGGTCAAGGTAGTGAACCTGTTAAGGACAGAGCC	3042
QY	2993	TAGTGTAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCAACGCTCAC	3052
Db	3043	TAGTGTAAATCCAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCAACGCTCAC	3102
QY	3053	TGACAGCCGAGGGAACAGAGATCATCTCTGCTGGAACGGAACATTTAGGGGCTTTGCAAG	3112
Db	3103	TGACAGCCGAGGGAACAGAGATCATCTCTGCTGGAACGGAACATTTAGGGGCTTTGCAAG	3162
QY	3113	TTTACTTTAAGCAAAACCAAGTACCTCAGACAGAAAGTCCGGGCTTTGACCACTACCAT	3172

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RESULT 9
 US-10-357-930-26815
 ; Sequence 26815, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
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 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281

;; PRIOR FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 62232
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 26815
;; LENGTH: 5145
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 5144, 5145
;; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26815

Query Match 81.0%; Score 4413; DB 18; Length 5145;
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Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db 4303 ACTTCATGTTCTCATGATGATCTTAAACCAAGACAGAAATGATATGATCTCAACAG 4362

QY	4313	CCGACTTGGTTAATGGGGAGATGAGACCCGACAGACCTACTAGTTGTGTCACAAAATAAATGT	43172
Db	4363	CCGACTTGGTTAATGGGGAGATGAGACCCGACAGACCTACTAGTTGTGTCACAAAATAAATGT	44222
QY	4373	GCTATGATGGGGTGTAAAGTGAAGGCAGAAAGGGTCAAGCCGATGTTTATGATATCTGGG	44322
Db	4423	GCTATGATGGGGTGTAAAGTGAAGGCAGAAAGGGTCAAGCCGATGTTTATGATATCTGGG	44822
QY	4433	AAAGTGTGTGTCAACGATTTGAGTTTATGATATCAATTTGAAATCTTTAAATCAAGAC	44922
Db	4483	AAAGTGTGTGTCAACGATTTGAGTTTATGATATCAATTTGAAATCTTTAAATCAAGAC	45422
QY	4493	AATTCACAGTTTCAACAGATGTTTATGATATGATACACACACCAATATGTGTAAACA	45522
Db	4543	AATTCACAGTTTCAACAGATGTTTATGATATGATACACACACCAATATGTGTAAACA	46022
QY	4553	GTTTCAACACTTCCAGAGTGTGTCAATGCCAAACATTTTAAAGAAAGAAAGCAGTAGC	46122
Db	4603	GTTTCAACACTTCCAGAGTGTGTCAATGCCAAACATTTTAAAGAAAGAAAGCAGTAGC	46622
QY	4613	TCTTTGCTTAACGATTTTCAAGAGGTTTGGGCACTTGTTTAAATGAGCTTGTCAAT	46722
Db	4663	TCTTTGCTTAACGATTTTCAAGAGGTTTGGGCACTTGTTTAAATGAGCTTGTCAAT	47222
QY	4673	TAGGGCTTCTCTGGGCGAATGGTCCCTCTCTTGGAACGTGTGATAGTACATCTTAC	47322
Db	4723	TAGGGCTTCTCTGGGCGAATGGTCCCTCTCTTGGAACGTGTGATAGTACATCTTAC	47822
QY	4733	AGCCTTAATGATCTGGTTACTAGTGTCAATATCAATTTCTTGGAATCGAGACTGCCGTG	47922
Db	4783	AGCCTTAATGATCTGGTTACTAGTGTCAATATCAATTTCTTGGAATCGAGACTGCCGTG	48422
QY	4793	GCGAAGGGGTGGCTTCGGAGGCAAGCTCTGGAAGCTGTTGATGTCCTTTAGTGGGGTGG	48522
Db	4843	GCGAAGGGGTGGCTTCGGAGGCAAGCTCTGGAAGCTGTTGATGTCCTTTAGTGGGGTGG	49022
QY	4853	TGGCTGG 4859	
Db	4903	TGGCTGG 4909	
RESULT 10			
US-10-357-930-26912			
Sequence 26912, Application US/10357930			
Publication No. US20040259086A1			
GENERAL INFORMATION:			
APPLICANT: Schlegel, Robert			
APPLICANT: Endege, Wilson			
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
TITLE OF INVENTION: HUMAN PROSTATE CANCER			
FILE REFERENCE: MRI-007BCN			
CURRENT APPLICATION NUMBER: US/10/357,930			
CURRENT FILING DATE: 2003-02-04			
PRIOR APPLICATION NUMBER: 09/785,276			
PRIOR FILING DATE: 2003-02-16			
PRIOR APPLICATION NUMBER: 60/183,319			
PRIOR FILING DATE: 2000-02-17			
PRIOR APPLICATION NUMBER: 60/189,862			
PRIOR FILING DATE: 2000-03-16			
PRIOR APPLICATION NUMBER: 60/207,454			
PRIOR FILING DATE: 2000-05-25			
PRIOR APPLICATION NUMBER: 60/211,314			
PRIOR FILING DATE: 2000-06-09			
PRIOR APPLICATION NUMBER: 60/219,007			
PRIOR FILING DATE: 2000-07-18			
PRIOR APPLICATION NUMBER: 60/255,281			
PRIOR FILING DATE: 2000-12-13			
NUMBER OF SEQ ID NOS: 62232			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 26912			

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/   LENGTH: 5145
/   TYPE: DNA
/   ORGANISM: Homo sapiens
/   FEATURE:
/   NAME/KEY: misc feature
/   LOCATION: 1, 5144, 5145
/   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26912

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Query Match	81.0%;	Score 4413;	DB 18;	Length 5145;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 4683;	Conservative	0;	Mismatches 3;	Indels 1;
			Gaps	1;

QY	173	GCCTTCAGTCCAGATGTAAGCTGTTGGACGCGCGGAGCAAAAGGTAAAGATATGATGAATG	232
Db	224	GCCTTCAGTCCAGATGTAAGCTGTTGGACGCGCGGAGCAAAAGGTAAAGATATGATGAATG	283
QY	233	CGCTGGCTCTCCAAAGCATCTTTTGTGTGGAAATGGTATTTCCACTCATCTCTTATGA	292
Db	284	CGCTGGCTCTCCAAAGCATCTTTTGTGTGGAAATGGTATTTCCAGTCACTCTCTTATGA	343
QY	293	ATCCAAATGTGAGGGGGTGCTTTGTGTGACGGAATCCTTTGCAAGAGACATCAACGGAAA	352
Db	344	ATCCAAATGTGAGGGGGTGCTTTGTGTGACGGAATCCTTTGCAAGAGACATCAACGGAAA	403
QY	353	GAGAAAGAGACATTCACCTTGGAGGGCTCTTGGCTGAAAATGGGTTTAACTCTCTTTGGC	412
Db	404	GAGAAAGAGACATTCACCTTGGAGGGCTCTTGGCTGAAAATGGGTTTAACTCTCTTTGGC	463
QY	413	AATCAACACACGCGCTGACTCATTAACCTTTTATGTAATGAGATGTGACCTTAGC	472
Db	464	AATCAACACACGCGCTGACTCATTAACCTTTTATGTAATGAGATGTGACCTTAGC	523
QY	473	ACACACCATTTACATCATCTGTGGCAATTTAAAGAGAGGTGGAGAAAAGAGACCTTATG	532
Db	524	ACACACCATTTACATCATCTGTGGCAATTTAAAGAGAGGTGGAGAAAAGAGACCTTATG	583
QY	533	TTGTCAATGGCCCATGATGATGATTTGGAATCTCAAAATTTGTACTGAGAGTTGGTCTTGC	592
Db	584	TTGTCAATGGCCCATGATGATGATTTGGAATCTCAAAATTTGTACTGAGAGTTGGTCTTGC	643
QY	593	TGGAAAGTGGAAACGGAAAAGTGGCTGAATTTGATAGCGCGCATTTGTGAAATCAATA	652
Db	644	TGGAAAGTGGAAACGGAAAAGTGGCTGAATTTGATAGCGCGCATTTGTGAAATCAATA	703
QY	653	CATCCCATTTTGGAAAGCCATTAATATCAACTGTCTCCAACTTATGAGAGCAAGTTGC	712
Db	704	CATCCCATTTTGGAAAGCCATTAATATCAACTGTCTCCAACTTATGAGAGCAAGTTGC	763
QY	713	AACGAGACAAAGTGTAAATTAACAAGCTCATCCAGCATTCAGCGCAACATTAAGTTGACA	772
Db	764	AACGAGACAAAGTGTAAATTAACAAGCTCATCCAGCATTCAGCGCAACATTAAGTTGACA	823
QY	773	TTGATTCAGTCAACAAGTTGTAGTTTATACATCAAAAGTCCCAAGATTTGCTCTCTCT	832
Db	824	TTGATTCAGTCAACAAGTTGTAGTTTATACATCAAAAGTCCCAAGATTTGCTCTCTCT	883
QY	833	CTTCAAGACTGTTTCTCACTGTACTTTCTGGGTAAATCTGAGAGAAGCTTCAACTCTGTT	892
Db	884	CTTCAAGACTGTTTCTCACTGTACTTTCTGGGTAAATCTGAGAGAAGCTTCAACTCTGTT	943
QY	893	ACCTGCTTGGACGGGTGGTTGTCTGAGTTCTCTGTTTCCCTGGGCTCTGTGTAAAGAA	952
Db	944	ACCTGCTTGGACGGGTGGTTGTCTGAGTTCTCTGTTTCCCTGGGCTCTGTGTAAAGAA	1003
QY	953	AATCACTAGTCCCTACCTGACATTTCTCAAGCTTGTCTTAACCTTTGGCCAACATTTGGG	1012
Db	1004	AATCACTAGTCCCTACCTGACATTTCTCAAGCTTGTCTTAACCTTTGGCCAACATTTGGG	1063
QY	1013	CAACCGGAATTTCTCCCAATCTTTATCTTGGCTGACGCGAGATGTCTTCAACAAGAGC	1072
Db	1064	CAACCGGAATTTCTCCCAATCTTTATCTTGGCTGACGCGAGATGTCTTCAACAAGAGC	1123

Qy 1073 TGATACAGCAGAAATGGATGGTATATGTGTAAATGCGACGTATACCTGTCCAAAGCCTG 1132
Db 1124 TGATGACAGCAAAATGGATGGTATATGTGTAAATGCGACCAATCTGTCCAAAGCCTG 1183
Qy 1133 ACTTTATCCCGAGCTCATTTTCCGTGCGTGTCCGTGTAAATGACAGCTTTTGTGAGAAA 1192
Db 1184 ACTTTATCCCGAGCTCATTTTCCGTGCGTGTCCGTGTAAATGACAGCTTTTGTGAGAAA 1243
Qy 1193 TTTTCCGCTGGTGGACAAATCAGTATGATTTTCATTGAGAAAGCAAAAGCCTCCAAATGAT 1252
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Qy 1253 GTGTCTAGTCACTGTTTAACTGGAGATCTCCCGCTCCGCAACAATGCTATCCGCTTACA 1312
Db 1304 GTGTCTAGTCACTGTTTAACTGGAGATCTCCCGCTCCGCAACAATGCTATCCGCTTACA 1363
Qy 1313 TCATGAAAGAGATGAGCACTGTCTTTAGATGAAAGCTTACAGATTTGTGAAAGAAAAGAC 1372
Db 1364 TCATGAAAGAGATGAGCACTGTCTTTAGATGAAAGCTTACAGATTTGTGAAAGAAAAGAC 1423
Qy 1373 CTACTATATCTCCAACTTCAATTTTCTGGGCGCAATCTGTGACATATGAGAAAGATTA 1432
Db 1424 CTACTATATCTCCAACTTCAATTTTCTGGGCGCAATCTGTGACATATGAGAAAGATTA 1483
Qy 1433 AGAAGCAGACTGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGACCTGTGAGAAAC 1492
Db 1484 AGAAGCAGACTGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGACCTGTGAGAAAC 1543
Qy 1493 CAAATGAACTGTCTCTGTCTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTCAATC 1552
Db 1544 CAAATGAACTGTCTCTGTCTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTCAATC 1603
Qy 1553 CACCTGTGCGGACCTGTCTCTCAGAGGGTGGACAGAAAAGCGGCTGTGATCCCGCA 1612
Db 1604 CACCTGTGCGGACCTGTCTCTCAGAGGGTGGACAGAAAAGCGGCTGTGATCCCGCA 1663
Qy 1613 GCGTGCCAGCGTGGCCAGCGTGGACCGCTGTGTTAGAGAACAGCCCGTGTATACAG 1672
Db 1664 GCGTGCCAGCGTGGCCAGCGTGGACCGCTGTGTTAGAGAACAGCCCGTGTATACAG 1723
Qy 1673 CGCTCAGTGGCTGACCTGTCTCCGACAGCAGGCTGGAAGACAAATAGCTCAAGCCTT 1732
Db 1724 CGCTCAGTGGCTGACCTGTCTCCGACAGCAGGCTGGAAGACAAATAGCTCAAGCCTT 1783
Qy 1733 CCTTCTCTCTGGAATGAAATCAGTTTATATTCAGCAGCAGATGGCAGCATCTTATACATG 1792
Db 1784 CCTTCTCTCTGGAATGAAATCAGTTTATATTCAGCAGCAGATGGCAGCATCTTATACATG 1843
Qy 1793 GCTTCTCTCTCAGAAAGATCTTTGGAATCTACTCAAACTTCCACTCTGTGATGGGA 1852
Db 1844 GCTTCTCTCTCAGAAAGATCTTTGGAATCTACTCAAACTTCCACTCTGTGATGGGA 1903
Qy 1853 CCAACAAAGCTATGCGCAGTTCTCCCTGTTCAGGAATATCGGAGAGCATCTCCGAAACCA 1912
Db 1904 CCAACAAAGCTATGCGCAGTTCTCCCTGTTCAGGAATATCGGAGAGCATCTCCGAAACCA 1963
Qy 1913 GTCTGATTAAGAGAGAGAGCAGCATCTCCCAAGAAAGCTGACAGCCGAGGCTTACAGCA 1972
Db 1964 GTCTGATTAAGAGAGAGAGCAGCATCTCCCAAGAAAGCTGACAGCCGAGGCTTACAGCA 2033
Qy 1973 GCGAGAGCAGAGATGAGATTCGAGTCCAGAACAGCAGAGTGGACCGCCCAAGAGATCC 2032
Db 2024 GCGAGAGCAGAGATGAGATTCGAGTCCAGAACAGCAGAGTGGACCGCCCAAGAGATCC 2083
Qy 2033 TTTTATCTCAGCTGATGGAAGTGGAGCGTGGAGAGCAATTTACCAACAGCTTCCCTT 2092
Db 2084 TTTTATCTCAGCTGATGGAAGTGGAGCGTGGAGAGCAATTTACCAACAGCTTCCCTT 2143
Qy 2093 TCGGCTTTTCCACAGCAGCAGACCTTCAGGAATGTCTGTGCTGTGGCTTTAAGGGCT 2152
Db 2144 TCGGCTTTTCCACAGCAGCAGACCTTCAGGAATGTCTGTGCTGTGGCTTTAAGGGCT 2203
Qy 2153 GGCACCTGGATATCTTGGCCCCCGACGCTCTACCCCTTCCCTGACAGAGCTGTAT 2212

Db 2204 GGCACCTGGATATCTTGGCCCCCGACGCTCTACCCCTTCCCTGACAGAGCTGTAT 2263
Qy 2213 TTTGCAAGAGTCTCCACATTTCTACTGTGCTGACCATCTGACGAGAGAGTGCAGAT 2272
Db 2264 TTTGCAAGAGTCTCCACATTTCTACTGTGCTGACCATCTGACGAGAGAGTGCAGAT 2323
Qy 2273 ACTGTGCTTACAGCTGACAGCAGCTGCTCACTTGTGAGAGCAAAATCTTATCTGTGCGCA 2332
Db 2324 ACTGTGCTTACAGCTGACAGCAGCTGCTCACTTGTGAGAGCAAAATCTTATCTGTGCGCA 2383
Qy 2333 GCGCGCAGAGCCAAAGTACAGAGCTGACTGCGCGCGAGCTGGCATGAGAGAGCCCT 2392
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Qy 2393 TTTGAAAGCAGTTTAAACGAGAGCTGCGCAATGGAAATTTGAGAGAGCATATGTCAG 2452
Db 2444 TTTGAAAGCAGTTTAAACGAGAGCTGCGCAATGGAAATTTGAGAGAGCATATGTCAG 2503
Qy 2453 AGAAGAGTCAAGGAGAGAGCTGGGAAAGTGGGCAAGTCAAGTCTTATGAGCAATTTT 2512
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Qy 2513 TGAATATCATTTAGAGTCTCTGAGAGAGAGCACTTGTGACTTCTATGACAAATTTT 2572
Db 2564 TGAATATCATTTAGAGTCTCTGAGAGAGAGCACTTGTGACTTCTATGACAAATTTT 2622
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Db 2623 TTTTCTGTTCAGAAAATATCCCTGTAAATCTGAAATATATATATATATATATATATAT 2682
Qy 2633 TATTTTGGAAAATGAGAGCTATGAGTAAAGCAACAGTGGATCAACCCAGTGTACT 2692
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Qy 2693 CTCTTAATCTGCAATTTGAGAGATCAGCTAATATCTTCTCAACAAAATGAAAGGCA 2752
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Qy 2753 GATGCTAAGATCCCCCTTACAGAGAGAGAAACATTTTATCTAGATTAACAATCTC 2812
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Qy 2813 TTTTCTTAAAGAAAGCAAGTCTTTGTGTGAGAGCAAAATCCCTTACATTTTAC 2872
Db 2863 TTTTCTTAAAGAAAGCAAGTCTTTGTGTGAGAGCAAAATCCCTTACATTTTAC 2922
Qy 2873 GTTGTCTACTTAAAGATCTCAAAATATATATCTTGTCCGAGCCCTTCAATGATACCT 2932
Db 2923 GTTGTCTACTTAAAGATCTCAAAATATATATCTTGTCCGAGCCCTTCAATGATACCT 2982
Qy 2933 TAGCGCTGAGATGAGCCAGCTTGGGGTCAAGTATGAGTACAGCTGTTAAGGACAGAGCC 2992
Db 2983 TAGCGCTGAGATGAGCCAGCTTGGGGTCAAGTATGAGTACAGCTGTTAAGGACAGAGCC 3042
Qy 2993 TAGTGTAAATCCCAAGAAATGATCTTATCCAAAGCTGATTCCAAACCAAGCTCAC 3052
Db 3043 TAGTGTAAATCCCAAGAAATGATCTTATCCAAAGCTGATTCCAAACCAAGCTCAC 3102
Qy 3053 TGAAGCGAGAGGACAGAGCATCTCTGTGACAGCACTTATGAGGCGCTTCCAAAG 3112
Db 3103 TGAAGCGAGAGGACAGAGCATCTCTGTGACAGCACTTATGAGGCGCTTCCAAAG 3162
Qy 3113 TCTACCTTAAGCAAAACCAAGTACTCAGACAGAAAGTGGGCTTTGACCACTACAT 3172
Db 3163 TCTACCTTAAGCAAAACCAAGTACTCAGACAGAAAGTGGGCTTTGACCACTACAT 3222
Qy 3173 ATCTGTAGCCCAATTTCTAGGCAATGTGAAATAGTATGATGATGATGATGATGATGAT 3232
Db 3223 ATCTGTAGCCCAATTTCTAGGCAATGTGAAATAGTATGATGATGATGATGATGATGAT 3282
Qy 3233 CCAATTCAACTGTCTATGACAAAAATCCCGTGGGCTAGATGAGATTAATTTT 3292

Db	3283	CCAAATTCAAACCTGCTATGCAAAAATTTCCCGTGGCCGATGAGATTAATTTTTTTTT	3342
Qy	3293	CTTCTGAGCTTTATGGAAGAAAGGAAACTGTCATAGATTCTAGCTGAACCAACAGAAAC	3352
Db	3343	CTTCTCAGCTTTATGAAGAGAAAGGAAACTGTCATAGATTCTAGCTGAACCAACAGAAAC	3402
Qy	3353	TGGCAATCATACGATTTTAAGCTAAAGTTGGGAGGCTTAACGAGTCTACTCCCTCTTGT	3412
Db	3403	TGGCAATCATACGATTTTAAGCTAAAGTTGGGAGGCTTAACGAGTCTACTCCCTCTTGT	3462
Qy	3413	AATCAAGAATTTGTTAAATGGGATGTGCAATCCCTTAAATAAAGATGAACCTTGTT	3472
Db	3463	AATCAAGAATTTGTTAAATGGGATGTGCAATCCCTTAAATAAAGATGAACCTTGTT	3522
Qy	3473	AAGCCAAATGAAATTTATTTGGGTGGTGAAGACAGACGACGACCTTCAAAATCTAGC	3532
Db	3523	AAGCCAAATGAAATTTATTTGGGTGGTGAAGACAGACGACGACCTTCAAAATCTAGC	3582
Qy	3533	CAAAAGAGATGTTTTTGCCCTTCTGCTCACTGAGATGATACAGTTGGTAAATGAT	3592
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Qy	3593	AATATGGCAGATTTTATATAGAACTTCTAGGAGGTAAATTAATGGAGATTAAGAAA	3652
Db	3643	AATATGGCAGATTTTATATAGAACTTCTAGGAGGTAAATTAATGGAGATTAAGAAA	3702
Qy	3653	GGTACAAATTGCTGAGAGAAACAGAGAAACCTGTTCCCTTGGGCTTTATCCCTCG	3712
Db	3703	GGTACAAATTGCTGAGAGAAACAGAGAAACCTGTTCCCTTGGGCTTTATCCCTCG	3762
Qy	3713	CATGCGATGGGCGTGAATGTTCTATGATGTGCTCAGACTTTCACATTTACTAGTAGGCT	3772
Db	3763	CATGCGATGGGCGTGAATGTTCTATGATGTGCTCAGACTTTCACATTTACTAGTAGGCT	3822
Qy	3773	GAGAGAGCTTTAGTGAAGAGAAATATTCAATTAATAACGTTGAAAGCTGAGAGA	3832
Db	3823	GAGAGAGCTTTAGTGAAGAGAAATATTCAATTAATAACGTTGAAAGCTGAGAGA	3882
Qy	3833	CCATTGAGTTTGATCAGTTGTAATAGTAGCAAGCAATGGCCAGCTGTTTGGAA	3892
Db	3883	CCATTGAGTTTGATCAGTTGTAATAGTAGCAAGCAATGGCCAGCTGTTTGGAA	3942
Qy	3893	AGCGTGGCCGGGTGCTCTGCTGAGGAAAGCAAAATCAAAATGAGCGAGAGCAAAAGGG	3952
Db	3943	AGCGTGGCCGGGTGCTCTGCTGAGGAAAGCAAAATCAAAATGAGCGAGAGCAAAAGGG	4002
Qy	3953	CGTCTCAGTCTCAACCTTCAATCATCTGATAGAAATCGGTCTGGCAGCTGAACATAG	4012
Db	4003	CGTCTCAGTCTCAACCTTCAATCATCTGATAGAAATCGGTCTGGCAGCTGAACATAG	4062
Qy	4013	AGGTACAATGAAACAAGTATAGTCAATTTGGCTTTCAAAATCTCTTGGCTTGAAT	4072
Db	4063	AGGTACAATGAAACAAGTATAGTCAATTTGGCTTTCAAAATCTCTTGGCTTGAAT	4122
Qy	4073	TATCAGCTACATATGGGTCTCTTTTGAAGCCTTAATTCAACAAGCAAGCTTTTGGG	4132
Db	4123	TATCAGCTACATATGGGTCTCTTTTGAAGCCTTAATTCAACAAGCAAGCTTTTGGG	4182
Qy	4133	GTGGGCGCTGGCGGGTGTGTCATGTTCTTTCCTTCTGTAAGTGTGCTAGTTGGTG	4192
Db	4183	GTGGGCGCTGGCGGGTGTGTCATGTTCTTTCCTTCTGTAAGTGTGCTAGTTGGTG	4242
Qy	4193	CCTGATATCAGGTTTTCTCGTTTTTGAAGAAATGGAACAGTTTTTGAACAGAGATGT	4252
Db	4243	CCTGATATCAGGTTTTCTCGTTTTTGAAGAAATGGAACAGTTTTTGAACAGAGATGT	4302
Qy	4253	ACTTCATGTTTCTATGTAATCTTAAACCAAGCAACAGATGATATGCTCAACAGAG	4312
Db	4303	ACTTCATGTTTCTATGTAATCTTAAACCAAGCAACAGATGATATGCTCAACAGAG	4362
Qy	4313	CCGACTGGTTATGGGAGATAGAGCCGACAGACCTCACTAGTTGTGCAAAATATGT	4372
Db	4363	CCGACTGGTTATGGGAGATAGAGCCGACAGACCTCACTAGTTGTGCAAAATATGT	4422

Oy		4373	GCGATGATGGGGGTGAAGATTGTAAGCCAGAAGAGGGTCACGCCCATTTGTTATGATACTGGG	4432
Dd		4423	GCTATGATGGGGTGTAAAGTAGAAGGCAGAAAGGGTCAGCCGACTTTGTATGATCACTGGG	4482
Oy		4433	AAAAGTCTGGTGCAACGATTTTGAGTAGTTTATGATATACATTGAATCTTTAATCAGAC	4492
Dd		4483	AAAGTCTGGTGCAACGATTTTGAGTAGTTTATGATATACATTGAATCTTTAATCAGAC	4542
Oy		4493	AATTCACAGTTTCAACAGTAGTATTTTGTATGTATGTAACAACAACCAAATGTGTAA	4552
Dd		4543	ATTCTCAAGTTTCAACAGTAGTATTTTGTATGTATGTAACAACAACCAAATGTGTAA	4602
Oy		4553	GTTTCACACCTTCACAGAGTGTGTCATGCCAAAACTGTTTTAAGAAAGAAACAGTAGC	4612
Dd		4603	GTTTCACACCTTCACAGAGTGTGTCATGCCAAAACTGTTTTAAGAAAGAAACAGTAGC	4662
Oy		4613	TCTCTGCTTAACGATGTTTCAGAGGTTTGAGGACATTGTTTTAATGAGCTTGTCAAT	4672
Dd		4663	TCCTTGCTTAACGATGTTTCAGAGGTTTGAGGACATTGTTTTAATGAGCTTGTCAAT	4722
Oy		4673	TAGGAGCTTCTCTGAGGCATAGTGTCCCTTCCTTCCTGGAACGTGATGATGACATCTAC	4732
Dd		4723	TAGGAGCTTCTCTGAGGCATAGTGTCCCTTCCTTCCTGGAACGTGATGATGACATCTAC	4782
Oy		4733	AGCCTTAGTCTGTGTTCACTAGTGCAGATPAATCAAGTTCTTGGAATCGAGACTGCCGTG	4792
Dd		4783	AGCCTTAGTCTGTGTTCACTAGTGCAGATPAATCAAGTTCTTGGAATCGAGACTGCCGTG	4842
Oy		4793	GCGAAGGGGGTGGCCTCGAGAGCAGGCGCTGAGACCTGTTGGAATGTTAGTGGGGTGG	4852
Dd		4843	GCGAAGGGGGTGGCCTCGAGAGCAGGCGCTGAGACCTGTTGGAATGTTAGTGGGGTGG	4902
Oy		4853	TGGCTGG 4859 	
Dd		4903	TGGCTGG 4909	
RESULT 11				
US-10-357-930-26923				
Sequence 26923, Application US/10357930				
Publication No. US20040259086A1				
GENERAL INFORMATION:				
APPLICANT: Schlegel, Robert				
APPLICANT: Endege, Wilson				
APPLICANT: Monahan, John				
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR				
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF				
FILE REFERENCE: MRI -007BCN				
CURRENT APPLICATION NUMBER: US/10/357,930				
CURRENT FILING DATE: 2003-02-04				
PRIORITY APPLICATION NUMBER: 09/785,276				
PRIORITY FILING DATE: 2003-02-16				
PRIORITY APPLICATION NUMBER: 60/183,319				
PRIORITY FILING DATE: 2000-02-17				
PRIORITY APPLICATION NUMBER: 60/189,862				
PRIORITY FILING DATE: 2000-03-16				
PRIORITY APPLICATION NUMBER: 60/207,454				
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PRIORITY APPLICATION NUMBER: 60/219,007				
PRIORITY FILING DATE: 2000-07-18				
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PRIORITY FILING DATE: 2000-12-13				
NUMBER OF SEQ ID NOS: 62232				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 26923				
LENGTH: 5145				
TYPE: DNA				
ORGANISM: Homo sapiens				
FEATURE:				

NAME/KEY: misc_feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26923

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 173 GCTTCACATCCAGTGTAAAGCTTTGGAGCCGCGGAGGAAAGTAAAGTAAATG 232
DB 224 GCTTCACATCCAGTGTAAAGCTTTGGAGCCGCGGAGGAAAGTAAAGTAAATG 283
QY 223 CGCTGGCTGCTCAAGCATCTTTTGTGTGAATGTATTCAGATCTCTTATGA 292
DB 284 CGCTGGCTGCTCAAGCATCTTTTGTGTGAATGTATTCAGATCTCTTATGA 343
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DB 344 ATCAATGTGAGGGCTGCTTTGTGAGCGAGTCTTTGCAAGACACATCAACGGGAAA 403
QY 353 GAGAAAGACATTCATTGAGGGCTGCTTTGTGAATGGTTAACTCTCTTTGCC 412
DB 404 GAGAAAGACATTCATTGAGGGCTGCTTTGTGAATGGTTAACTCTCTTTGCC 463
QY 413 AGTACACACAGCTGACCTCAATACCTTTTATGATGAGTGGCTGAGCTTTGAGC 472
DB 464 AGTACACACAGCTGACCTCAATACCTTTTATGATGAGTGGCTGAGCTTTGAGC 523
QY 473 ACACCAACCATTAATCATCTGTGGCAATTAAGAAAGGTGGAAAAGAGACTTATG 532
DB 524 ACACCAACCATTAATCATCTGTGGCAATTAAGAAAGGTGGAAAAGAGACTTATG 583
QY 533 TTGTGATGGCCCATGAGATGATTTGGAATCTCAATTTGTACTGAGAGTGTGGCTTGC 592
DB 584 TTGTGATGGCCCATGAGATGATTTGGAATCTCAATTTGTACTGAGAGTGTGGCTTGC 643
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DB 644 TGGAAAGTGAACGGAAAAGTGTGCTAATTTGATGAGCGGCAATTTGTGGAATCAATA 703
QY 653 CATCCACATTTTGGAAACCATTAATCAATGCTGCCAGCTTAAGAGGAAAGTTC 712
DB 704 CATCCACATTTTGGAAACCATTAATCAATGCTGCCAGCTTAAGAGGAAAGTTC 763
QY 713 AACGAGACAAAGTGAATTAACAGAGCTATCCAGCATTCAGCGAAACATAAGTTGACA 772
DB 764 AACGAGACAAAGTGAATTAACAGAGCTATCCAGCATTCAGCGAAACATAAGTTGACA 823
QY 773 TTGATTTGAGTCAGAAAGTGTGATTTAGATCAAAAGCTCCCAAGATGTGCTCTCT 832
DB 824 TTGATTTGAGTCAGAAAGTGTGATTTAGATCAAAAGCTCCCAAGATGTGCTCTCTCT 883
QY 833 CTTCAGACTGTTTTCTCACTGTAATCTTGGGTAAACTGAGAAAGCTTCACTCTGTTCC 892
DB 884 CTTCAGACTGTTTTCTCACTGTAATCTTGGGTAAACTGAGAAAGCTTCACTCTGTTCC 943
QY 893 ACCTGCTTGACAGGTGGTGTGCTGATCTCTCGTTGTTCCCTGAGCTCTGTGAAGAA 952
DB 944 ACCTGCTTGACAGGTGGTGTGCTGATCTCTCGTTGTTCCCTGAGCTCTGTGAAGAA 1003
QY 953 AATTCACCTGATCCCTACCTGACCTTCTCAGCCCTGCTGTTTACCTGTTGCCAACTTGGGC 1012
DB 1004 AATTCACCTGATCCCTACCTGACCTTCTCAGCCCTGCTGTTTACCTGTTGCCAACTTGGGC 1063
QY 1013 CAACCCGAAATCTTCCCAATCTTTATCTTGGCTGCGACGAGATGTCTCAACAAGAGC 1072
DB 1064 CAACCCGAAATCTTCCCAATCTTTATCTTGGCTGCGACGAGATGTCTCAACAAGAGC 1123
QY 1073 TGAATACAGAGAAATGGATTTGGTTATGTGTTAAATGCAAGCTATACCTGTCCAAAGCTG 1132
DB 1124 TGAATACAGAGAAATGGATTTGGTTATGTGTTAAATGCAAGCTATACCTGTCCAAAGCTG 1183

QY 1133 ACTTATCCCGAGTCTCATTTCTGCTGTCGCTGTGAATGACAGCTTTTGTGAGAAA 1192
DB 1184 ACTTATCCCGAGTCTCATTTCTGCTGTCGCTGTGAATGACAGCTTTTGTGAGAAA 1243
QY 1193 TTTTGGCGGTGTGAGCAATTCAGTAAATTTCAATTTGAGAAAAGCAAGCTTCAATGAT 1252
DB 1244 TTTTGGCGGTGTGAGCAATTCAGTAAATTTCAATTTGAGAAAAGCAAGCTTCAATGAT 1303
QY 1253 GTGTTCTAGTACAGCTTTTACCTGGGATCTCCGCTCCGACCAATGCTTATGCTTCA 1312
DB 1304 GTGTTCTAGTACAGCTTTTACCTGGGATCTCCGCTCCGACCAATGCTTATGCTTCA 1363
QY 1313 TCATGAAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAAGAC 1372
DB 1364 TCATGAAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAAGAC 1423
QY 1424 CTACTATATCTCAAACTTCAATTTTGTGGCCAACTCTGACATGATGAAGAAATTA 1483
DB 1433 AGAACAGACTGAGCATCAAGGGCCAAAGACAAATCAAGCTGTGACCTGAGAGAGC 1492
QY 1484 AGAACAGACTGAGCATCAAGGGCCAAAGACAAATCAAGCTGTGACCTGAGAGAGC 1543
QY 1493 CAAATGAACCTGTCTGCTGTCTCAAGAGGTGAGACAGAAAAGGAGAGAGCCCTCAGTC 1552
DB 1544 CAAATGAACCTGTCTGCTGTCTCAAGAGGTGAGACAGAAAAGGAGAGAGCCCTCAGTC 1603
QY 1553 CACCTGTGCGGACTCTGTCTAATCTTCAAGAGGAGACAAAGGCCGTGCAATCCGCCA 1612
DB 1604 CACCTGTGCGGACTCTGTCTAATCTTCAAGAGGAGACAAAGGCCGTGCAATCCGCCA 1663
QY 1613 GCGTCCAGAGTCCAGCCAGCGTGTGAGCCGTGCTTGAAGAGACAGCCCGTGTGAACG 1672
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QY 1673 CGCTCAGTGGGCTCAGCTGTCCGACAGCAGGCTGGAAGACAGAAATGAGCTCAAGCCTT 1732
DB 1724 CGCTCAGTGGGCTCAGCTGTCCGACAGCAGGCTGGAAGACAGAAATGAGCTCAAGCCTT 1783
QY 1733 CTTTCTCTGTGATATCAATCAATTCATATTCAGCCAGGATGAGCAGATCTTTACATG 1792
DB 1784 CTTTCTCTGTGATATCAATCAATTCATATTCAGCCAGGATGAGCAGATCTTTACATG 1843
QY 1793 GCTTCTCTCATCAAGAAATGCTTTGAAATCTTCAAACTTCACTTCTGTGATGAGGA 1852
DB 1844 GCTTCTCTCATCAAGAAATGCTTTGAAATCTTCAAACTTCACTTCTGTGATGAGGA 1903
QY 1853 CCAACAGACTATGACAGTCTCCCTGTTCAGAACTATGAGAGAGATCCCGAAACCA 1912
DB 1904 CCAACAGACTATGACAGTCTCCCTGTTCAGAACTATGAGAGAGATCCCGAAACCA 1963
QY 1913 GTCTGTATGAAGAGAAAGCCAGATCCCAAGAAAGCTGACAGCCGACCTTCAAGCA 1972
DB 1964 GTCTGTATGAAGAGAAAGCCAGATCCCAAGAAAGCTGACAGCCGACCTTCAAGCA 2023
QY 1973 GCGAGACAGCAATTTGATTCGCTCAGAACACAGCAGTGTGCAACGCGCCAGAGGTCC 2032
DB 2024 GCGAGACAGCAATTTGATTCGCTCAGAACACAGCAGTGTGCAACGCGCCAGAGGTCC 2083
QY 2033 TTTTATCTCCATCTGACATGGAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTT 2092
DB 2084 TTTTATCTCCATCTGACATGGAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTT 2143
QY 2093 TCGGCTTTTCCACAGCAGCAGACCTCAAGAGTCTGTGCGCTGTGAGCTTAAAGGCT 2152
DB 2144 TCGGCTTTTCCACAGCAGCAGACCTCAAGAGTCTGTGCGCTGTGAGCTTAAAGGCT 2203
QY 2153 GGCACCTGGATATTTTGGCCCGCCAGACCTTACCTTCCCTTCAACAGCAGCTGTGAT 2212
DB 2204 GGCACCTGGATATTTTGGCCCGCCAGACCTTACCTTCCCTTCAACAGCAGCTGTGAT 2263
QY 2213 TTGCAACAGAGTCTTCACTTCTGCTCAGCAGCTACAGAGGAGGAGTCCAGTT 2272

Db	2264	TTGGCA CAGAGTCTCTACACTTTACTCTGCTCAGCCACTTACGGAGGCACTGCAATT	2323
Qy	2273	ACTTGTGCTTCAAGCTGCAAGCCTGACCTCCACTTGGCGAACCMAATCTAATCTGTGCGCA	2332
Db	2324	ACTGTGCTTCAAGCTGCAAGCCTGACCTCCACTTGGCGAACCMAATCTAATCTGTGCGCA	2383
Qy	2333	GGCGGCGAAGCCCAAGTGA CAGAGCTGACTCCGCGGGAGCTGGCATGAAGAGCCCTT	2392
Db	2384	GGCGGCGAAGCCCAAGTGA CAGAGCTGACTCCGCGGGAGCTGGCATGAAGAGGCCCCCT	2443
Qy	2393	TTGAAAAGCACTTTAAACGCAGAAAGCTGCAATGGAAATTGGAGAGACATCATGTCTAG	2452
Db	2444	TTGAAAAGCACTTTAAACGCAGAAAGCTGCAATGGAAATTGGAGAGACATCATGTCTAG	2503
Qy	2453	AGAAACAGCTCAGCGGAGAAAGCTGGGGGAAAGTGGGCAATGCTAAGCTTTTGGGGCGCA	2512
Db	2504	AGAAACAGCTCAGCGGAGAAAGCTGGGGGAAAGTGGGCAATGCTAAGCTTTTGGGGCGCA	2563
Qy	2513	TGGAAATCAATTGAGGTCTCTGAGAAAGAAAGACCTGTGACTTCTATAGACAAATTTT	2572
Db	2564	TGGAAATCAATTGAGGTCTCTGAGAAAGAAAGACCTGTGACTTCTATAGACAA -TTTTT	2622
Qy	2573	TTTTCTGTGTCACAAAAAATTCCTGTAAATCTGAAATATATATATGATCATACATATA	2632
Db	2623	TTTTCTGTGTCACAAAAAATTCCTGTAAATCTGAAATATATATATGATCATACATATA	2682
Qy	2633	TATTTTGGAAATGAGAGTATGTGTAAAGCAACAGTGGATCAACCCAGTTGTTACT	2692
Db	2683	TATTTTGGAAATGAGAGTATGTGTAAAGCAACAGTGGATCAACCCAGTTGTTACT	2742
Qy	2693	CTCTTAACATCTGCAATTTGAGAGATCACTAATACCTCTCTCA CAAAAATGGAAGGCA	2752
Db	2743	CTCTTAACATCTGCAATTTGAGAGATCACTAATACCTCTCTCA CAAAAATGGAAGGCA	2802
Qy	2753	GATGCTAGAAATCCCCCTTGA CGGAGGAAAAACATTTATTCAGTGAATTAACATCTTC	2812
Db	2803	GATGCTAGAAATCCCCCTTGA CGGAGGAAAAACATTTATTCAGTGAATTAACATCTTC	2862
Qy	2813	TTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTGGAGACAAAAATCCCTCACTCAATTTTCAC	2872
Db	2863	TTGTTCTTAAAAAAGCAAGTGTCTTTGGTGTGGAGACAAAAATCCCTCACTCAATTTTCAC	2922
Qy	2873	GTGTGCTACTAAGAATCTCAATATATAGTCTTTGTCCGAGCCCTTCCATAGTACACTT	2932
Db	2923	GTGTGCTACTAAGAATCTCAATATATAGTCTTTGTCCGAGCCCTTCCATAGTACACTT	2982
Qy	2933	TAGCGCTGAGACTGAGCAGCTTGGGGGTCAAGTAGAGTAACCTGTTTGGGACAGAGCC	2992
Db	2983	TAGCGCTGAGACTGAGCAGCTTGGGGGTCAAGTAGAGTAACCTGTTTGGGACAGAGCC	3042
Qy	2993	TAGTGTAAATCCCAAGAGAAATGATTCCTATTCAAAGCTGATTCA CAAACCCAGCTCACC	3052
Db	3043	TAGTGTAAATCCCAAGAGAAATGATTCCTATTCAAAGCTGATTCA CAAACCCAGCTCACC	3102
Qy	3053	TGACAGCCGAGGGACAGAGCATCACTGTGTCGAGCGAACATTAAGGGGCTTGGCCAAAG	3112
Db	3103	TGACAGCCGAGGGACAGAGCATCACTGTGTGTCGAGCGAACATTAAGGGGCTTGGCCAAAG	3162
Qy	3113	TCTACCTTTAGGCAAAACCCAGTACCTTCAGCAGAGAAAGTCCGGGCTTTGACCACTACAT	3172
Db	3163	TCTACCTTTAGGCAAAACCCAGTACCTTCAGCAGAGAAAGTCCGGGCTTTGACCACTACAT	3222
Qy	3173	ATCTGCTAGCCCAATTTCTAGGGCAATGTGTAATGTGATAGTACCTATGATCAACTTTTCAGA	3232
Db	3223	ATCTGCTAGCCCAATTTCTAGGGCAATGTGTAATGTGATAGTACCTATGATCAACTTTTCAGA	3282
Qy	3233	CCAAATCAAACTGTCTATGACAAAAATCCCTGTGGGCTAGATGAGAGTAATTTTTTTTTT	3292
Db	3283	CCAAATCAAACTGTCTATGACAAAAATCCCTGTGGGCTAGATGAGAGTAATTTTTTTTTT	3342
Qy	3293	CTTCTGAGCTTTATGAAAGAGAGGAAACTGTCTAGATTCACTGTAACCAACAGAAACC	3352

Db	3343	CTTCTCAGCTTTATGAAAGAAAGGAAACCTGTCATGGAATTCACTGAAACAACAGAAAC	3402
Qy	3353	TGGCAACATCAGCATTTTAAGCTTAAGGTTGGAGGCTAACGAGCTACCTCCCTTTGTA	3412
Db	3403	TGGCAACATCAGCATTTTAAGCTTAAGGTTGGAGGCTAACGAGCTACCTCCCTTTGTA	3462
Qy	3413	AATCAAAAGAAATGGTTTAAATGGGATGTGCATCCTTTAAATAAAGATGAACCTGGTTTC	3472
Db	3463	AATCAAGAAATGTTTAAATGGGATGTGCATCCTTTAAATAAAGATGAACCTGGTTTC	3522
Qy	3473	AAGCCAAATGTGAATTTATTTGGTTGGTACAGACGACGACCTTCAAAATCTCAGC	3532
Db	3523	AAGCCAAATGTGAATTTATTTGGTTGGTACAGACGACGACCTTCAAAATCTCAGC	3582
Qy	3533	CAAAAGCAATGTTTTTGGCCCTTTCTGCTTCACTGCATGATACAGTTGGTAAATGTAAAT	3592
Db	3583	CAAAAGCAATGTTTTTGGCCCTTTCTGCTTCACTGCATGATACAGTTGGTAAATGTAAAT	3642
Qy	3593	AATATGCGAATTTTATAGAGAAACCTTCCTGGGAGGTAATATATAGGAAAGTTAAGAA	3652
Db	3643	AATATGCGAATTTTATAGAGAAACCTTCCTGGGAGGTAATATATAGGAAAGTTAAGAA	3702
Qy	3653	GGTACAAATTCGCTAGAGAGAAAGCAGAAACCTGTTTCTTATGGCTTTTATCCCTCGG	3712
Db	3703	GGTACAAATTCGCTAGAGAGAAAGCAGAAACCTGTTTCTTATGGCTTTTATCCCTCGG	3762
Qy	3713	CATGCGATGGGGCTGATGTTTCTATGATTCGCTCAGACTTTCACATTTACTAGGCT	3772
Db	3763	CATGCGATGGGGCTGATGTTTCTATGATTCGCTCAGACTTTCACATTTACTAGGCT	3822
Qy	3773	GAGAGAGGCTTTTAAATGAGAAAGAAATATTCAGAAATAAACGGTTTGAAAGCTGAGAA	3832
Db	3823	GAGAGAGGCTTTTAAATGAGAAAGAAATATTCAGAAATAAACGGTTTGAAAGCTGAGAA	3882
Qy	3833	CCATTTGAGTTTGAATCAGTTGTGAATATAGATGCAAAAGCCATGGCCAACTGTTTGGAA	3892
Db	3883	CCATTTGAGTTTGAATCAGTTGTGAATATAGATGCAAAAGCCATGGCCAACTGTTTGGAA	3942
Qy	3893	ACGCTGGCCGGCGTGTCTTCAGTGGAAAAAGCAAAATCAAAATGAGACGAGCAAAAGGG	3952
Db	3943	ACGCTGGCCGGCGTGTCTTCAGTGGAAAAAGCAAAATCAAAATGAGACGAGCAAAAGGG	4002
Qy	3953	CGTCCCTCAGTCCCTCAACCTTCAATTCATCTGTATGGAATGGGTCTGGACCTTAACATAG	4012
Db	4003	CGTCCCTCAGTCCCTCAACCTTCAATTCATCTGTATGGAATGGGTCTGGACCTTAACATAG	4062
Qy	4013	AGGTCATGTGAACAAGATAGTAGCAGATTTGGCTTCAAAACATCCCTCGGCTTAGATT	4072
Db	4063	AGGTCATGTGAACAAGATAGTAGCAGATTTGGCTTCAAAACATCCCTCGGCTTAGATT	4122
Qy	4073	TATCAGCTCACAATGTGGGTCTCTTTTGAAGCCTTAATTCACAAACAGCAGCTTTTGGGG	4132
Db	4123	TATCAGCTCACAATGTGGGTCTCTTTTGAAGCCTTAATTCACAAACAGCAGCTTTTGGGG	4182
Qy	4133	GTTGGGGCTGGGCGGGGTGTGTACTATGTTCTTCCCTCCTGTAAATGTGTCAGTTGCTG	4192
Db	4183	GTTGGGGCTGGGCGGGGTGTGTACTATGTTCTTCCCTCCTGTAAATGTGTCAGTTGCTG	4242
Qy	4193	CCTCGATCTCAGGTTTTTCTGTGTTTTGAGAAATGACAGTTTTTTTGAACAGGATGTG	4252
Db	4243	CCTCGATCTCAGGTTTTTCTGTGTTTTGAGAAATGACAGTTTTTTTGAACAGGATGTG	4302
Qy	4253	ACTTCATGTTTTCTATGTGTACTTTTAAACCAAGACAGATGATATGATCTCAACACAGA	4312
Db	4303	ACTTCATGTTTTCTATGTGTACTTTTAAACCAAGACAGATGATATGATCTCAACACAGA	4362
Qy	4313	CCGACTTTGGTTATGGGGATGATGACCCGCAACGACTCAGTTGGTGCACAAATTAATGT	4372
Db	4363	CCGACTTTGGTTATGGGGATGATGACCCGCAACGACTCAGTTGGTGCACAAATTAATGT	4422
Qy	4373	GCTATGATGGGGGTGAAGTGAAGCAGAAAGGGTCAAGCCGCAATGTTATGATCTGGG	4432
Db	4423	GCTATGATGGGGGTGAAGTGAAGCAGAAAGGGTCAAGCCGCAATGTTATGATCTGGG	4482

OY	4453	AAAAGCGTGGCAACGATTTGAGTTAGTTTTAGTATACATGGAATCTTTATCAGAC	44952
Db	4443	AAAGCGTGGTCAACGATTTGAGTTAGTTTTAGTATACATGGAATCTTTAATCAGAC	4542
OY	4493	ATTCTCAAGTTTCAACAGTAGTTTTGATGTATATACACACACCAATGTGTACA	4552
Db	4543	ATTCTCAAGTTTCAACAGTAGTTTTGATGTATATATACACACACCAATGTGTACA	4602
OY	4553	GTTACCACTTCCAGAGTGTGTATGCCCCAAAACATGTTTAAGAAAGGAAGATAGC	4612
Db	4603	GTTACCACTTCCAGAGTGTGTATGCCCCAAAACATGTTTAAGAAAGGAAGATAGC	4662
OY	4613	TCCTTGTCAACAGATGTTTCAAGAGGTTTGCGGCACTTGTTTTATATAGCTTCTGTCA	4672
Db	4663	TCCTTGTCAACAGATGTTTCAAGAGGTTTGCGGCACTTGTTTTATATAGCTTCTGTCA	4722
OY	4673	TAGGGCTTCTCTTGCCCAATGCTCCCTTCTCTTGGAACGTGATGTATCAATCCTAC	4732
Db	4723	TAGGGCTTCTCTTGCCCAATGCTCCCTTCTCTTGGAACGTGATGTATCAATCCTAC	4782
OY	4733	AGCCTTAGTGTCTGGTTCACATAGTGTGATATACAGTCTTGGAATGGAACGTGCCGTG	4792
Db	4783	AGCCTTAGTGTCTGGTTCACATAGTGTGATATACAGTCTTGGAATGGAACGTGCCGTG	4842
OY	4793	GCGAAGGGGTGGCCTCGAGGCAAGGCTCTGAGACTGTTGAGTCTTTAAGTGGGGTGG	4852
Db	4843	GCGAAGGGGTGGCCTCGAGGCAAGGCTCTGAGACTGTTGAGTCTTTAAGTGGGGTGG	4902
OY	4853	TGGCTGG 4859	
Db	4903	TGGCTGG 4909	

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RESULT 12
US-10-357-930-27145
; Sequence 27145, Application US/10357930
; Publication NO. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357, 930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785, 276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183, 319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189, 862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207, 454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211, 314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219, 007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255, 281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 27145
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5144..5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-27145

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Query Match	81.0%	Score 4413;	DB 18;	Length 5145;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 4683; Conservative	0;	Mismatches 3;	Indels 1;	Gaps 1

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Db	224	GCTTCACTCCAGGTAAAGCTGTTGGAGCCCGGAGCAAAAGGTAAAGATGAATGAATG	283
QY	233	CGCTGGCTGCTCAAAAGCATCTTTTGTTGTGGAAATGTTATTCAGTCATCTCTTAATGA	292
Db	284	CGCTGGCTGCTCAAAAGCATCTTTTGTTGTGGAAATGTTATTCAGTCATCTCTTAATGA	343
QY	293	ATCAAAATGTAGGGGCTGCTTTGTGGAGAGGAGTCCTTTGGAAAGCAATCAACGGGAAA	352
Db	344	ATCAAAATGTAGGGGCTGCTTTGTGGAGAGGAGTCCTTTGGAAAGCAATCAACGGGAAA	403
QY	353	GAGAAAGAGACATTCACCTTGGAGGGGCTCTTGCTGAAATATGGGTTTAACTCTCTTTGGC	412
Db	404	GAGAAAGAGACATTCACCTTGGAGGGGCTCTTGCTGAAATATGGGTTTAACTCTCTTTGGC	463
QY	413	AGTCAACAACAGCCTGACCTTATACACTTTTATGATCAATGTAGAGTGCTGAGCCTTTGAGC	472
Db	464	AGTCAACAACAGCCTGACCTTATACACTTTTATGATCAATGTAGAGTGCTGAGCCTTTGAGC	523
QY	473	AACACCAACATTATCAATCATCGTGGGCAAAATTAAGAAAGAGGTGGGAAAAGAGACATTATG	532
Db	524	AACACCAACATTATCAATCATCGTGGGCAAAATTAAGAAAGAGGTGGGAAAAGAGACATTATG	583
QY	533	TTGTCAATGGCCATGAGAGATGATTTGGAACTCAAAATTTGTACTGAGAGTTGGTGCTCTGC	592
Db	584	TTGTCAATGGCCATGAGAGATGATTTGGAACTCAAAATTTGTACTGAGAGTTGGTGCTCTGC	643
QY	593	TGGAAGGTGGAACGGAAAAAGTGCTCTTAATTGATAGCCGCGCCATTGTGTGAATACAAAT	652
Db	644	TGGAAGGTGGAACGGAAAAAGTGCTCTTAATTGATAGCCGCGCCATTGTGTGAATACAAAT	703
QY	653	CATCCCAACATTTTGGAGGCCATTATATCACTGCTCCAACTTATGAAAGGGAAGGTGTC	712
Db	704	CATCCCAACATTTTGGAGGCCATTATATCACTGCTCCAACTTATGAAAGGGAAGGTGTC	763
QY	713	AACAGGACAAAGTGTATTAATCAGAGGCTCATCCAGATTCAGACGAAACATTAAGTTTGAACA	772
Db	764	AACAGGACAAAGTGTATTAATCAGAGGCTCATCCAGATTCAGACGAAACATTAAGTTTGAACA	823
QY	773	TTGATTTGAGTCAGAAAGGTGTGATTAATCGATCAAAAGCTCCCAAGATGTTCCTCTCTCT	832
Db	824	TTGATTTGAGTCAGAAAGGTGTGATTAATCGATCAAAAGCTCCCAAGATGTTCCTCTCTCT	883
QY	833	CTTCAAGCTGTTTCTCACTGTGTAATCTTCGGGGTAAATCGGAAAGAGCTTCAACTCTGTGTC	892
Db	884	CTTCAAGCTGTTTCTCACTGTGTAATCTTCGGGGTAAATCGGAAAGAGCTTCAACTCTGTGTC	943
QY	893	ACCTGCTTGCAGGTGGGTTGCTGAGTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGAAA	952
Db	944	ACCTGCTTGCAGGTGGGTTGCTGAGTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGAAA	1003
QY	953	AATCAACTCTAGTCCCTACCTGCAATTTCTAGCCTTGCTTACCTGTTGCCAATCTGGGC	1012
Db	1004	AATCAACTCTAGTCCCTACCTGCAATTTCTAGCCTTGCTTACCTGTTGCCAATCTGGGC	1063
QY	1013	CAACCCGAAATCTTCCCAATCTTATATCTTGGCTGACGCGAGATGTCCTCAACAGAGAGC	1072
Db	1064	CAACCCGAAATCTTCCCAATCTTATATCTTGGCTGACGCGAGATGTCCTCAACAGAGAGC	1123
QY	1073	TGATACAGACAAATGGGATTTGGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCTG	1132
Db	1124	TGATACAGACAAATGGGATTTGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCTG	1183
QY	1133	ACTTTATTCCTCCGAGTCTCATTTCTCTGGGTGCTGCTGGAATGACAGCTTTTGTGAGAAA	1192
Db	1184	ACTTTATTCCTCCGAGTCTCATTTCTCTGGGTGCTGCTGGAATGACAGCTTTTGTGAGAAA	1243

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Db 1544 CAAATGAACCTGTCCCTGTGTCTCAGAGGGTGGACAGAAAGCAGAGACGCCCTCAGTC 1603
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Db 1604 CACCCGTGCCCCACTCTGTCTACTCTCAGAGCAGCAGAGCAAAAAGCCCTGTGATCCGCCA 1663
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Db 1664 GCGTGCCACGCGTCCAGCAGCTGAGCCGCTCGTGTAGAGGACAGCCCGCTGTGACAGG 1723
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Db 1844 GCTTCTCTCATCAGAAAGTGTCTTGGAACTACTACAAACCTTCCACTACTCTGAGTGGGA 1903
QY 1853 CCAAAAGCTATGCCAGATTCTCCCTGTTCAAGAACTATTCGAGAGCATCTCCGAAACCA 1912
Db 1904 CCAAAAGCTATGCCAGATTCTCCCTGTTCAAGAACTATTCGAGAGCATCTCCGAAACCA 1963
QY 1913 GTCTGATTAAGGAGAGCAGCATCCCAAGAAAGCTGACAGCCGCAAGGCTTCAACA 1972
Db 1964 GTCTGATTAAGGAGAGCAGCATCCCAAGAAAGCTGACAGCCGCAAGGCTTCAACA 2023
QY 1973 GCCAGAGCAAGGATTTGATTCGCTCAGAACCAAGCAGAGTGGACCGCCAGAGGTCCC 2032
Db 2024 GCCAGAGCAAGGATTTGATTCGCTCAGAACCAAGCAGAGTGGACCGCCAGAGGTCCC 2083
QY 2033 TTTTATCTCCACTGATGAGAGTGGAGGCTGGAGAGCAATTTACACACAGCTTCTTT 2092
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QY 2213 TTGGCA CAGAGTCTCTCACTTCTACTGTGCTCAGGCACTTACGAGAGAGGAGGAGGCTT 2272
Db 2264 TTGGCA CAGAGTCTCTCACTTCTACTGTGCTCAGGCACTTACGAGAGAGGAGGAGGCTT 2323
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Db 2324 ACTCTGCTTACAGCTGACGCGAGCTGCCACTTTCGAGAGCAAAAGTCTATTTCTGTGGCA 2383
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QY 2453 AGAAGAGTCAAGGAGAGAGCTGGGAGAAAGTGGGCACTGCTAGCTTTTGGGAGCA 2512
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QY 2513 TGAATATCATTGAGTCTCTGAGAGAAAGACATTTGTGACTTATAGACATTTT 2572
Db 2564 TGAATATCATTGAGTCTCTGAGAGAAAGACATTTGTGACTTATAGACAA -TTTTT 2622
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Db 2623 TTTTCTGTTCACAAAAAATTCCTGTAAATCTGAAATATATATGTAATACATATA 2682
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QY 2693 CTCTTAATCTGCTATTTGAGAGATCAGCTAATATCTTCTCAACAAAAATGAGAGGCA 2752
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QY 2753 GATGCTGAATCCCCCTAGACGAGAGAAACATTTTATGAGTAATTAACATCTC 2812
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Db 2923 GTTGTGTAATCTAGAAATCTCAAAATATATAGTCTTTGTCCGACCTTCCATATGACCT 2982
QY 2933 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTATGAGACCTGTTAGAGAGAGGCC 2992
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Db 3343 CTTCACGCTTTATGAGAGAGAGAACTGTATGAGATTCAGCTGACCAAGAAC 3402
QY 3353 TGGCAACATCAAGATTTAAGTATGAGTGGAGGCTTACAGCTTACTCTCTTTGTA 3412

Db	3403	GGCAACATCAGATTTAACGTAAAGTTGGAGGCTAACGATCACTCCTCTTTGTA	3465
Qy	3413	AATCAAGATGTTTAAATGGAAATGTCAATCCTTTAATAAAGATGAATTGGTTTC	3472
Db	3463	AATCAAGAAATTGTTTAAATGGGATTTGTCAATCCTTTAATAAAGATGAATTGGTTTC	3522
Qy	3473	AAGCAAAATGGAATTTATTTGGGTTGGATGAGAGACAGACACTTCAAAATTCAGC	3533
Db	3523	AAGCAAAATGGAATTTATTTGGGTTGGATGAGAGACAGACACTTCAAAATTCAGC	3583
Qy	3533	CAAAAGCATGTTTTTGGCCTTCTGCTTCACTGATGGAATCACTTGGTAAATGTAT	3592
Db	3583	CAAAAGCATGTTTTTGGCCTTCTGCTTCACTGATGGAATCACTTGGTAAATGTAT	3642
Qy	3593	AATATGGCAGAAATTTTATATGAAACCTTCTAGGAGGTAAATATATGGAAGATTAAGAA	3653
Db	3643	AATATGGCAGAAATTTTATATGAAACCTTCTAGGAGGTAAATATATGGAAGATTAAGAA	3702
Qy	3653	GGTAACAAATTCGTGAGAGAAACAGAAACCTGTTTCTTATGGCTTTATCCCTCGG	3712
Db	3703	GGTAACAAATTCGTGAGAGAAACAGAAACCTGTTTCTTATGGCTTTATCCCTCGG	3762
Qy	3713	CATGCGATGGGCTGATGTTTCTATGATTCCTCAGACCTTTCACATTTACTAGTGGGCT	3772
Db	3763	CATGCGATGGGCTGATGTTTCTATGATTCCTCAGACCTTTCACATTTACTAGTGGGCT	3822
Qy	3773	GAGAGAGCTTTAGTAGAGAAAGAAATATTCAGAAATMAAACGGTTGAGAAAGCTGAGAGA	3832
Db	3823	GAGAGAGCTTTAGTAGAGAAAGAAATATTCAGAAATMAAACGGTTGAGAAAGCTGAGAGA	3882
Qy	3833	CCATTGAAGTTTGATCAGTTGTGAATAGATGCAAAAGCCATGCGCACTGTTTTGAA	3892
Db	3883	CCATTGAAGTTTGATCAGTTGTGAATAGATGCAAAAGCCATGCGCACTGTTTTGAA	3942
Qy	3893	ACCGTGGCGGGGTCTTCAGTGGAAAAAGCAATCAAAATGAGCGAGCAAAAGGGG	3952
Db	3943	ACCGTGGCGGGGTCTTCAGTGGAAAAAGCAATCAAAATGAGCGAGCAAAAGGGG	4002
Qy	3953	GGTCCCTCAGTCTTCAACCTAACATCACTGATGGAATCGGTCTTGGCAGCTGAACATAGG	4012
Db	4003	GGTCCCTCAGTCTTCAACCTAACATCACTGATGGAATCGGTCTTGGCAGCTGAACATAGG	4062
Qy	4013	AGGTCACTGGAACAGATGATATGTGCAGATTTGGCTTCAACATCTCTGCTGTGAGTTT	4072
Db	4063	AGGTCACTGGAACAGATGATATGTGCAGATTTGGCTTCAACATCTCTGCTGTGAGTTT	4122
Qy	4073	TATCAGCTACAAATGTGGGTCTCTTTGAAGCTTAATTCACACAGACGTTTTTGGGG	4132
Db	4123	TATCAGCTACAAATGTGGGTCTCTTTGAAGCTTAATTCACACAGACGTTTTTGGGG	4182
Qy	4133	GTGGGGCTGGGCGGGGTGTGTCAATGTTCTTTCCTTCTGTGAAGTGTGCGTAAATGTG	4192
Db	4183	GTGGGGCTGGGCGGGGTGTGTCAATGTTCTTTCCTTCTGTGAAGTGTGCGTAAATGTG	4242
Qy	4193	CCTCGTATCTCAGGTTTTTCTCTGTTTTTGAAGAAATGACAGATTTTTTGAACAGAGATG	4252
Db	4243	CCTCGTATCTCAGGTTTTTCTCTGTTTTTGAAGAAATGACAGATTTTTTGAACAGAGATG	4302
Qy	4253	ACTTCATGTTTCTATGTGTGACTTTAAACACGACACAGATGATATGATCTCACAACGA	4312
Db	4303	ACTTCATGTTTCTATGTGTGACTTTAAACACGACACAGATGATATGATCTCACAACGA	4362
Qy	4313	CCGACTTGATATGAGGAGATGATAGCCGCAACGACTCAGTAGTTGTCACAAATTAATGT	4372
Db	4363	CCGACTTGATATGAGGAGATGATAGCCGCAACGACTCAGTAGTTGTCACAAATTAATGT	4422
Qy	4373	GCTATGATGGGTTGTAAGTGAAGGACAGAAAGGCTCAGCCGCAATTTGTTATGATACCTGGG	4432
Db	4423	GCTATGATGGGTTGTAAGTGAAGGACAGAAAGGCTCAGCCGCAATTTGTTATGATACCTGGG	4482
Qy	4433	AAAGTGTGTGTCAACGATTTGATTTAGTTTAAATATACATTAATCTTAAATCAAC	4492
Db	4483	AAAGTGTGTGTCAACGATTTGATTTAGTTTAAATATACATTAATCTTAAATCAAC	4542

OY	4433	ATTTCACGTTTCCACAGTAGTCTTTTGAATGTATGTACACACACACAAATGTGTAA	4555
Db	4543	ATTTCACAGTTTCCACAGTAGTCTTTTGAATGTATGTACACACACAAATGTGTAA	4603
OY	4553	GTTTCACCACTTCCAGAGTGTGGTTCATGCGCCAAACATGTTTAAAGAAAGCACTAGC	4613
Db	4603	GTTTCACCACTTCCAGAGTGTGGTTCATGCGCCAAACATGTTTAAAGAAAGCACTAGC	4663
OY	4613	TCCTTGTCTAACGATGTTTCCAGAGGTTTGGGGCACTTGTTTAAATGAGCTTGTCAAT	4722
Db	4663	TCCTTGTCTAACGATGTTTCCAGAGGTTTGGGGCACTTGTTTAAATGAGCTTGTCAAT	4733
OY	4673	TAGGGCTCTCTTGGCCATNGGCCCCCTTCCTTGGAACTGAGATGTATCATCTCAG	4733
Db	4723	TAGGGCTCTCTTGGCCATNGGCCCCCTTCCTTGGAACTGAGATGTATCATCTCAG	4783
OY	4733	AGCCTTAGTGTGTGTTACTAGTGTACATATACATTCAGTCTTGGAAATGCAGACTCCGTG	4793
Db	4783	AGCCTTAGTGTGTGTTACTAGTGTACATATACATTCAGTCTTGGAAATGCAGACTCCGTG	4843
OY	4853	TGGCTGG 4859	4855
Db	4903	TGGCTGG 4909	4903
RESULT 13			
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APPLICANT: Schlegel, Robert			
APPLICANT: Endesleg, Wilson			
APPLICANT: Monahan, John			
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NUMBER OF SEQ ID NOS: 62232			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 27149			
LENGTH: 5145			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: 1, 5144, 5145			
OTHER INFORMATION: n = A,T,C or G			
US-10-357-930-27149			
Query Match	81.0%	Score 4413;	DB 18; Length 5145;
Best Local Similarity	99.9%	Pred. No. 0;	
Matches 4683; Conservative	0;	Mismatches	3; Indels 1; Gaps 1;

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QY 293 ATCAATGTGAGGGGCTGCTTGTGAGCGGAGCTTGTGAGAGAGCATCAACGGGAAA 352
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QY 1913 GTCCTGATTAAGAGAGAGACAGATCCCAAGAGCTGAGACCCGCAAGCTTACAGACA 1972
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Oy 4373 GCTATGATGGGCTGTAAGTGAAGGACAGAGAGGCTCAGCCGACTTGTATGATCTGGG 4432
Db 4423 GCTATGATGGGCTGTAAGTGAAGGACAGAGAGGCTCAGCCGACTTGTATGATCTGGG 4482
Oy 4433 AAAAGTGTGTCACAGATTGATGATTTTGAATTAATGATGAATCTTAAATCAAGC 4492
Db 4483 AAAAGTGTGTCACAGATTGATGATTTTGAATTAATGATGAATCTTAAATCAAGC 4542
Oy 4493 ATTCTCAAGTTTCAACAGATGTTTGTATGTTATGTAACACACACCAATGTTGAACA 4552
Db 4543 ATTCTCAAGTTTCAACAGATGTTTGTATGTTATGTAACACACCAATGTTGAACA 4602
|||||

OY	4553	GTTCACCACTTCCAAAGTGTGTCAATGCCAAACAATGTTTAAAGAAAGAAAGCATAGC	4612
Db	4603	GTTCACCACTTCCAAAGTGTGTCAATGCCAAACAATGTTTAAAGAAAGAAAGCATAGC	4662
OY	4613	TCCTTGCTAACGATGTTTCAGAGGTTTGAGCACTTGTTTATAGCTTCCTGTCATT	4672
Db	4663	TCCTTGCTAACGATGTTTCAGAGGTTTGAGCACTTGTTTATAGCTTCCTGTCATT	4722
OY	4673	TAGGAGCTTCCTTGAGCCATAGGCCCCCTCCTTGCGAACTGTGATGTAGTCAACTCTAC	4732
Db	4723	TAGGAGCTTCCTTGAGCCATAGGCCCCCTCCTTGCGAACTGTGATGTAGTCAACTCTAC	4782
OY	4733	AGCCTTATGTGCTGTTCACTAATGTCCAGATATCATGTTCTTGAAATCGAAGCTCCGTG	4792
Db	4783	AGCCTTATGTGCTGTTCACTAATGTCCAGATATCATGTTCTTGAAATCGAAGCTCCGTG	4842
OY	4793	GCGAAGAGGATGAGCCTCGAGGCGAGGCTGTGAGCTGTGGAATGCTTTAGTGGGGTGG	4852
Db	4843	GCGAAGAGGATGAGCCTCGAGGCGAGGCTGTGAGCTGTGGAATGCTTTAGTGGGGTGG	4902
OY	4853	TGGCTGG 4859	
Db	4903	TGGCTGG 4909	

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RESULT 14
US-10-357-930-28675
/ Sequence 28675, Application US/10357930
/ Publication No. US20040259086A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Endege, Wilson
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ TITLE OF INVENTION: HUMAN PROSTATE CANCER
/ FILE REFERENCE: MRI-007HCN
/ CURRENT APPLICATION NUMBER: US/10/357, 930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785, 276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183, 319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189, 862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207, 454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211, 314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219, 007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255, 281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 28675
/ LENGTH: 5145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: misc feature
/ LOCATION: 1, 5144, 5145
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28675

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Query Match	81.0%;	Score 4413;	DB 18;	Length 5145;
Best Local Similarity:	88.0%			

Best local similarity 99.9%; Pred. NO. 0;
Matches 4693; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Oy 173 GCTTTCAGTCCAGTGAAGCTGTGGAGCGCGGAGCAGTAAGTAAAGATGATCTAATG 232
 Db 224 GCTTTCAGTCCAGTGAAGCTGTGGAGCGCGGAGCAGTAAGTAAAGATGATCTAATG 283

QY	233	CGCTGGCTGCTCCAAAGCATTCTTTTGTGGAAATGGTATTTCAGTCACTCTTTATGA	292
Db	284	CGCTGGCTGCTCCAAAGCATTCTTTTGTGGAAATGGTATTTCAGTCACTCTTTATGA	343
QY	293	ATCAAAATGAGGGGCTGCTTTGTGGACGAGTCTTTGCAAGACATCAACGGGAAA	352
Db	344	ATCAAAATGAGGGGCTGCTTTGTGGACGAGTCTTTGCAAGACATCAACGGGAAA	403
QY	353	GAGAAAGAACATTCCTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCTTTGCG	412
Db	404	GAGAAAGAACATTCCTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCTTTGCG	463
QY	413	AGTACACACACGCTGACCTCAATCACTTTTATGTAACAATGAGTGGCTGAGCTTTGAGC	472
Db	464	AGTACACACACGCTGACCTCAATCACTTTTATGTAACAATGAGTGGCTGAGCTTTGAGC	523
QY	473	ACACCAACCATTCATCATCTGTGGCAAAATTTAAAGAGAGTGGGAAAAGAGCATTAATG	532
Db	524	ACACCAACCATTCATCATCTGTGGCAAAATTTAAAGAGAGTGGGAAAAGAGCATTAATG	583
QY	533	TTGTCAATGGCCCATAGAGATGATTTGGAACTCAAAATGTTAACTGAGAGTTGGTCTTGC	592
Db	584	TTGTCAATGGCCCATAGAGATGATTTGGAACTCAAAATGTTAACTGAGAGTTGGTCTTGC	643
QY	593	TGGAAATGGGAAACGAAAAAGTGCCTGCTAAATGTAGACGGGCAATTTGTGGAAATCAATA	652
Db	644	TGGAAATGGGAAACGAAAAAGTGCCTGCTAAATGTAGACGGGCAATTTGTGGAAATCAATA	703
QY	653	CATCCCACTTTTGGAGACCATTAATCAACTGCTCCAGCTTAATGAAGGAAAGTTGC	712
Db	704	CATCCCACTTTTGGAGACCATTAATCAACTGCTCCAGCTTAATGAAGGAAAGTTGC	763
QY	713	AACAGACAAAGTGTAAATTAACAGAGCTATCCAGCACTTACGGCAACATTAAGGTGACA	772
Db	764	AACAGACAAAGTGTAAATTAACAGAGCTATCCAGCACTTACGGCAACATTAAGGTGACA	823
QY	773	TTGATTGCAATGACAGAGTTGATTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCT	832
Db	824	TTGATTGCAATGACAGAGTTGATTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCT	883
QY	833	CTTCAGACTGTTTTCTCACTGTGTAATCTTGGGTAATCGAGAAAGAATTCAACTCTGTTC	892
Db	884	CTTCAGACTGTTTTCTCACTGTGTAATCTTGGGTAATCGAGAAAGAATTCAACTCTGTTC	943
QY	893	ACCTGCTTGACAGTGGGTTTGTCTAGATCTCTCGTTTCTCGGCTCTGTGAAGAAA	952
Db	944	ACCTGCTTGACAGTGGGTTTGTCTAGATCTCTCGTTTCTCGGCTCTGTGAAGAAA	1003
QY	953	AATCACTCTAATGCCATCTGCATTTCTCAGCCTTGCTTAACCTGTTGCCAACATTGGGC	1012
Db	1004	AATCACTCTAATGCCATCTGCATTTCTCAGCCTTGCTTAACCTGTTGCCAACATTGGGC	1063
QY	1013	CAACCCGAATCTTCCCAATCTTTAATCTTGGCTGCGACGAGATGTCTCAACAAAGAGC	1072
Db	1064	CAACCCGAATCTTCCCAATCTTTAATCTTGGCTGCGACGAGATGTCTCAACAAAGAGC	1123
QY	1073	TGATACAGCAGATGGGATTTGTATGTGTAAATGCGACATTAACCTGTCCAAAGCTG	1132
Db	1124	TGATACAGCAGATGGGATTTGTATGTGTAAATGCGACATTAACCTGTCCAAAGCTG	1183
QY	1133	ACCTTAATCCCGAGTCAATTTCTGTGGTGGCTGTGGAATGACAGTTTGTGAGAAAA	1192
Db	1184	ACCTTAATCCCGAGTCAATTTCTGTGGTGGCTGTGGAATGACAGTTTGTGAGAAAA	1243
QY	1193	TTTTGCGGTGTTGACAAATCAATGATTTCAATTGAGAAAGCAAAAGCTCCAAATGAT	1252
Db	1244	TTTTGCGGTGTTGACAAATCAATGATTTCAATTGAGAAAGCAAAAGCTCCAAATGAT	1303
QY	1253	GTGTTCTAATGCACTGTTTAATGCTGGGATCTCCGCTCCGCAACCATGTGCTTAC	1312
Db	1304	GTGTTCTAATGCACTGTTTAATGCTGGGATCTCCGCTCCGCAACCATGTGCTTAC	1363

1313 TCATGAAAGAGATGAGCATGTCTTTAGTAGTAAGCTTACAGATTTGTGAAAGAAAAAGAC 1372
1364 TCATGAAAGAGATGAGCATGTCTTTAGTAGTAAGCTTACAGATTTGTGAAAGAAAAAGAC 1423
1373 CTACATATATCTCCAAATTTCAATTTTCTGGGCAACTCTGAGCATATGAGAAAGATTA 1432
1424 CTACATATATCTCCAAATTTCAATTTTCTGGGCAACTCTGAGCATATGAGAAAGATTA 1483
1433 AGAACCAAGCTGAGCATCAGGGCCAAAGAGCAATCTCAAGCTGTGACCTGAGAAAGC 1492
1484 AGAACCAAGCTGAGCATCAGGGCCAAAGAGCAATCTCAAGCTGTGACCTGAGAAAGC 1543
1493 CAATGAACTGTCTCTGTCTGAGAGGTGAGCAGAAAAGCAGAGCCCTCAGTC 1552
1544 CAATGAACTGTCTCTGTCTGAGAGGTGAGCAGAAAAGCAGAGCCCTCAGTC 1603
1553 CAACCTGTGCGGACCTGTCTACCTTACAGAGGACAGCAAAAGCCCTGACCTCCGCA 1612
1604 CAACCTGTGCGGACCTGTCTACCTTACAGAGGACAGCAAAAGCCCTGACCTCCGCA 1663
1613 GCGTGCCCAAGGCGTCCAGCCGTCAGCCGTCGTTTGAAGGACAGCCCGCTGATCAGG 1672
1664 GCGTGCCCAAGGCGTCCAGCCGTCAGCCGTCGTTTGAAGGACAGCCCGCTGATCAGG 1723
1673 CGCTCAGTGGGCTGACCTGTCCGAGACAGGCTGAAAGACAGCAATAGCTCAAGCTT 1732
1724 CGCTCAGTGGGCTGACCTGTCCGAGACAGGCTGAAAGACAGCAATAGCTCAAGCTT 1783
1733 CCTTCTCTGTGATATCAATATCAATTTTCAAGCCAGACATGGACAGATCTTTACATG 1792
1784 CCTTCTCTGTGATATCAATATCAATTTTCAAGCCAGACATGGACAGATCTTTACATG 1843
1793 GCTTCTCTCATCAAGATGTTTGAATCTAACAACCTTCCACTCTCTGATGAGGGA 1852
1844 GCTTCTCTCATCAAGATGTTTGAATCTAACAACCTTCCACTCTCTGATGAGGGA 1903
1853 CCAACCAAGCTATGACAGTTCCTCCCTGTTCAGGAACTATCGAGAGACATCCCGAAACA 1912
1904 CCAACCAAGCTATGACAGTTCCTCCCTGTTCAGGAACTATCGAGAGACATCCCGAAACA 1963
1913 GTCTGATTAAGAGGAGCCAGACATCCCAAGAGCTGACACCGCCAGGCTTTACACA 1972
1964 GTCTGATTAAGAGGAGCCAGACATCCCAAGAGCTGACACCGCCAGGCTTTACACA 2023
1973 GCGAGAGAGAGGATTTGATTCGGTCAGAACCAAGAGAGTGGCACCCGCCAGAGGTCCC 2032
2024 GCGAGAGAGAGGATTTGATTCGGTCAGAACCAAGAGAGTGGCACCCGCCAGAGGTCCC 2083
2033 TTTTATCTCACTGATGAAAGTGGAGCGTGAAGCAATTAACAACAGCTTCTTT 2092
2084 TTTTATCTCACTGATGAAAGTGGAGCGTGAAGCAATTAACAACAGCTTCTTT 2143
2093 TCGGCTTTTCAACAGCAGACGACCTCAAGAAATCTGTGGCTTGAAGGCT 2152
2144 TCGGCTTTTCAACAGCAGCAGACCTCAAGAAATCTGTGGCTTGAAGGCT 2203
2153 GGCACCTGGGATATCTTGGCCCCCAGACCTTACCCCTTCTGACAGCAGCTGTAT 2212
2204 GGCACCTGGGATATCTTGGCCCCCAGACCTTACCCCTTCTGACAGCAGCTGTAT 2263
2213 TTGGCAGAGAGCTCACTTCTACTGTGCTCAGCCATCTAGGAGAGCAGTGGCAGT 2272
2264 TTGGCAGAGAGCTCACTTCTACTGTGCTCAGCCATCTAGGAGAGCAGTGGCAGT 2323
2273 ACTGTGCTTACAGCTGACGACGCTGACCTTGGGAGACCAAGTCTATCTGTGCGCA 2332
2324 ACTGTGCTTACAGCTGACGACGCTGACCTTGGGAGACCAAGTCTATCTGTGCGCA 2383
2333 GCGGCGAAGAGCAAGTGAAGAGTGAATGCGGCGGAGAGTGGAGATGAAGAGAGCCCT 2392
2384 GCGGCGAAGAGCAAGTGAAGAGTGAATGCGGCGGAGAGTGGAGATGAAGAGAGCCCT 2443
2393 TTGAAGAGAGTGAAGAGAGAGCTGCAAAATGGAATTTGAGAGAGACATCATGTGAG 2452

2444 TTGAAGAGAGTGAAGAGAGCTGCAAGAGCTGCAAAATGGAATTTGAGAGAGACATCATGTGAG 2503
2453 AGAACAGCTCACGGGAAGAGCTGGGGAAGAGGAGAGCTGAGCTTTCTGGGAGAGA 2512
2504 AGAACAGCTCACGGGAAGAGCTGGGGAAGAGGAGAGCTGAGCTTTCTGGGAGAGA 2563
2513 TGAAGATCATGAGGCTCTCTGAGAGAGAGACATTTGAGCTTCTATAGACAAATTTT 2572
2564 TGAAGATCATGAGGCTCTCTGAGAGAGAGACATTTGAGCTTCTATAGACAAATTTT 2622
2573 TTTTCTGTTCACAAAAAATTCCTGTAAATCTGAAATATATATATATGATACATATTA 2632
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2633 TATTTTGAAGAAATGAGAGCTATGTTGAAGAGCAAGGTGATCAACCCAGTTGTACT 2692
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2753 GATGTAGAAATCCCCCTTACAGAGAGAAACCAATTTTATTCAGTGAATTAACATCTTC 2812
2803 GATGTAGAAATCCCCCTTACAGAGAGAAACCAATTTTATTCAGTGAATTAACATCTTC 2862
2813 TTGTTCTTAAAAAGCAAGTGTCTTTGATGTTGAAGAGCAAAATTCCTCTACATTTTAC 2872
2863 TTGTTCTTAAAAAGCAAGTGTCTTTGATGTTGAAGAGCAAAATTCCTCTACATTTTAC 2922
2873 GTTGTGCTACTTGAAGATCTCAAAATTAATGATCTTTGTCCGAGCCCTTCATATGATCACT 2932
2923 GTTGTGCTACTTGAAGATCTCAAAATTAATGATCTTTGTCCGAGCCCTTCATATGATCACT 2982
2933 TAGGCTGAGACTGAGCCAGCTTGGGGGTCAAGTATGAGACCTGTTTAGGAGACAGAGCC 2992
2983 TAGGCTGAGACTGAGCCAGCTTGGGGGTCAAGTATGAGAGACCTGTTTAGGAGACAGAGCC 3042
2993 TAGTGTAAATTCAGAGAAATGATCTTATCAAAAGCTGATTCACAAACCCAGCTCAC 3052
3043 TAGTGTAAATTCAGAGAAATGATCTTATCAAAAGCTGATTCACAAACCCAGCTCAC 3102
3053 TGACAGCCGAGAGACAGAGATCATCTGTGAGCGGACCAATTAGGGGCTTGGCAAGG 3112
3103 TGACAGCCGAGAGACAGAGATCATCTGTGAGCGGACCAATTAGGGGCTTGGCAAGG 3162
3113 TCTACCTTGAAGCAAAACCAATACCTCAGACAGGAAATCGGGGCTTTGACCACTACCAT 3172
3163 TCTACCTTGAAGCAAAACCAATACCTCAGACAGGAAATCGGGGCTTTGACCACTACCAT 3222
3173 ATCTGTAGCCATTTTCTAGGACTTGTGAATGAGTAGTACTGATCACTTTTACGA 3232
3223 ATCTGTAGCCATTTTCTAGGACTTGTGAATGAGTAGTACTGATCACTTTTACGA 3282
3233 CCAATTCAACTGTCTATGACCAAAATTCCTGGGGCTTAAATGAGATATTTT 3292
3283 CCAATTCAACTGTCTATGACCAAAATTCCTGGGGCTTAAATGAGATATTTT 3342
3293 CTCTCAGCTTATGAAGAGAGGAAACTCTTATGATTCAGCTGAAACCAAGAGAAC 3352
3343 CTCTCAGCTTATGAAGAGAGGAAACTCTTATGATTCAGCTGAAACCAAGAGAAC 3402
3353 TGGCAACATCAAGATTAAGTTAAGTTGGAGGCTAACGAGTCACTCCCTCTTTGTA 3412
3403 TGGCAACATCAAGATTAAGTTAAGTTGGAGGCTAACGAGTCACTCCCTCTTTGTA 3462
3413 AATCAAGAAATTTGTTAAAAAGGAGATGTCATCTTAAATTAAGATGAACCTGTTTC 3472
3463 AATCAAGAAATTTGTTAAAAAGGAGATGTCATCTTAAATTAAGATGAACCTGTTTC 3522
3473 AAGCAATGTGATTTATTTGGTGTGAGACAGACGACCTTCAATTTCTCAGC 3532

Db 3523 AAGCCAAATGATATTTATTTGGGTTGGTAGCAGAGCAGCAGCCTTCAAAATTTCTCAGG 3582
 QY 3533 CAAGCAGATGTTTGGCCCTTCTGCTCACTGCATNGCATAGTTGGTAAATATAT 3592
 Db 3583 CAAGCAGATGTTTGGCCCTTCTGCTCACTGCATNGCATAGTTGGTAAATATAT 3642
 QY 3593 AATATGCGAATTTTATAGAAATCTTCTAGGAGGATAAATATATGGAATTAAGAA 3652
 Db 3643 AATATGCGAATTTTATAGAAATCTTCTAGGAGGATAAATATGGAATTAAGAA 3702
 QY 3653 GGTACAAATTTGCTAGAGAGAGAGAAACCTGTTCTTCTAGTGGCTTTTATCCCTCGG 3712
 Db 3703 GGTACAAATTTGCTAGAGAGAGAGAAACCTGTTCTTCTAGTGGCTTTTATCCCTCGG 3762
 QY 3713 CATGCATGAGGAGCTGATGTTTCTATGATTTGCCCTCAGACTTTTCACTTTACTATGAGGCT 3772
 Db 3763 CATGCATGAGGAGCTGATGTTTCTATGATTTGCCCTCAGACTTTTCACTTTACTATGAGGCT 3822
 QY 3773 GAGAGAGGCTTTAGTAGAGAGAGAAATATTCAGAATTAACGGTTGAGAAAGCTGAGAGA 3832
 Db 3823 GAGAGAGGCTTTAGTAGAGAGAGAAATATTCAGAATTAACGGTTGAGAAAGCTGAGAGA 3882
 QY 3833 CCATTGAGTTTGAATGATTTGGAATAGAGTGAAGCCATGCGCCAGCTGTTTGGAA 3892
 Db 3883 CCATTGAGTTTGAATGATTTGGAATAGAGTGAAGCCATGCGCCAGCTGTTTGGAA 3942
 QY 3893 AGCGTGGCCGGCGTGTCTTCACTGAGAAAGCAATCAAAATGAGAGCAGACCAAGGGG 3952
 Db 3943 AGCGTGGCCGGCGTGTCTTCACTGAGAAAGCAATCAAAATGAGAGCAGACCAAGGGG 4002
 QY 3953 GCTTCTCAGTCTTCACTGAGAAATCACTGATGAAATGGTCTTGGAGCTGAAATAGG 4012
 Db 4003 GCTTCTCAGTCTTCACTGAGAAATCACTGATGAAATGGTCTTGGAGCTGAAATAGG 4062
 QY 4013 AGGTCACTGGAACAAGTGAATGAGCAATTTGCTTCAACATCTCTCGGCTTGAAGTT 4072
 Db 4063 AGGTCACTGGAACAAGTGAATGAGCAATTTGCTTCAACATCTCTCGGCTTGAAGTT 4122
 QY 4073 TATCAGCTACAAATGAGGCTCTCTTTTGAAGCTTAATTCACACAGAGCTTTTGGGG 4132
 Db 4123 TATCAGCTACAAATGAGGCTCTCTTTTGAAGCTTAATTCACACAGAGCTTTTGGGG 4182
 QY 4133 GTGGGGCTGGGGGGGAGTGTGATGTTCTTCTCTGTAAGTGTGCTAGTTGGTG 4192
 Db 4183 GTGGGGCTGGGGGGGAGTGTGATGTTCTTCTCTGTAAGTGTGCTAGTTGGTG 4242
 QY 4193 CCTGCTATCTCAGTCTTCTCTGTTTGAAGAAATGACAGTCTTTTGAACAGAGTGTG 4252
 Db 4243 CCTGCTATCTCAGTCTTCTCTGTTTGAAGAAATGACAGTCTTTTGAACAGAGTGTG 4302
 QY 4253 ACTTCATGTTTCTTATGAGTCTTAAACCGACACGAATGATGATCTCAACACAGA 4312
 Db 4303 ACTTCATGTTTCTTATGAGTCTTAAACCGACACGAATGATGATCTCAACACAGA 4362
 QY 4313 CCGACTTGGTATGAGGAGTGAATGAGCCGACAGACTTCACTAGTTGTCACAAATATGT 4372
 Db 4363 CCGACTTGGTATGAGGAGTGAATGAGCCGACAGACTTCACTAGTTGTCACAAATATGT 4422
 QY 4373 GCTATGATGGGCTGTAAGTGAAGGAGAGAGGGTCAAGCTGTTGTTATGATCTGGG 4432
 Db 4423 GCTATGATGGGCTGTAAGTGAAGGAGAGAGGGTCAAGCTGTTGTTATGATCTGGG 4482
 QY 4433 AAAAGTGTGCTGACAGATTTGATGTTTATGATATACATTGAAATCTTTAATCAGAC 4492
 Db 4483 AAAAGTGTGCTGACAGATTTGATGTTTATGATATACATTGAAATCTTTAATCAGAC 4542
 QY 4493 ATTCTAAGTTTCAACAGATTTTATGATTTATGATACACACCAAAATGTTTACA 4552
 Db 4543 ATTCTAAGTTTCAACAGATTTTATGATTTATGATACACACCAAAATGTTTACA 4602
 QY 4553 GTTCAACAATTTGAGAGTGTGATGCTCCAAAACATGTTTAAAGAAAGAGAGATAGC 4612
 Db 4603 GTTCAACAATTTGAGAGTGTGATGCTCCAAAACATGTTTAAAGAAAGAGAGATAGC 4662

QY 4613 TCTTCTTACAGATGTTTCAAGAGGTTTGGGGCATTGCTGTTTATATAGCTTCTGTCA 4672
 Db 4663 TCTTCTTACAGATGTTTCAAGAGGTTTGGGGCATTGCTGTTTATATAGCTTCTGTCA 4722
 QY 4673 TAGGGCTTCTTGGCCATGAGTCCCTTCTTCTGGAACGTGTATGATCACTTCTAC 4732
 Db 4723 TAGGGCTTCTTGGCCATGAGTCCCTTCTTCTGGAACGTGTATGATCACTTCTAC 4782
 QY 4733 AGCTTTAGTCTGTTTCACTAGTGTCAATATCAATCAATTTGGAATCGAGATCGCGTG 4792
 Db 4783 AGCTTTAGTCTGTTTCACTAGTGTCAATATCAATCAATTTGGAATCGAGATCGCGTG 4842
 QY 4793 GCGAAGGGGTGGCTCCGAGGAGAGCTCTGAGAGCTCTTGTGATGTTTATAGTGGGTGG 4852
 Db 4843 GCGAAGGGGTGGCTCCGAGGAGAGCTCTGAGAGCTCTTGTGATGTTTATAGTGGGTGG 4902
 QY 4853 TGGCTGG 4859
 Db 4903 TGGCTGG 4909

RESULT 15
 US-10-648-593-115
 ; Sequence 115, Application us/10648593
 ; Publication No. US20040106132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
 ; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
 ; FILE REFERENCE: D0273 NP
 ; CURRENT APPLICATION NUMBER: US/10/648,593
 ; PRIOR FILING DATE: 2003-08-26
 ; PRIOR APPLICATION NUMBER: 60/406,385
 ; PRIOR FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 557
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 115
 ; LENGTH: 4790
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-648-593-115

Query Match 78.2%; Score 4262; DB 18; Length 4790;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4782; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
 QY 355 GAAAGACATTCACCTTGAAGGGCTTGTCTGAAATGAGGTTTAACTCTCTTTTGGCAG 414
 Db 1 GAAAGACATTCACCTTGAAGGGCTTGTCTGAAATGAGGTTTAACTCTCTTTTGGCAG 60
 QY 415 TCACCAACGAGCTGACCTTATACCTTTTATGTAATGATGAGTGGCTGAGCTTTTGAAC 474
 Db 61 TCACCAACGAGCTGACCTTATACCTTTTATGTAATGATGAGTGGCTGAGCTTTTGAAC 120
 QY 475 ACCACATTAATCATCTGTCGCAATTAAGAGAGGTTGAGAAAGAGACTTATTTGT 534
 Db 121 ACCACATTAATCATCTGTCGCAATTAAGAGAGGTTGAGAAAGAGACTTATTTGT 180
 QY 121 ACCACATTAATCATCTGTCGCAATTAAGAGAGGTTGAGAAAGAGACTTATTTGT 180
 QY 535 GTCATGCCCCATGAGATGATGAACTCAATTTGTTACTGAGAGTGTGTGCTGTG 594
 Db 181 GTCATGCCCCATGAGATGATGAACTCAATTTGTTACTGAGAGTGTGTGCTGTG 240
 QY 595 GAAAGTGAACGAAAGAAAGTGTGCTAATGATGATACCGGCAATTTGTGATCAATCA 654
 Db 241 GAAAGTGAACGAAAGAAAGTGTGCTAATGATGATACCGGCAATTTGTGATCAATCA 300
 QY 655 TCCCAATTTTGAAGCCATTATATCAACTGCTCCAAGCTTATGAGAGGTTGCA 714
 Db 301 TCCCAATTTTGAAGCCATTATATCAACTGCTCCAAGCTTATGAGAGGTTGCA 360
 QY 715 CAGGACAAAGTGTATTAATTCAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACATT 774

Db	361	CAGGACAAAGTGTATTAACAAGCTCATCCAGCAATTCAGCAAACTAAGGTGACATT	420
Oy	775	GATTGCAGTCAGAAAGGTGTAGTTTAACATCAAAAGCTCCCAAGATGTTGCTCTCTCT	834
Db	421	GATTGCAGTCAGAAAGGTGTAGTTTAACATCAAAAGCTCCCAAGATGTTGCTCTCTCT	480
Oy	835	TCAGACTGTTTTCTCACTGTACTCTGGGTAACTGAGAAAGCTTCAACTCTGTTAC	894
Db	481	TCAGACTGTTTTCTCACTGTACTCTGGGTAACTGAGAAAGCTTCAACTCTGTTAC	540
Oy	895	CTGCTTGACAGGTGGGTGGTGGTCTAGTCTCTCGTGTGTTCCCTGGCTCTGTGAAGAAA	954
Db	541	CTGCTTGACAGGTGGGTGGTGGTCTAGTCTCTCGTGTGTTCCCTGGCTCTGTGAAGAAA	600
Oy	955	TCCACTAGTCCCTACCTGACATTTCTCAGCCTTGCTTACCTGTTGCCAACTTGGGCA	1014
Db	601	TCCACTAGTCCCTACCTGACATTTCTCAGCCTTGCTTACCTGTTGCCAACTTGGGCA	660
Oy	1015	ACCGGAATCTTCCCAATCTTATCTTGCTGCTGCAGCGAGATGTCTCAACAGAGCTG	1074
Db	661	ACCGGAATCTTCCCAATCTTATCTTGCTGCTGCAGCGAGATGTCTCTCAACAGAGCTG	720
Oy	1075	ATACAGCAGAAATGGGATTTGTTATGTGTAAATGCCAGTAACTGTGTCAAAGCTGAC	1133
Db	721	ATACAGCAGAAATGGGATTTGTTATGTGTAAATGCCAGTAACTGTGTCAAAGCTGAC	780
Oy	1135	TTTATCCCCGAGTCTCATTTCTCGCGTGCCTGTGAATGACAGCTTTTGTAGAAATT	1199
Db	781	TTTATCCCCGAGTCTCATTTCTCGCGTGCCTGTGAATGACAGCTTTTGTAGAAATT	840
Oy	1195	TTGCGGTGGTTGGACAAATCAGTAGATTCTTAAGAAAGCAAAAGCCTCCATAGATGT	1254
Db	841	TTGCGGTGGTTGGACAAATCAGTAGATTCTTAAGAAAGCAAAAGCCTCCATAGATGT	900
Oy	1255	GTTCTAGTGCATGTTTAGTGGGATCTCCGCTCGCCACATGGCTATGCGCTTACATC	1313
Db	901	GTTCTAGTGCATGTTTAGTGGGATCTCCGCTCGCCACATGGCTATGCGCTTACATC	960
Oy	1315	ATGAAGAGATGGAATGCTTTAGTGAAGCTTACAGATTTGTGAAGAAAAAGAAAGCCT	1377
Db	961	ATGAAGAGATGGAATGCTTTAGTGAAGCTTACAGATTTGTGAAGAAAAAGAAAGCCT	1022
Oy	1375	ACTATATCTCCAACTTCAATTTCTGGGCAACTCTGSACTATAGAAAGAAAGATTAA	1434
Db	1021	ACTATATCTCCAACTTCAATTTCTGGGCAACTCTGSACTATAGAAAGAAAGATTAA	1081
Oy	1435	AAACGACTGAGCATCAGGGCCAAAGCAAACTCAGACTGCTGCACCTGGAGAGCCA	1494
Db	1081	AAACGACTGAGCATCAGGGCCAAAGCAAACTCAGACTGCTGCACCTGGAGAGCCA	1140
Oy	1495	AATGAACCTGCTCCGCTGTCTCAAGAGGTGGAAGAAAGGGAAGGCCCTCTAGTCA	1555
Db	1141	AATGAACCTGCTCCGCTGTCTCAAGAGGTGGAAGAAAGGGAAGGCCCTCTAGTCA	1200
Oy	1555	CCCTGTGCCGACTCTGTCTACCTCAGAGGACAGAGCAAAAGGCCGCTGTACTCCGCAAC	1614
Db	1201	CCCTGTGCCGACTCTGTCTACCTCAGAGGACAGAGCAAAAGGCCGCTGTACTCCGCAAC	1266
Oy	1615	GTCGCCAGCTGTCAGGCGTGCAGCCGTTGCTGTTAAGAGCAGCCGCTGTGTACAGCG	1674
Db	1261	GTCGCCAGCTGTCAGGCGTGCAGCCGTTGCTGTTAAGAGCAGCCGCTGTGTACAGCG	1322
Oy	1675	CTCAATGGGCTGCACCTGTCCGCAACAGGCTGTGAAGACAGAAATTAAGTCAAGGTTCC	1733
Db	1321	CTCAATGGGCTGCACCTGTCCGCAACAGGCTGTGAAGACAGAAATTAAGTCAAGGTTCC	1380
Oy	1735	TTCTCTCTGATATCAAAATCAGTTTCATTTACAGCAGATGGCAGACTCTTACATGGC	1794
Db	1381	TTCTCTCTGATATCAAAATCAGTTTCATTTACAGCAGATGGCAGACTCTTACATGGC	1444
Oy	1795	TTCTCTCATCAGAAATGCTTTGGAATATACAAACTTCCACTACTCTGTAGTGAACC	1854

[illegible]

QY 2935 GCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTAGTAGACCTGTTAGGACAGAGCTTA 2994
| | | | |
Db 2980 GCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTAGTAGACCTGTTAGGACAGAGCTTA 2939
| | | | |
QY 2995 GTGGTAATCCAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCACTG 3054
| | | | |
Db 2640 GTGGTAATCCAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCACTG 2699
| | | | |
QY 3055 ACAGCCGAGGAGACAGAGCACTCTGCTGAGACGACCTTGGGGCTTTGCCAAGGTC 3114
| | | | |
Db 2700 ACAGCCGAGGAGACAGAGCACTCTGCTGAGACGACCTTGGGGCTTTGCCAAGGTC 2759
| | | | |
QY 3115 TACCTTAGACAAACCCAGTACCTCAGACAGAGAAAGCGGGCTTTGACCACTACCAATAT 3174
| | | | |
Db 2760 TACCTTAGACAAACCCAGTACCTCAGACAGAGAAAGCGGGCTTTGACCACTACCAATAT 2819
| | | | |
QY 3175 CTGGTAGCCATTTTCTAGGCAATTTGGAATAGGTAGGTAGTACACTTTTCAGACC 3234
| | | | |
Db 2820 CTGGTAGCCATTTTCTAGGCAATTTGGAATAGGTAGGTAGTACACTTTTCAGACC 2879
| | | | |
QY 3235 AATTCAAACGTCTATGCACAAAATTCGCGTGGGCTTATAGTGAATAATTTTTTTTCT 3294
| | | | |
Db 2880 AATTCAAACGTCTATGCACAAAATTCGCGTGGGCTTATAGTGAATAATTTTTTTTCT 2939
| | | | |
QY 3295 TCTCAGCTTATGAGAGAGAGGAACTGTAGATTCAGCTGAAACACAGAGAACTG 3354
| | | | |
Db 2940 TCTCAGCTTATGAGAGAGAGGAACTGTAGATTCAGCTGAAACACAGAGAACTG 2999
| | | | |
QY 3355 GCACATCAGATTTTAAAGTTAGGTGGAGGCTAACAGTCTACCTCCCTTTGTAA 3414
| | | | |
Db 3000 GCACATCAGATTTTAAAGTTAGGTGGAGGCTAACAGTCTACCTCCCTTTGTAA 3059
| | | | |
QY 3415 TCAGAAATTTGTTAAATGGATGTCAATCTTTAATAATAAGATGAATGGTTTCA 3474
| | | | |
Db 3060 TCAGAAATTTGTTAAATGGATGTCAATCTTTAATAATAAGATGAATGGTTTCA 3119
| | | | |
QY 3475 GCCAATGTGAATTTATTTGGGTGGTAGACAGACAGACCTTCAAAATTCAGCCA 3534
| | | | |
Db 3120 GCCAATGTGAATTTATTTGGGTGGTAGACAGACAGACCTTCAAAATTCAGCCA 3179
| | | | |
QY 3535 AAGCAGATGTTTTTCCCTTCTGCTTCACTGATGATACAGTGTGTAATAATGAATA 3594
| | | | |
Db 3180 AAGCAGATGTTTTTCCCTTCTGCTTCACTGATGATACAGTGTGTAATAATGAATA 3239
| | | | |
QY 3595 TATGCAAGATTTTATAGAAAATTCTTAGAGAGTAAATTAATGAGAGATTAAGAAA 3654
| | | | |
Db 3240 TATGCAAGATTTTATAGAAAATTCTTAGAGAGTAAATTAATGAGAGATTAAGAAA 3299
| | | | |
QY 3655 TACAAATGTGAGAGAGAGAGAAAGCTGTTTCTTAGAGGCTTTATATCCCTCGGA 3714
| | | | |
Db 3300 TACAAATGTGAGAGAGAGAGAAAGCTGTTTCTTAGAGGCTTTATATCCCTCGGA 3359
| | | | |
QY 3715 TGGCAATGGGCTGATGTTTCTATATGCTCAGACTTTCATTACTAGTAGGGCTGA 3774
| | | | |
Db 3360 TGGCAATGGGCTGATGTTTCTATATGCTCAGACTTTCATTACTAGTAGGGCTGA 3419
| | | | |
QY 3775 GAGAGGCTTTTGTAGAGAGAGAAATTTTCAAGATTTAAACGTTGAGAAAGCTGAGAGACC 3834
| | | | |
Db 3420 GAGAGGCTTTTGTAGAGAGAGAAATTTTCAAGATTTAAACGTTGAGAAAGCTGAGAGACC 3479
| | | | |
QY 3835 ATTAGATTTTGTATGATGTGATATAGAGTGCAGAACCTAGGCAAGCTGTTTTTGGAAAC 3894
| | | | |
Db 3480 ATTAGATTTTGTATGATGTGATATAGAGTGCAGAACCTAGGCAAGCTGTTTTTGGAAAC 3539
| | | | |
QY 3895 GCTGGCCGGCGCTGCTTCAAGTGAAGAAACCAATCAAAATGAGACGAGCAAAAGGGCG 3954
| | | | |
Db 3540 GCTGGCCGGCGCTGCTTCAAGTGAAGAAACCAATCAAAATGAGACGAGCAAAAGGGCG 3599
| | | | |
QY 3955 TCTCAGTCTCAACCTATCAATCACTGTATGGAATCGTCTGCGACGCTGAACATGAGAG 4014
| | | | |
Db 3600 TCTCAGTCTCAACCTATCAATCACTGTATGGAATCGTCTGCGACGCTGAACATGAGAG 3659
| | | | |

QY 4015 GTCACTGAAACAAGTATAGTGCAGATTTGGCTTTCAAAACATCTCTGCGCTTGATTTTA 4074
| | | | |
Db 3660 GTCACTGAAACAAGTATAGTGCAGATTTGGCTTTCAAAACATCTCTGCGCTTGATTTTA 3719
| | | | |
QY 4075 TCAGCTAACAAATGTGGGTCTCTTTTGAAGCCTTTAATTCACACAGCAGCTTTTGGGGGT 4134
| | | | |
Db 3720 TCAGCTAACAAATGTGGGTCTCTTTTGAAGCCTTTAATTCACACAGCAGCTTTTGGGGGT 3779
| | | | |
QY 4135 GGGGCTGGGCGGATGTGTCAATGTCTTCTCTCTGTATAGTGTAGTGTCTGCC 4194
| | | | |
Db 3780 GGGGCTGGGCGGATGTGTCAATGTCTTCTCTCTGTATAGTGTGTGTGTCTGCC 3839
| | | | |
QY 4195 TCGATCTCAGTTTTTCTCTGTTTTTGAAGATGACAGTTTTTGAACAGATGTGAC 4254
| | | | |
Db 3840 TCGATCTCAGTTTTTCTCTGTTTTTGAAGATGACAGTTTTTGAACAGATGTGAC 3899
| | | | |
QY 4255 TTCAATGTTTCTATGATGACTTCTTAAACAGACACAGATATGATGCTAACACAGACC 4314
| | | | |
Db 3900 TTCAATGTTTCTATGATGACTTCTTAAACAGACACAGATATGATGCTAACACAGACC 3959
| | | | |
QY 4315 GACTTGTATGGGATATGATGACCGACAGACCTCACTAGTGTGACAAATATATGTGC 4374
| | | | |
Db 3960 GACTTGTATGGGATATGATGACCGACAGACCTCACTAGTGTGACAAATATATGTGC 4019
| | | | |
QY 4375 TATGATGGGATGTAAAGTGAAGGAGAGAGGCTCAGCCGCTTTATATATCTGGAA 4434
| | | | |
Db 4020 TATGATGGGATGTAAAGTGAAGGAGAGAGGCTCAGCCGCTTTATATATCTGGAA 4079
| | | | |
QY 4435 AGTCTGTCAACGATTTGATGATGTTTATGATATATATGAAATCTTAAATCAGACAT 4494
| | | | |
Db 4080 AGTCTGTCAACGATTTGATGATGTTTATGATATATATGAAATCTTAAATCAGACAT 4139
| | | | |
QY 4495 TCTCAATTTCAACAGTATTTTGAATGTATATACACACACCAATATGTAAACAGT 4554
| | | | |
Db 4140 TCTCAATTTCAACAGTATTTTGAATGTATATATACACACCAATATGTAAACAGT 4199
| | | | |
QY 4555 TCAACATTTCAAGATGTGTCAATGCCCCCAAAACATGTTTAAAGAAAGAGATGATC 4614
| | | | |
Db 4200 TCAACATTTCAAGATGTGTCAATGCCCCCAAAACATGTTTAAAGAAAGAGATGATC 4259
| | | | |
QY 4615 CTGCTTAACGATTTTCAAGAGGTTTGGGCACTTGGTTTATAGACTTCTGTCAATTA 4674
| | | | |
Db 4260 CTGCTTAACGATTTTCAAGAGGTTTGGGCACTTGGTTTATAGACTTCTGTCAATTA 4319
| | | | |
QY 4675 GGGCTTCTGTGGCCATGATGCCCTTCTCTCTGAGAACTGTATATGATCAATCTTACAG 4734
| | | | |
Db 4320 GGGCTTCTGTGGCCATGATGCCCTTCTCTCTGAGAACTGTATATGATCAATCTTACAG 4379
| | | | |
QY 4735 CTTTATGCTGTGTTCACTAGTGTCAATATCAGTTCTTGGAAATCGAGATGCGGTGAC 4794
| | | | |
Db 4380 CTTTATGCTGTGTTCACTAGTGTCAATATCAGTTCTTGGAAATCGAGATGCGGTGAC 4439
| | | | |
QY 4795 GAAAGGGGTGGCTCCGAGAGCAGGCTGTGAGAGTGTCTTGAATGCTTTAGGTGGGTGTG 4854
| | | | |
Db 4440 GAAAGGGGTGGCTCCGAGAGCAGGCTGTGAGAGTGTCTTGAATGCTTTAGGTGGGTGTG 4499
| | | | |
QY 4855 GCTGGCTCTCTTCAAGATGATATTTGGGAAACCTCGGCTCTACTAGGGGTGATACAGAT 4914
| | | | |
Db 4500 GCTGGCTCTCTTCAAGATGATATTTGGGAAACCTCGGCTCTACTAGGGGTGATACAGAT 4559
| | | | |
QY 4915 GGTGATTTTAAAGAGCAAACTAGACTTCTATATGAGAGAGTGTGGAATGATTTAGGA 4974
| | | | |
Db 4560 GGTGATTTTAAAGAGCAAACTAGACTTCTATATGAGAGAGTGTGGAATGATTTAGGA 4619
| | | | |
QY 4975 CATGTGTAAAGTTATAGTGAAGAGCTGTAATATGTTTAAATAGATATATAGTGTCTTTTGA 5034
| | | | |
Db 4620 CATGTGTAAAGTTATAGTGAAGAGCTGTAATATGTTTAAATAGATATATAGTGTCTTTTGA 4679
| | | | |
QY 5035 AGTAAAGCCAGCTGTTGAACGTTTAACTGTGCAATTTCTCAATTTTGAATGTGTATGATG 5094
| | | | |
Db 4680 AGTAAAGCCAGCTGTTGAACGTTTAACTGTGCAATTTCTCAATTTTGAATGTGTATGATG 4739
| | | | |
QY 5095 TTAATGTATGAAATGATTTAAATTAATCAAAACCTGTGATCCTGTTATATCAT 5145
| | | | |

Db	1392	CAATTTTCTGGGCGAACTCTGGACCTATGAGAAAGAAATTAAGAACCAACATCGAGCAATC	1451
QY	1452	AGGGCCAAAGAGCAAACTCAAGCTGTGCACTTGAGAGCCAAATGAACTGTCCCTGCG	1511
Db	1452	AGGGCCAAAGAGCAAACTCAAGCTGTGCACTTGAGAGCCAAATGAACTGTCCCTGCG	1511
QY	1512	TGCTCAGAGGGGTGGACAGAAAAGCGAAGACGCCCTCACTGATCCACTCCTGTGCCACTCTGC	1571
Db	1512	TGCTCAGAGGGGTGGACAGAAAAGCGAAGACGCCCTCACTGATCCACTCCTGTGCCACTCTGC	1571
QY	1572	TACCTCAGAGGCAAGCAAGAGCCCGTGCATCCGCGCAGCGTCCAGCGTGCCTCAG	1631
Db	1572	TACCTCAGAGGCAAGCAAGAGCCCGTGCATCCGCGCAGCGTCCAGCGTGCCTCAG	1631
QY	1632	CGTGCAGCCGTGCTGTATGAGAGCAGCCCCGTGTATCAGGCGCTCACTGGGGCTGCACCT	1691
Db	1632	CGTGCAGCCGTGCTGTATGAGAGCAGCCCCGTGTATCAGGCGCTCACTGGGGCTGCACCT	1691
QY	1692	GTCGCGAGCAGGCTGGAGAGCAGCAATAGCTCAAGGGTTCCTCTCTCGATATCAAA	1751
Db	1692	GTCGCGAGCAGGCTGGAGAGCAGCAATAGCTCAAGGGTTCCTCTCTCGATATCAAA	1751
QY	1752	ATCAGTTTCATATTCAGCCAGCATGCGCAGCATCTTATACATGGCTTCTCTCATCAGAGA	1811
Db	1752	ATCAGTTTCATATTCAGCCAGCATGCGCAGCATCTTATACATGGCTTCTCTCATCAGAGA	1811
QY	1812	TGCTTTGGAAATCTCAAAACCTTCCACTACTGTGATGGAGCCAAAGAGCTATGCGCAGTT	1871
Db	1812	TGCTTTGGAAATCTCAAAACCTTCCACTACTGTGATGGAGCCAAAGAGCTATGCGCAGTT	1871
QY	1872	CTCCCTGTTTACGAACTATGCGAGCAGACTCCCGAAAACAATCCTGTATGAGAGGAGC	1931
Db	1872	CTCCCTGTTTACGAACTATGCGAGCAGACTCCCGAAAACAATCCTGTATGAGAGGAGC	1931
QY	1932	CAGCAATCCCAAGAGCTGCGAGACCGCGAGGCTTTCAGACGACGAGCAAGCGATTTGCA	1991
Db	1932	CAGCAATCCCAAGAGCTGCGAGACCGCGAGGCTTTCAGACGACGAGCAAGCGATTTGCA	1991
QY	1992	TTCCGTCAGAACCAAGCAGTGTGCAACCGCCAGAGGTCCTTTTATCTCACTGCATCG	2051
Db	1992	TTCCGTCAGAACCAAGCAGTGTGCAACCGCCAGAGGTCCTTTTATCTCACTGCATCG	2051
QY	2052	AAGTGGAGCGTGGAGGCAATTAACACACAGCTTCTTTTGCGCTTTCCACAGACCA	2111
Db	2052	AAGTGGAGCGTGGAGGCAATTAACACACAGCTTCTTTTGCGCTTTCCACAGACCA	2111
QY	2112	GCAGCACTTCAAGAGTCTGTGCCTGTGGGCTTAAAGGCTGCGACCTCGGATATCTTGGG	2171
Db	2112	GCAGCACTTCAAGAGTCTGTGCCTGTGGGCTTAAAGGCTGCGACCTCGGATATCTTGGG	2171
QY	2172	CCCCCAGACCTCTACCCCTTCCCTGACACAGCACTGGTATTTTGGCACAGAGTCTTACA	2231
Db	2172	CCCCCAGACCTCTACCCCTTCCCTGACACAGCACTGGTATTTTGGCACAGAGTCTTACA	2231
QY	2232	CTTCTACTCTGCTCTCAGGCATCTACGGAAGGAGTGCATTAATCTCTGCTTACAGCTGCG	2291
Db	2232	CTTCTACTCTGCTCTCAGGCATCTACGGAAGGAGTGCATTAATCTCTGCTTACAGCTGCG	2291
QY	2292	CCAGCTGCCCATTTGGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAAGAGCAAGTGA	2351
Db	2292	CCAGCTGCCCATTTGGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAAGAGCAAGTGA	2351
QY	2352	CAGAGCTGACCTCGGGGGGAGCTGGCATTAAGAGAGCCCTTTGAAAAGCATTTTAAACG	2411
Db	2352	CAGAGCTGACCTCGGGGGGAGCTGGCATTAAGAGAGCCCTTTGAAAAGCATTTTAAACG	2411
QY	2412	CAGAACTGCGCAATGGAATTTGAGAGAGCATCATGTACAGAGAACAGGTCAACGGGAGAA	2471
Db	2412	CAGAACTGCGCAATGGAATTTGAGAGAGCATCATGTACAGAGAACAGGTCAACGGGAGAA	2471
QY	2472	GCTGGGGAAAGTGGGCGTCAAGTCTAGCTTTTGGGACAGATGGAATCATTTAGAGTCTC	2531
Db	2472	GCTGGGGAAAGTGGGCGTCAAGTCTAGCTTTTGGGACAGATGGAATCATTTAGAGTCTC	2531

Db	2472	GC	GGGGAAGTGGGCA	GTCA	GTAGCTTT	CGGCGAGCA	TGAAATCAT	TGAGGTCTC	2531		
Oy	2532	CT	GAGAGAAAGCA	CTTG	GTGCTTA	TATAGCAATTTT	TTTTTTTCTG	TCCAGAAAA	2591		
Db	2532	CT	GAGAGAAAGCA	CTTG	TGCTTA	TATAGCAATTTT	TTTTTTTCTG	TCCAGAAAA	2590		
Oy	2592	ATT	CCCTGTAATCT	GAAATATAT	TATGTACAT	TATATATTTT	TGGAAAA	TGAGC	2651		
Db	2591	ATT	CCCTGTAATCT	GAAATATAT	TATGTACAT	TATATATTTT	TGGAAAA	TGAGC	2650		
Oy	2652	TAT	GGTTAAAGCA	CAGGTG	ATCAACCA	GTGTATCTCT	CTTAACATCTG	CAATTTG	2711		
Db	2651	TAT	GGTTAAAGCA	CAGGTG	ATCAACCA	GTGTATCTCT	CTTAACATCTG	CAATTTG	2710		
Oy	2712	AGA	ATCACTTA	TATCTCTCA	CAAAAA	TGAAAGG	CAGATGCTA	GAATCC	2771		
Db	2711	AGA	ATCACTTA	TATCTCTCA	CAAAAA	TGAAAGG	CAGATGCTA	GAATCC	2770		
Oy	2772	GAC	GAGAAAA	CCATTTTAT	TACGTGAATTA	CAATCTCT	TGTTCTTA	AAAAAGCA	2831		
Db	2771	GAC	GAGAAAA	CCATTTTAT	TACGTGAATTA	CAATCTCT	TGTTCTTA	AAAAAGCA	2830		
Oy	2832	TG	CTTGGTGTG	AGAGCAAAAT	CCCCTACATTTT	CACGTTG	GTGCTTA	GAGATC	2891		
Db	2831	TG	CTTGGTGTG	AGAGCAAAAT	CCCCTACATTTT	CACGTTG	GTGCTTA	GAGATC	2890		
Oy	2892	TC	AAATATTAG	CTTTGTCG	AGACCTTTCAT	TATGACCTTA	AGCCTGA	ACTGA	2951		
Db	2891	TC	AAATATTAG	CTTTGTCG	AGACCTTTCAT	TATGACCTTA	AGCCTGA	ACTGA	2950		
Oy	2952	GCT	TGGGGGT	CAGGATAG	ACCTGT	TTTGGGACAG	CGCTGATG	TGTTAATCC	3011		
Db	2951	GCT	TGGGGGT	CAGGATAG	ACCTGT	TTTGGGACAG	CGCTGATG	TGTTAATCC	3010		
Oy	3012	AAT	ATCTTATTC	CAACCTGATTA	CCAAACCA	CGCTCA	CTGACAG	CCGAGGAC	3071		
Db	3011	AAT	ATCTTATTC	CAACCTGATTA	CCAAACCA	CGCTCA	CTGACAG	CCGAGGAC	3070		
Oy	3072	GC	ATCACTCTG	CTGGA	CGGACCA	TTTGGGGCTT	GCAAGCTT	TACTTA	GAGCAAA	3131	
Db	3071	GC	ATCACTCTG	CTGGA	CGGACCA	TTTGGGGCTT	GCAAGCTT	TACTTA	GAGCAAA	3130	
Oy	3132	AG	TACTCAG	ACAGAAAGT	CGGGCTTT	TGACCACTA	CACTATCTG	TAGCCATTTCT	3191		
Db	3131	AG	TACTCAG	ACAGAAAGT	CGGGCTTT	TGACCACTA	CACTATCTG	TAGCCATTTCT	3190		
Oy	3192	AG	GATTTGTA	TATAGTATAGT	ACTAGTAC	CACTTT	CAGCCAA	TTCATCTG	TATG	3251	
Db	3191	AG	GATTTGTA	TATAGTATAGT	ACTAGTAC	CACTTT	CAGCCAA	TTCATCTG	TATG	3250	
Oy	3252	CAC	AAATTC	CCGTTGG	CCCTAGATG	AGATTAATTTTT	TTTTCTCT	CAGCTT	TATGAGAC	3311	
Db	3251	CAC	AAATTC	CCGTTGG	CCCTAGATG	AGATTAATTTTT	TTTTCTCT	CAGCTT	TATGAGAC	3310	
Oy	3312	GA	AGGAAA	CTGTCT	TAGATTA	CACTGTAAC	CAACAGAA	CTTG	CAACATCA	CGATTTAA	3371
Db	3311	GA	AGGAAA	CTGTCT	TAGATTA	CACTGTAAC	CAACAGAA	CTTG	CAACATCA	CGATTTAA	3370
Oy	3372	GC	TAAAGTTGG	AGGCTTA	ACGATCA	CCCTCT	TGTATATCA	AAATGTTTAA	3431		
Db	3371	GC	TAAAGTTGG	AGGCTTA	ACGATCA	CCCTCT	TGTATATCA	AAATGTTTAA	3430		
Oy	3432	AT	GGGATTTG	CAATCTTTAA	TAAAGATGA	ATTGGTT	CAAGCCAA	TGTGAATTTAT	3491		
Db	3431	AT	GGGATTTG	CAATCTTTAA	TAAAGATGA	ATTGGTT	CAAGCCAA	TGTGAATTTAT	3490		
Oy	3492	TT	GGGTTG	TAGAGAG	CAAGCA	CCCTCA	ATTTCT	CAGCCAA	AGCATGTTTGGC	3551	
Db	3491	TT	GGGTTG	TAGAGAG	CAAGCA	CCCTCA	ATTTCT	CAGCCAA	AGCATGTTTGGC	3550	
Oy	3552	CT	TTTCTG	CTTCACTG	ATGATAG	TACGTTGGT	TAAATGTA	TATATG	CAAGATTTTATA	3611	
Db	3551	CT	TTTCTG	CTTCACTG	ATGATAG	TACGTTGGT	TAAATGTA	TATATG	CAAGATTTTATA	3610	

Oy	3612	GGAAACCTCCAGGGAGGTAATTAATGGAAGATTAGAAAGAGTACAAATTGCTGAGAG	3671
Db	3611	GGAAACCTCCAGGGAGGTAATTAATGGAAGATTAGAAAGAGTACAAATTGCTGAGAG	3670
Oy	3672	AAGCAGGAAACCTGCTCCTAGTGGCTTTATATCCCTCGGCATGCGCATGGGGCTGATGT	3731
Db	3671	AAGCAGGAAACCTGCTCCTAGTGGCTTTATATCCCTCGGCATGCGCATGGGGCTGATGT	3730
Oy	3732	TTCTATGATTTGCTCAGACTTTCACATTTACTAGTA	3767
Db	3731	TTCTATGATTTGCTCAGACTTTCACATTTACTAGTA	3766

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1       RESULT 17
2       US-10-425-114-26234
3       ; Sequence 26234, Application US/10425114
4       ; Publication NO. US2004003488A1
5       ; GENERAL INFORMATION:
6       ; APPLICANT: Liu, Jingdong
7       ; APPLICANT: Zhou, Yihua
8       ; APPLICANT: Kowalc, David K.
9       ; APPLICANT: Screen, Steven E
10      ; APPLICANT: Tabaska, Jack E
11      ; APPLICANT: Cao, Yongwei
12      ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
13      ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
14      ; FILE REFERENCE: 38-21(53)313 B
15      ; CURRENT APPLICATION NUMBER: US/10/425,114
16      ; CURRENT FILING DATE: 2003-04-28
17      ; NUMBER OF SEQ ID NOS: 73128
18      ; SEQ ID NO 26234
19      ; LENGTH: 3625
20      ; TYPE: DNA
21      ; ORGANISM: Homo sapiens
22      ; FEATURE:
23      ; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
24      ; US-10-425-114-26234

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Query Match 59.4%; Score 3238; DB 17; Length 3625;

Best Local Similarity 99.9%; Pred.No. 0;
Matches 3458; Conservative 0; Mismatches 2; Indels 1; Gaps 1

Qy	12	GAGAGGAGAGCATCGGACGGGACGGCAGCGGGAGCGCAGCGGCGCTCTCGGCTCCGG	71
Db	166	GAGAGGAGAGCATCGGACGGGACGGCAGCGGAGCGCAGCGGCGCTCTCGGCTCCGG	225
Qy	72	GCGCGCCCTCCCAAGTCCGGAGGCGAGGGGGGCCGAGGGGAGACGCGGTGACAACTTT	131
Db	226	GCGCGCCCTCCCAAGTCCGGAGGCGAGGGGGGCCGAGGGGAGACGCGGTGACAACTTT	285
Qy	132	CGTTTCCCTCTGAGGGAAATTGGAGGTGGCGGGCCCAAAAGCTTTCAGTCCAGGTAA	191
Db	286	CGTTTCCCTCTGAGGGAAATTGGAGGTGGCGGGCCCAAAAGCTTTCAGTCCAGGTAA	345
Qy	192	GCTGTGGAGCGCGGAGCAAAAGTAAAGATGATTAATGCGTGGCTGCTCCAAAGCA	251
Db	346	GCTGTGGAGCGCGGAGCAAAAGTAAAGATGATTAATGCGTGGCTGCTCCAAAGCA	405
Qy	252	TCTTTGTGTGGGAATGGTTAATTCAGATCTCTTTTAAATGAAATGTAAGGGGGCTGC	311
Db	406	TCTTTGTGTGGGAATGGTTAATTCAGATCTCTTTTAAATGAAATGTAAGGGGGCTGC	465
Qy	312	TTTGTGACGAGATCTTTGCAAGACATCAACGGGAAAGAGAAAGACATTCATT	371
Db	466	TTTGTGACGAGATCTTTGCAAGACATCAACGGGAAAGAGAAAGACATTCATT	525
Qy	372	GGAAGGCTCTTGCTGAAAATGGGTTTAATCTCTCTTTTGCAGTCAACCAAGCTGAAC	431
Db	526	GGAAGGCTCTTGCTGAAAATGGGTTTAATCTCTCTTTTGCAGTCAACCAAGCTGAAC	585
Qy	432	TGATACATTTTAATGACAAATGAGATGGCTGAAGCTTTGACACACCACTTAATATATC	491

Db	586	CCATACACTTTTAGTACAAATGGAAGGCGTGAAGCCTTTGAGCACACCAATATCAATC	645
Qy	492	GTGGCAATTTAAAGAAGAGGTGGGAAAAAGAGACTTATTGTTCATAGGCCCATAGAGT	551
Db	646	GTGGCAAAATTAAAGAAGAGGTGGGAAAAAGAGACTTATTGTTCATAGGCCCATAGAGAT	705
Qy	552	GATTGGAACCTCAAAATTGTTACTGAGAGGTGGTGGCTGGCTGGAAAGTGGAAACGGAAAA	611
Db	706	GATTGGAACCTCAAAATTGTTACTGAGAGGTGGTGGCTGGCTGGAAAGTGGAAACGGAAAA	765
Qy	612	AGTCTGCTAATTTGATATAGCCCGCAATTTGTGGAATATACATATACATCCCAATTTTGGAAAGC	671
Db	766	AGTCTGCTAATTTGATATAGCCCGCAATTTGTGGAATATACATATATATCCCAATTTTGGAAAGC	825
Qy	672	CATTATATATCAACTGCTCCAGCTTATGAGCGAAGTTTGCAACGAGACAAAGTGTAAAT	731
Db	826	CATTATATATCAACTGCTCCAGCTTATGAGCGAAGTTTGCAACGAGACAAAGTGTAAAT	885
Qy	732	TACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTTGAACATTTGATTCAGATCAAGAAGT	791
Db	886	TACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTTGAACATTTGATTCAGATCAAGAAGT	945
Qy	792	TGTAGTTTACGATCAAAAGCTCCCAAGATGTTGGCCTCTCTCTTCAGACTGTTTTCTCAC	851
Db	946	TGTAGTTTACGATCAAAAGCTCCCAAGATGTTGGCCTCTCTCTTCAGACTGTTTTCTCAC	1001
Qy	852	TGTACTTCGCGGTAACTGAGAAAGCTTCAACTGTGTGCACTGCTTGCAAGTGGGTT	911
Db	1006	TGTACTTCGCGGTAACTGAGAAAGAGCTTCAACTGTGTGCACTGCTTGCAAGTGGGTT	1066
Qy	912	TGCTGAGTTCCTCTGTTGTTTTCCCTGGCCTCTGTGAAAGAAATTCACCTATGCTCCATAC	971
Db	1066	TGCTGAGTTCCTCTGTTGTTTTCCCTGGCCTCTGTGAAAGAAATTCACCTATGCTCCATAC	1122
Qy	972	CTGCATTTCTCAGGCTTGCTTAACCTGTGTGSCAAACATGGGCAACCCGAAATTTCTTCCCAA	1033
Db	1126	CTGCATTTCTCAGGCTTGCTTAACCTGTGTGSCAAACATGGGCAACCCGAAATTTCTTCCCAA	1188
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Qy	1092	TGCTTATGTGTAAATGCGCAAGCTATACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCA	1155
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Qy	1272	AGCTGGAGATCTCCGCTCCGCGACATGCTATGCTTACATCATGAAGAAGATGAGACAT	1333
Db	1426	AGCTGGAGATCTCCGCTCCGCGACCAATGCTATGCTTACATCATGAAGAAGATGAGACAT	1488
Qy	1332	GTCTTTTATGATGAAAGCTTACAGATTTTGTGAAAGAAAAAGAAAGAAAGAAAGCTTATATCTCCAAACTT	1399
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Db 3585 ATGGGATTTGCAATCTTTAAATTAAGATGAATCTTGTTTC 3625
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RESULT 18
US-09-964-277-1
Sequence 1, Application US/09964277
Patent No. US20020137170A1
GENERAL INFORMATION:
APPLICANT: Lucbe, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.434
CURRENT APPLICATION NUMBER: US/09/964,277
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3496
TYPE: DNA

[illegible]

QY	3191	TAGGATTTGTAATAGGATAGGTACTAGTCAACCTTTTCAGACCAATTCAACTGTCTAT	3250
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Db	3275	GCACAAATTCCTCGTGGGCTTAGATGAGATAAATTTTTTTTCTTCAGCTTATGAA	3334
QY	3311	AGAAAGGGAATATGCTCTAGGATTCAGCTGAACCAACAGAACTTGGCAACATCAGATTTA	3370
Db	3335	AGAAAGGGAATATGCTCTAGGATTCAGCTGAACCAACAGAACTTGGCAACATCAGATTTA	3394
QY	3371	AGCTAAGTTGGAGGCTAAAGATCTACCTCCCTCTTTGTAATCAAGAATGTTTAA	3430
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QY	3431	AAATGGATTTGCATCTCTTAAATAAAGATGAACCTTGCTTTC	3472
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RESULT 19
US-09-816-494-1
Sequence 1, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USNS THEREFOR
FILE REFERENCE: 10448-030002
CURRENT FILING DATE: US/09/816,494
PRIOR APPLICATION NUMBER: 2001-03-23
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589) ... (2583)
US-09-816-494-1

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	Query Match	56.5%;	Score 3079;	DB 9;	Length 3544;	
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	Matches 3299;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1	
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QY	353	GAGAAAGACATTCACCTTGTGAGAGGCTCTTGTCTGAAAAATGGTTTAACTCTCTTTGGC	412			
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Qy 3473 AA 3474
Db 3523 AA 3524
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RESULT 20
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Currie, Roly A.O.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MP103-0180NMIM
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; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2586)
US-10-377-072-25
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Query Match 56.5%; Score 3079; DB 17; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3299; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db 344 ATCAATGTGAGGGGCTGTTGTGAGCGAGTCTTTGCAAGACATCAACGGAA 403
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Qy 653 CATCCCAATTTTGAAGCCATTAATCAATCTGCTCCAAAGCTTATGAAGGAAGTTGC 712
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US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MPI03-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; PRIOR FILING DATE: 2003-02-27
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
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; PRIOR APPLICATION NUMBER: US 09/843,297

; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
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; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Query Match 56.5%; Score 3079; DB 18; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3299; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 173 GCTTTCAGTCCAGTGTAAAGCTGTGAGCGCGGAGCAAAAGTAAAGATGTAAATG 232
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Db 2923 GTTGTGCTATCAAGAGATCTCAATATATAGCTTTGTGCGGACCTTCCATAGTACAGCT 2982
Qy 2933 TAGCGCTGAGACTGAGCAGCTTGGGGGTCAAGTGAAGACCTGTGTAAGGAGACAGGCC 2992
Db 2983 TAGCGCTGAGACTGAGCAGCTTGGGGGTCAAGTGAAGACCTGTGTAAGGAGACAGGCC 3042
Qy 2993 TAGGTGTAATCCAAAGAAATGATCTTATCAAAAGCTGATTCACAAACCAAGCTCACCC 3052
Db 3043 TAGGTGTAATCCAAAGAAATGATCTTATCAAAAGCTGATTCACAAACCAAGCTCACCC 3102

QY	3053	TGACAGCCGAGGGACACAGAGCATCTCTGCTGACCGACCAATTAGGCGCCTTGCAAG	3112
Db	3103	TGACAGCCGAGGGACACAGAGCATCTCTGCTGACCGACCAATTAGGCGCCTTGCAAG	3162
QY	3113	TCTACCTTAGAGCAACCAGACTCTAGACAGAAATCGGGGCTTGACCATCAAT	3172
Db	3163	TCTACCTTAGAGCAACCAGACTCTAGACAGAAATCGGGGCTTGACCATCAAT	3222
QY	3173	ATCTGCTAGCCATTTTCTAGGCATTTGGAAATAGGTAGTACATAGTCACATTTTCAGA	3232
Db	3223	ATCTGCTAGCCATTTTCTAGGCATTTGGAAATAGGTAGTACATAGTCACATTTTCAGA	3282
QY	3233	CCAATTCAAATGTCTATGCACAAAATCCCGTGGGCTAATGAGAGTAATTTTTTTT	3292
Db	3283	CCAATTCAAATGTCTATGCACAAAATCCCGTGGGCTAATGAGAGTAATTTTTTTT	3342
QY	3293	CTTCTAGCCTTATGAGAGAGGAAACTGTCTAGAGTTTCAGCTGAAACCAACGAAAC	3352
Db	3343	CTTCTAGCCTTATGAGAGAGGAAACTGTCTAGAGTTTCAGCTGAAACCAACGAAAC	3402
QY	3353	TGGCAACATCAACGATTTAAGCTAAGGTTGGAGGCTAACGAGTTACTCCCTCTTTGTA	3412
Db	3403	TGGCAACATCAACGATTTAAGCTAAGGTTGGAGGCTAACGAGTTACTCCCTCTTTGTA	3462
QY	3413	AATCAAGAATTTGTTAAATAGGATGTGTCAATCTTTAAATAAAGATGAACCTGGTTTC	3472
Db	3463	AATCAAGAATTTGTTAAATAGGATGTGTCAATCTTTAAATAAAGATGAACCTGGTTTC	3522
QY	3473	AA 3474	
Db	3523	AA 3524	

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RESULT 22
US-10-370-715B-261
; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;      Pacin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE OF INVENTION: Related Diseases
; FILE REFERENCE: PI94BR1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 261
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-370-715B-261

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Query Match	56.3%	Score 3069	DB 18	Length 3521
Best Local Similarity	99.9%	Pred. No. 0		
Matches 3459	Conservative 0	Mismatches 3	Indels 2	Gaps 2
OY	12	GAGGAGGAGACGACGCGAGACGAGACGCGACGCCCTCTCTGGCTCCGCG	71	
Db	38	GAGGAGGAGACGACGCGAGCGGACGCGAGCGCAGCGCCCTCTCGGCTCCGCG	97	
OY	72	GCGGCGCTCCCAAGTCCCGGAGGCGAGGGGGCCCCGAGGGAGACGCCGTGACAACTTT	131	
Db	98	GCGGCGCTCCCAAGTCCCGGAGGCGAGGGGGCCCCGAGGGAGACGCCGTGACAACTTT	157	
OY	132	CGTTCCCTCGAGGGAGTTGGGAGGTGGCGGCCCAAAAGCTTTCAGTCCAAGTTAA	191	

Db	158	CGTTTCCCTCTGAGGGAATTGGGAGGCTGGCGGGCCCCAAAAGCTTTCAGTCCAGTGAAT	217
Qy	192	GCTGTTGAGCCGCGGAGCAAAAGTAAAGAATGATGTAAATGCGCTGGCTTCCAAAGCA	251
Db	218	GCTGTGGAGCGCGGAGCAAAAGTAAAGAATGATGTAAATGCACTGGCTCTCCAAAGCA	277
Qy	252	TCTTTTGTGTGGAATGATTAATTCACGTATCTCTTAATGAATCAATATGAGGGGCTCG	311
Db	278	TCTTTTGTGTGGAATGATTAATTCACGTATCTCTTAATGAATCAATATGAGGGGCTCG	337
Qy	312	TTTGTGACGAGATCTTTGCAAGACATCAACCGGAAAGAAAGAGACTTCATT	371
Db	338	TTTGTGACGAGATCTTTGCAAGACATCAACCGGAAAGAAAGAGACTTCATT	397
Qy	372	GGAGGGCTCTGTGTGAAAAATGGGTTTAATCTCTCTTTGGCAGTCAACACGCTGACC	431
Db	398	GGAGGGCTCTGTGTGAAAAATGGGTTTAATCTCTCTTTGGCAGTCAACACGCTGACC	457
Qy	432	TCATACACTTTTAAGTACATGAGAGTGGCTGTAGACACTTGAACAACCACTTAATCATC	491
Db	458	TCATACACTTTTAAGTACATGAGAGTGGCTGTAGACACTTGAACAACCACTTAATCATC	517
Qy	492	GTGGCAATTTAAAGAGAGGTGGAAAAAGAGACTTAATGTGTATGATGCCATGAGAT	551
Db	518	GTGGCAATTTAAAGAGAGGTGGAAAAAGAGACTTAATGTGTATGATGCCATGAGAT	577
Qy	552	GATTGGAATCAAAATTTGTTACTGAGAGAGTTGGTGTCTGTCTGGAAAAATGGGAAACGGAAA	611
Db	578	GATTGGAATCAAAATTTGTTACTGAGAGAGTTGGTGTCTGTCTGGAAAAATGGGAAACGGAAA	637
Qy	612	AGTGTCTTAATGATGATGACCGGCCCATTTGTGAAATACAAATACATCCCATATTTGGAAGC	671
Db	638	AGTGTCTTAATGATGATGACCGGCCCATTTGTGAAATACAAATACATCCCATATTTGGAAGC	697
Qy	672	CAATTAATACACATCTCCACAGCTTATGAAGGAGGTGTGCAACGAGCAAAAGTGTAAAT	731
Db	698	CAATTAATACACATCTCCACAGCTTATGAAGGAGGTGTGCAACGAGCAAAAGTGTAAAT	757
Qy	732	TACAGAGCTCATCCAGCAATTCAGCAAAATTAAGTTGACATTTGATTCAGTCAAGAGGT	791
Db	758	TACAGAGCTCATCCAGCAATTCAGCAAAATTAAGTTGACATTTGATTCAGTCAAGAGGT	817
Qy	792	TGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCCTCTCTCTTCAGACTGTTTTCTCAC	851
Db	818	TGTAGTTTACGATCAAAGCTCCCAAGATGTTGCCCTCTCTCTTCAGACTGTTTTCTCAC	877
Qy	852	TGTAATTCGCGGTAACCTGGAAGAGGTTCAACTGTACCGCTGTGAGAGGTGTT	911
Db	878	TGTAACTTCGGGTAACTGGAAGAGGTTCAACTGTGTACCGCTGTGAGAGGTGTT	937
Qy	912	TGCTGAGTTCCTCGTTGTTTTCCCTGGCTCTGTGAGAGAAATCACTTAATCCCTCAC	971
Db	938	TGCTGAGTTCCTCGTTGTTTTCCCTGGCTCTGTGAGAGAAATCACTTAATCCCTCAC	997
Qy	972	CTGCAATTTCTCAGCGCTGCTTAAGTGTGTTCCAAATATGGGCAACCGGAATTTCTTCCAA	1031
Db	998	CTGCAATTTCTCAGCGCTGCTTAAGTGTGTTCCAAATATGGGCAACCGGAATTTCTTCCAA	1057
Qy	1032	TCTTATCTTGGCTGCAGCAGAGATGTCTCAACAAGAGCTGATACAGCAGATGGGAT	1091
Db	1058	TCTTATCTTGGCTGCAGCAGAGATGTCTCAACAAGAGCTGATACAGCAGATGGGAT	1117
Qy	1092	TGCTTAATGTGTTAATGCGAGCTATACCTGTCCAAAGCTGACTTTATCCCGAGTCTCA	1151
Db	1118	TGCTTAATGTGTTAATGCGAGCAATTAACCTGTCCAAAGCTGACTTTATCCCGAGTCTCA	1177
Qy	1152	TTTCCGTGATGCTGTGATGATGACAGCTTTTGTGAAAAATTTTGGCGATGTGACAA	1211
Db	1178	TTTCCGTGATGCTGTGATGATGACAGCTTTTGTGAAAAATTTTGGCGATGTGACAA	1237
Qy	1212	ATCAGTGAATTTCAATGAGAAAGCAAAAGCTCCCAATGATATGTTCTAGTGAATCTGTT	1271
Db	1238	ATCAGTGAATTTCAATGAGAAAGCAAAAGCTCCCAATGATATGTTCTAGTGAATCTGTT	1297

QY 1272 AGCTGGAGATCTCCCGCTCCGACCATGCTATCGCCCTACATCATGAAGAAGATGGAAT 1331
DB 1298 AGCTGGAGATCTCCCGCTCCGACCATGCTATCGCCCTACATCATGAAGAAGATGGAAT 1357
QY 1332 GTCTTTAGTAGAAGCTTACAGATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1391
DB 1358 GTCTTTAGTAGAAGCTTACAGATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1417
QY 1392 CAATTTTCTGGGCGCAATCTCTGAGACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1451
DB 1418 CAATTTTCTGGGCGCAATCTCTGAGACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1477
QY 1452 AGGGCGAAG 1511
DB 1478 AGGGCGAAG 1537
QY 1512 TGTCTCAGAGAGGTGAG 1571
DB 1538 TGTCTCAGAGAGGTGAG 1597
QY 1572 TACCTCAG 1631
DB 1598 TACCTCAG 1657
QY 1632 CGTGAGAGCGGTGAG 1691
DB 1658 CGTGAGAGCGGTGAG 1717
QY 1692 GTCCGAG 1751
DB 1718 GTCCGAG 1777
QY 1752 ATCAGTTTCAATTTAG 1811
DB 1778 ATCAGTTTCAATTTAG 1837
QY 1812 TGCTTTGAGATCTACAG 1871
DB 1838 TGCTTTGAGATCTACAG 1897
QY 1872 CTCCCTCTGTTAG 1931
DB 1898 CTCCCTCTGTTAG 1957
QY 1932 CAGCATCCCCAAG 1991
DB 1958 CAGCATCCCCAAG 2017
QY 1992 TTCCGTGAG 2051
DB 2018 TTCCGTGAG 2077
QY 2052 AAGTGGAG 2111
DB 2078 AAGTGGAG 2137
QY 2112 GCAAGCATCTCAAG 2171
DB 2138 GCAAGCATCTCAAG 2197
QY 2172 CCCCCAG 2231
DB 2198 CCCCCAG 2257
QY 2232 CTTCTACTCTGAG 2291
DB 2258 CTTCTACTCTGAG 2317
QY 2292 CCAAGTGGAG 2351
DB 2318 CCAAGTGGAG 2377

QY 2352 CAGAGCTGACTCGCGCGGAG 2411
DB 2378 CAGAGCTGACTCGCGCGGAG 2437
QY 2412 CAGAGCTGCGAATGGAATTTGAG 2471
DB 2438 CAGAGCTGCGAATGGAATTTGAG 2497
QY 2472 GCTGGGAG 2531
DB 2498 GCTGGGAG 2557
QY 2532 CTGAG 2591
DB 2558 CTGAG 2616
QY 2592 ATTCCTGTAAATCTGAAAT 2651
DB 2617 ATTCCTGTAAATCTGAAAT 2676
QY 2652 TATGTTGTAAG 2710
DB 2677 TATGTTGTAAG 2736
QY 2711 GAGAGATCAGCTAATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2770
DB 2737 GAGAGATCAGCTAATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2796
QY 2771 AGAGGAG 2830
DB 2797 AGAGGAG 2856
QY 2831 GTGTCTTTGTTGTTGAG 2890
DB 2857 GTGTCTTTGTTGTTGAG 2916
QY 2891 CTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2950
DB 2917 CTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2976
QY 2951 AGCTTGGGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3010
DB 2977 AGCTTGGGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3036
QY 3011 AAATGATCTTATCCAAAGCTATTTCAAAACCAAGCTATTTCAAAACCAAGCTATTTCAAAACCA 3070
DB 3037 AAATGATCTTATCCAAAGCTATTTCAAAACCAAGCTATTTCAAAACCAAGCTATTTCAAAACCA 3096
QY 3071 AGCATCACTGCTGAG 3130
DB 3097 AGCATCACTGCTGAG 3156
QY 3131 CAGTACCTCAG 3190
DB 3157 CAGTACCTCAG 3216
QY 3191 TAGGATTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3250
DB 3217 TAGGATTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3276
QY 3251 GCAGAGAAATTCGCGTGGGCTGAG 3310
DB 3277 GCAGAGAAATTCGCGTGGGCTGAG 3336
QY 3311 AGAAGGAGAACTGTCTAGAGATTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3370
DB 3337 AGAAGGAGAACTGTCTAGAGATTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3396
QY 3371 AGCTAAGTTGGAG 3430
DB 3397 AGCTAAGTTGGAG 3456
QY 3431 AATGGAGTTGTCATCTTTTAAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3474

Db 3457 AATGGATTGTCATCTTTAAATAAAGATGAACCTTGTTCAA 3500

RESULT 23

US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDM5
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (127)...(2121)
US-10-257-026-1

Query Match 52.1%; Score 2837; DB 17; Length 3059;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3057; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 412 CAGTACCCACGACCGCTGACCTCATACCTTTAGTACATGAGAGGCTTTGAG 471
Db 1 CAGTACCCACGACCGCTGACCTCATACCTTTAGTACATGAGAGGCTTTGAG 60
QY 472 CACACCACCATTAATCATCTGTGCAAAATTAAGAAGAGGTGGAAAAAGAGCTTAAT 531
Db 61 CACACCACCATTAATCATCTGTGCAAAATTAAGAAGAGGTGGAAAAAGAGCTTAAT 120
QY 532 GTTGTCAATGCGCCATGAGATGATTTGAACTCAATTTGTTACTGAGAGGTTGTGCTCTG 591
Db 121 GTTGTCAATGCGCCATGAGATGATTTGAACTCAATTTGTTACTGAGAGGTTGTGCTCTG 180
QY 592 CTGGAAGTGAAGGAAAAAGTGTGCTTAATTAATGATCCGCGCCATTTGTGAAATACAT 651
Db 181 CTGGAAGTGAAGGAAAAAGTGTGCTTAATTAATGATCCGCGCCATTTGTGAAATACAT 240
QY 652 ACATCCCATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAGCGAAGTTG 711
Db 241 ACATCCCATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAGCGAAGTTG 300
QY 712 CAAAGGACCAAGTGTTAATTAAGAGCTCATCCAGCTTCAAGCGAAAATTAAGTTGAC 771
Db 301 CAAAGGACCAAGTGTTAATTAAGAGCTCATCCAGCTTCAAGCGAAAATTAAGTTGAC 360
QY 772 ATTGATTGACGTGAGAGGTTGATTAAGATCAAGTCCCAAGATGTTGCCCTCTC 831
Db 361 ATTGATTGACGTGAGAGGTTGATTAAGATCAAGTCCCAAGATGTTGCCCTCTC 420
QY 832 TCTTCAAGCTGTTTCTCACTGTAATCTGTGGTAACTGAGAGAGCTTCAACTCTGT 891
Db 421 TCTTCAAGCTGTTTCTCACTGTAATCTGTGGTAACTGAGAGAGCTTCAACTCTGT 480
QY 892 CACCTGCTGAGAGTGGTTGTGCTGAGTCTCTGTTTCCCTGGCTCTGTGAAGA 951
Db 481 CACCTGCTGAGAGTGGTTGTGCTGAGTCTCTGTTTCCCTGGCTCTGTGAAGA 540
QY 952 AATATCACTAGTCCCTACCTGATTTCTGAGCTTGTCTTACCTGTTGCAACATTTGG 1011
Db 541 AATATCACTAGTCCCTACCTGATTTCTGAGCTTGTCTTACCTGTTGCAACATTTGG 600
QY 1012 CCAATCCGAATTTTCCCAATCTTATCTTGAGCTGCGAGGAGATGTCTCAACAAGAG 1071
Db 601 CCAATCCGAATTTTCCCAATCTTATCTTGAGCTGCGAGGAGATGTCTCAACAAGAG 660

QY 1072 CTGATACAGAGAAATGGGATTTGTTAATGTTAAATGCGACCTATACCTGTCCAAAGCT 1131
Db 661 CTGATACAGAGAAATGGGATTTGTTAATGTTAAATGCGACCAATACCTGTCCAAAGCT 720
QY 1132 GACTTATATCCCGAGTCTCATATTTCTCGTGTGCTGCTGGAATGACAGCTTTTGAAGAA 1191
Db 721 GACTTATATCCCGAGTCTCATATTTCTCGTGTGCTGCTGGAATGACAGCTTTTGAAGAA 780
QY 1192 ATTTTGGCGGTGTGAGCAAAATCAATGATTTCAATGAGAAAGCAAAAGCTTCAATGGA 1251
Db 781 ATTTTGGCGGTGTGAGCAAAATCAATGATTTCAATGAGAAAGCAAAAGCTTCAATGGA 840
QY 1252 TGTGTTCTAGTCACTGTTTGTAGTGGATCCCGCTCCGCAACATGCGTATGCGCTAC 1311
Db 841 TGTGTTCTAGTCACTGTTTGTAGTGGATCCCGCTCCGCAACATGCGTATGCGCTAC 900
QY 1312 ATCATGAAGAGATGAGATGATCTTTAGATGAATGACATTAATTTGTGAAAGAAAAAGA 1371
Db 901 ATCATGAAGAGATGAGATGATCTTTAGATGAATGACATTAATTTGTGAAAGAAAAAGA 960
QY 1372 CCTACTATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACATATGAGAGAGATT 1431
Db 961 CCTACTATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACATATGAGAGAGATT 1020
QY 1432 AAGAACCAGACTGAGGATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTGAGAGAG 1491
Db 1021 AAGAACCAGACTGAGGATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTGAGAGAG 1080
QY 1492 CCAATGAACCTGTCTCTGTGTCTCAGAGAGGTGACAGAAAAAGAGAGAGAGAGAGAG 1551
Db 1081 CCAATGAACCTGTCTCTGTGTCTCAGAGAGGTGACAGAAAAAGAGAGAGAGAGAGAG 1140
QY 1552 CCACCTGTGCGCATCTGTCTACTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1611
Db 1141 CCACCTGTGCGCATCTGTCTACTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1612 AGCGTGCCAGCGTGCAGCGTGCAGCGCTCCCTGTGAGAGAGAGAGAGAGAGAGAGAG 1671
Db 1201 AGCGTGCCAGCGTGCAGCGTGCAGCGCTCCCTGTGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1672 GCGCTCAGTGGGCTGCACTGTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1731
Db 1261 GCGCTCAGTGGGCTGCACTGTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1732 TCCCTCTCTGGAATTCATTAATGATTTCAATTTGAGAGAGAGAGAGAGAGAGAGAG 1791
Db 1321 TCCCTCTCTGGAATTCATTAATGATTTCAATTTGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1792 GCGCTCTCTCATCAGAGAGTGTGGAATTAATCAAACTTCCACTGCTGAGTGG 1851
Db 1381 GCGCTCTCTCATCAGAGAGTGTGGAATTAATCAAACTTCCACTGCTGAGTGG 1440
QY 1852 ACCAACAAGTATGCGAGTTCCTCCCTGTTCAAGAACTATGAGAGAGAGAGAGAGAG 1911
Db 1441 ACCAACAAGTATGCGAGTTCCTCCCTGTTCAAGAACTATGAGAGAGAGAGAGAGAG 1500
QY 1912 AGTCTGATTAAG 1971
Db 1501 AGTCTGATTAAG 1560
QY 1972 AGCAG 2031
Db 1561 AGCAG 1620
QY 2032 CTTTATATCTCACTGATGAGAGTGGAGCGTGGAGCAATTAACACACAGCTTCTT 2091
Db 1621 CTTTATATCTCACTGATGAGAGTGGAGCGTGGAGCAATTAACACACAGCTTCTT 1680
QY 2092 TTGCGCTTTTCCAG 2151
Db 1681 TTGCGCTTTTCCAG 1740
QY 2152 TGGCACTGGATATCTTGAGCCGCCAGAGCTTCAACCTTCCCTGAGCAGAGAGCTGTAT 2211

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Db      1741 TGGCACTGGGATATCTTGGCCCCCGAGACTCTACCCCTTCCCTACCGAGCGAGCTGGAT 1800
Qy      2212 TTTGGCAGAGATCCCACTTCTACTGTGCTGAGCCATTAGAGGAGCGAGT 2271
Db      1801 TTTGGCAGAGATCCCACTTCTACTGTGCTGAGCCATTAGAGGAGCGAGT 1860
Qy      2272 TACTGTGCTGAGCTGAGCGAGCTGCGCACTTGGAGAGCAAGTCTATTCTGTGCG 2331
Db      1861 TACTGTGCTGAGCTGAGCGAGCTGCGCACTTGGAGAGCAAGTCTATTCTGTGCG 1920
Qy      2332 AGCGCGGAGAGCCCAAGTGAAGAGCTGACTGCGCGGAGCTGCGATGAGAGAGCC 2391
Db      1921 AGCGCGGAGAGCCCAAGTGAAGAGCTGACTGCGCGGAGCTGCGATGAGAGAGCC 1980
Qy      2392 TTTGAAAAGCAATTAAACGAGAGCTGCCAAATGGAATTTGGAGAGAGCTCATGTCA 2451
Db      1981 TTTGAAAAGCAATTAAACGAGAGCTGCCAAATGGAATTTGGAGAGAGCTCATGTCA 2040
Qy      2452 GAGAACAGATCAAGGAGAGCTGGGAGAAAGTGGCAGTCAAGTCTAGCTTTTGGGAGC 2511
Db      2041 GAGAACAGATCAAGGAGAGCTGGGAGAAAGTGGCAGTCAAGTCTTTTGGGAGC 2100
Qy      2512 ATGGAATCATTTGAGGTCTCTGAGAGAGAGACCTTGTGACTTCTATAGCAATTTT 2571
Db      2101 ATGGAATCATTTGAGGTCTCTGAGAGAGAGACCTTGTGACTTCTATAGCAATTTT 2159
Qy      2572 TTTTCTGTTTCAAAAAAATCCCTGTAATCTGGAATATATATATATATATATATAT 2631
Db      2160 TTTTCTGTTTCAAAAAAATCCCTGTAATCTGGAATATATATATATATATATATAT 2219
Qy      2632 ATATTTTGGAAAATGAGAGCTATGCTATGTAATGAAAGAGTGAATCAACCCAGTTTAC 2691
Db      2220 ATATTTTGGAAAATGAGAGCTATGCTATGTAATGAAAGAGTGAATCAACCCAGTTTAC 2279
Qy      2692 TCTCTTAAATCTGATTTGAGAGTCACTATATCTTCTCAACAAAATGAGAGGAGC 2751
Db      2280 TCTCTTAAATCTGATTTGAGAGTCACTATATCTTCTCAACAAAATGAGAGGAGC 2339
Qy      2752 AGAGCTGTAATCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
Db      2340 AGAGCTGTAATCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2399
Qy      2812 CTGTGTTCTTAAAGAGAGTCTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2871
Db      2400 CTGTGTTCTTAAAGAGAGTCTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2459
Qy      2872 CGTGTGCTACTAGAGATCTCAATATATAGTCTTGTCCGAGCCCTTCAATAGTACCC 2931
Db      2460 CGTGTGCTACTAGAGATCTCAATATATAGTCTTGTCCGAGCCCTTCAATAGTACCC 2519
Qy      2932 TTAGCGCTGAGAGCTGAGCGAGCTGGGGGTCAAGTATGAGTCACTGTTAGGAGAGC 2991
Db      2520 TTAGCGCTGAGAGCTGAGCGAGCTGGGGGTCAAGTATGAGTCACTGTTAGGAGAGC 2579
Qy      2992 CTAGTGTGTAATCCAGAGAAATGATCTATCCAAAGCTGATTCACAAACCAAGCTAC 3051
Db      2580 CTAGTGTGTAATCCAGAGAAATGATCTATCCAAAGCTGATTCACAAACCAAGCTAC 2639
Qy      3052 CTGACAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3111
Db      2640 CTGACAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2699
Qy      3112 GTCTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3171
Db      2700 GTCTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2759
Qy      3172 TATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3231
Db      2760 TATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2819
Qy      3232 ACGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3291

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Db      2820 ACGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2879
Qy      3292 TCTTCTGAGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3351
Db      2880 TCTTCTGAGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2939
Qy      3352 CTGGCAATCATCAGATTTAAAGCTTAAAGTGGAGGCTTAAAGAGTCACTCCCTTTGT 3411
Db      2940 CTGGCAATCATCAGATTTAAAGCTTAAAGTGGAGGCTTAAAGAGTCACTCCCTTTGT 2999
Qy      3412 AATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3471
Db      3000 AATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3059

RESULT 24
US-10-296-115-520
; Sequence 520, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseg Inc
; TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 520
; LENGTH: 2966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2966)
; OTHER INFORMATION: n = a,t,c or g
US-10-296-115-520

Query Match      48.1%; Score 2624; DB 17; Length 2966;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2844; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy      582 GGTGGCTCTGCTGGAAGAGTGAACGAGAAAGTCTGCTAATATATATATATATATATAT 641
Db      67 GGTGGCTCTGCTGGAAGAGTGAACGAGAAAGTCTGCTAATATATATATATATATATAT 126
Qy      642 GGAATTAACAATATATATATATATATATATATATATATATATATATATATATATATAT 701
Db      127 GGAATTAACAATATATATATATATATATATATATATATATATATATATATATATATAT 186
Qy      702 GCGAAGGTTGCAACAGAGCAAAAGTGTATATATATATATATATATATATATATATATAT 761
Db      187 GCGAAGGTTGCAACAGAGCAAAAGTGTATATATATATATATATATATATATATATATAT 246
Qy      762 TAAAGTTGACATTTATATATATATATATATATATATATATATATATATATATATATAT 821
Db      247 TAAAGTTGACATTTATATATATATATATATATATATATATATATATATATATATATAT 306
Qy      822 TGCCCTCTCTCTGAGAGCTGTTTCTCACTGTACTTCTGAGTAACTGAGAGAGAGCTT 881
Db      307 TGCCCTCTCTCTGAGAGCTGTTTCTCACTGTACTTCTGAGTAACTGAGAGAGAGCTT 366
Qy      882 CAATCTGTTTCACTGCTTGGAGGTTGCTGAGTCTCTGCTGTTTCCCTGGGCT 941
Db      367 CAATCTGTTTCACTGCTTGGAGGTTGCTGAGTCTCTGCTGTTTCCCTGGGCT 426
Qy      942 CTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
Db      427 CTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
Qy      1002 CAACATTTGGGCAACCGGAATTTTCCCAATCTTATCTTGGCTGAGAGAGATGTCT 1061

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Db 487 CAACATTGGGCGAACCCGGAATTCCTCCCAATCTTTATCTTGCGTCCAGGAGATGTCTT 546
Qy 1062 CAACAAGAGCTGTATAGAGAGATGGGATTTGGTTATGTGTAAATGCCAGTAAACCTTG 1121
Db 547 CAACAAGAGAGCTGTATAGAGAGATGGGATTTGGTTATGTGTAAATGCCAGCAATCTTG 606
Qy 1122 TCCAAAGCTGAGCTTTATCCCCAGTCTCATTTCCGCGTGTGCTGTGAATGACAGCTT 1181
Db 607 TCCAAAGCTGAGCTTTATCCCCAGTCTCATTTCCGCGTGTGCTGTGAATGACAGCTT 666
Qy 1182 TTGTGAGAAAATTTTGGCCGTGTGTGACAAATCAGTAAATTTTCATTGAGAAAAGCAAAAGC 1241
Db 667 TTGTGAGAAAATTTTGGCCGTGTGTGACAAATCAGTAAATTTTCATTGAGAAAAGCAAAAGC 726
Qy 1242 CTCGAATGATGTGTCTAGTGACATGTTTAAAGTGGAGATCTCCCGCTCCGCCACCATCTGC 1301
Db 727 CTCGAATGATGTGTCTAGTGACATGTTTAAAGTGGAGATCTCCCGCTCCGCCACCATCTGC 786
Qy 1302 TATCGCTCATCATGATGAGAGATGAGACATGCTTTAGATGAACTTACAGATTTGTGA 1361
Db 787 TATCGCTCATCATGATGAGAGATGAGACATGCTTTAGATGAACTTACAGATTTGTGA 846
Qy 1362 AGAAAAAAGACCTATATATCTTCAAACCTTCAATTTTGTGGGCCAACTCTGTGACTATGA 1421
Db 847 AGAAAAAAGACCTATATATCTTCAAACCTTCAATTTTGTGGGCCAACTCTGTGACTATGA 906
Qy 1422 GAAGAAGATTAAGAACAGAGCTGAGAGCATCAGGGCCCAAGAGCAAACTCAACTCTGCA 1481
Db 907 GAAGAAGATTAAGAACAGAGCTGAGAGCATCAGGGCCCAAGAGCAAACTCAACTCTGCA 966
Qy 1482 CCTGGAAGAACCAATGAACCTGTCCCTGCTGTCTCAGAGGGTGAAGAAAAGGAGAC 1541
Db 967 CCTGGAAGAACCAATGAACCTGTCCCTGCTGTCTCAGAGGGTGAAGAAAAGGAGAC 1026
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Qy 1602 GCATCCCGCAGAGCTGCGGAGGCTCCAGCGTGCAGCGCTGTGTAGAGAACAGGCC 1661
Db 1087 GCATCCCGCAGAGCTGCGGAGGCTCCAGCGTGCAGCGCTGTGTAGAGAACAGGCC 1146
Qy 1662 GCTGGTACAGGCGCTCAGTGSGCTGACCTGTCCGAGACAGGCTGGAAGACAGCATTA 1721
Db 1147 GCTGGTACAGGCGCTCAGTGSGCTGACCTGTCCGAGACAGGCTGGAAGACAGCATTA 1206
Qy 1722 GCTCAAGGCTCTCTCTGTGGAATGAATCAATTCATTTTCAAGCAGATGGCAGC 1781
Db 1207 GCTCAAGGCTCTCTCTGTGGAATGAATCAATTCATTTTCAAGCAGATGGCAGC 1266
Qy 1782 ATCTTACATGAGCTTCTCTCATCAGAAAGCTTTGGAATATACAAACCTTCACTAC 1841
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Qy 1842 TCTGATAGGAGCAACAAGCTATGTCAGTCTTCCCTGTTCAGAACTATGAGAGCAGC 1901
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Qy 1902 TCCGAAAACAGTCTGTATAGAGAGAGAGAGATCCCAAGAGCTGCGACACCGCAG 1961
Db 1387 TCCGAAAACAGTCTGTATAGAGAGAGAGAGATCCCAAGAGCTGCGACACCGCAG 1446
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Db 1447 GCCTTACAGAGCAGAGCAAGCATTGCAATTCGCTGAGAACAGCAGCAGTGGCACCGC 1506
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Qy 2082 CAGCTTCTTTTCCGCTTTTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2141
Db 1567 CAGCTTCTTTTCCGCTTTTCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC

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Db 1627 CCTTAAAGGCTGGCAGCTCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAG 1686
Qy 2202 CAGCTGTATTTTGGCACAAGAGTCTTCACTTTACTCTGTGAGCATCTACGAGG 2261
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Qy 2262 CAGTGCAGTAACTCTGCTCAGCTGAGCAGCTGCGCCACTTGGCGGAGCAAGTCTA 2321
Db 1747 CAGTGCAGTAACTCTGCTCAGCTGAGCAGCTGCGCCACTTGGCGGAGCAAGTCTA 1806
Qy 2322 TTCTGTGCGCAGGCGGAGAACGCAAGTGAAGAAGCTGACTCGGCGGAGCTGAGTGA 2381
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Qy 2382 AGAGAGCCCCCTTGAAGAGAGCTTTAAACGAGAACTGCGCAATGGAATTTGAGAGAG 2441
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Qy 2442 CATCATGTCAAGAGAACAGTCTACGGAAGAGCTGGGGAAGAGTGGAGCTAGCTTACCTT 2501
Db 1927 CATCATGTCAAGAGAACAGTCTACGGAAGAGCTGGGGAAGAGTGGAGCTAGCTTACCTT 1986
Qy 2502 TTGGGCGAGCATGGAATCATTTGAGTCTCTGAGAAAGAAAGACCTTGTGACTTATA 2561
Db 1987 TTGGGCGAGCATGGAATCATTTGAGTCTCTGAGAAAGAAAGACCTTGTGACTTATA 2046
Qy 2562 GACAAATTTTTTTTTCTGTGCACAAAAAATTTCCCTGTAAATCTGAAATATATATATGT 2621
Db 2047 GACAA-TTTTTTTTTTCTGTGCACAAAAAATTTCCCTGTAAATCTGAAATATATATATGT 2105
Qy 2622 ACATACATATATATTTTTTGGAAAAATGAGCTATGATGTAAGAAACAAAGGTGATCAAC 2681
Db 2106 ACATACATATATATTTTTTGGAAAAATGAGCTATGATGTAAGAAACAAAGGTGATCAAC 2165
Qy 2682 CAGTGTATCTCTTAAACATCTGCATTTGAGAGATCAGTAAATCTTCTCAACAAA 2741
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Qy 2862 ACCATTTTCAAGTGTGCTATAGAGATCTGAAATATAGCTTTGTCCGACCTTCC 2921
Db 2346 ACCATTTTCAAGTGTGCTATAGAGATCTGAAATATAGCTTTGTCCGACCTTCC 2405
Qy 2922 ATAGTACACCTTACGCTGAGACTGAGCAGCTTGGGGGTCAAGTATGAGACCTGTTA 2981
Db 2406 ATAGTACACCTTACGCTGAGACTGAGCAGCTTGGGGGTCAAGTATGAGACCTGTTA 2465
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Db 2466 GGGACAGAGCTTATGTGTAAATTCAGAGAAATGATCTATCAAAAGCTATTCACAAAC 2525
Qy 3042 CCAAGCTCACTGACAGCGGAGGAGACAGAGATCACTGTGTGAGACGACCATTAAGGG 3101
Db 2526 CCAAGCTCACTGACAGCGGAGGAGACAGAGATCACTGTGTGAGACGACCATTAAGGG 2585
Qy 3102 CCTTGCAGAGTCTACTTAAAGCAAAACCACTACCTGACAGAGAAAGTGGGGCTTTG 3161
Db 2586 CCTTGCAGAGTCTACTTAAAGCAAAACCACTACCTGACAGAGAAAGTGGGGCTTTG 2645
Qy 3162 ACCACTACCATATCTGTGATGCCATTTTCTAGAGCAATGTGAATAGTATGATGCTA 3221
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 Qy 3282 AATTTTTTTTCTCTACGCTTTATGAAAGAGAGGAAATCTGTAGATTCACTGAAC 3341
 Db 2766 AATTTTTTTTCTCTACGCTTTATGAAAGAGAGGAAATCTGTAGATTCACTGAAC 2825
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 Db 2886 CCTCTTTGTAATCAAGAAATTTGTTT 2912

RESULT 25

US-10-168-506-2
 : Sequence 2, Application US/10168506
 : Publication No. US20040053229A1
 : GENERAL INFORMATION:
 : APPLICANT: PLOWMAN, GREGORY D.
 : APPLICANT: MARTINEZ, RICARDO
 : APPLICANT: MAYHE, DAVID
 : APPLICANT: MANNING, GERRARD
 : APPLICANT: SUDARSHANAM, SUCHA
 : APPLICANT: HILL, RON
 : APPLICANT: FLANAGAN, PETER
 : TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
 : FILE REFERENCE: 038602/1351
 : CURRENT APPLICATION NUMBER: US/10/168, 506
 : PRIOR FILING DATE: 2002-06-21
 : PRIOR APPLICATION NUMBER: PCT/US00/34736
 : NUMBER OF SEQ ID NOS: 76
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 2
 : LENGTH: 2732
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-10-168-506-2

Query Match 45.1%; Score 2459; DB 17; Length 2732;

Beet Local Similarity 99.9%; Pred. No. 0;
 Matches 2729; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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 Db 61 TCGGCTCCGCGCGCGCGCTCGCAATCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGCG 120
 Qy 121 GTGCACTTCTGTTTCCCTCTGAGGGAATTGGAGGTCGCGCGGCCCAAAAGCTTTAG 180
 Db 121 GTGCACTTCTGTTTCCCTCTGAGGGAATTGGAGGTCGCGCGGCCCAAAAGCTTTAG 180
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 Db 241 GCTCCAAAGCATCTTTTGTGTGATGTTATTCAGATCATCTTTTATGATCAAAATG 300
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 Db 301 TGAGAGGCTGCTTTTGTGAGCGAGTCTTTTGAAGACATCAACGCGGAAAGAGAAAGA 360
 Qy 361 GACATTCACCTTGAGAGGCTTTGTGAAGATGGGTTTAACCTCTCTTTTGTGCAAGTCA 420

Db 361 GACATTCACCTTGAGAGGCTTTGTGAAGATGGGTTTAACCTCTCTTTTGTGCAAGTCA 420
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 Db 421 CCAAGCTCACTCATACCTTTTATGATACAAATGAGATGAGCTTAGAGACACACAC 480
 Qy 481 ATTACATCATGTGGCAATTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 Db 481 ATTACATCATGTGGCAATTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 Qy 541 GCCCATGAGATGATGGAATCAATTTGTATCTGAGAGGTTGTTGCTCTGCTGAGAAAT 600
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 Db 601 GGAAGGAAAAAGTCTCTAATGATGAGCGGCAATTTTGTGATACAAATCAATCCAC 660
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 Qy 781 AGTCAGAAAGTTGATGTTAAGATCAAAAGCTCCCAAGATGTTGCTCTCTCTCAAG 840
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 Db 1321 AGATGAGATGTTTAAAGTGAAGCTTACAGATTTGTGAAGAAAAAGCTTACTATA 1380
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Db 1501 CCGTCCCTGCTGCTCAGAGGGTGGACAGAAAAGGAGAGCGCCCTCAGTCCACCTCT 1560
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Db 1561 GCCGACTGTGCTACCTCAGAGGAGAGAGCAAAAGGCCGTGATCCCGCAGCGTGGCC 1620
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QY 1861 CTATGCGAATGCTCCCTGCTTGAAGAACTATCGAGACAGACTCCGAAACAGTCTGAT 1920
Db 1861 CTATGCGAATGCTCCCTGCTTGAAGAACTATCGAGACAGACTCCGAAACAGTCTGAT 1920
QY 1921 AAGGAGAAAGCCAGCATCCCAAGAAAGCTGCAAGCCGCAAGGCTTGAAGACCAAG 1980
Db 1921 AAGGAGAAAGCCAGCATCCCAAGAAAGCTGCAAGCCGCAAGGCTTGAAGACCAAG 1980
QY 1981 AAGCATTTGATTCGGTGAAGCAAGCAGCAGTGGCAACGCCAGAGTCCCTTATCT 2040
Db 1981 AAGCATTTGATTCGGTGAAGCAAGCAGCAGTGGCAACGCCAGAGTCCCTTATCT 2040
QY 2041 CCACTGCAATCGAAGTGGAGCGTGAAGGACATTTACACACACAGCTTCTTTCGGCTT 2100
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Db 2521 ATTGAGGTCTCTGAGAGAAAGACATTTGATGATTTTCTTCTTCTTCTTCTTCTTCTTCT 2580

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Db 2640 GAAATGAGGCTATGATGTAAAGCAACAGGTGATCAACCCAGTGTACTCTCTTAC 2699
QY 2701 ATCTGCAATTTAGAGATCAAGTAAATCTCTCT 2733
Db 2700 ATCTGCAATTTAGAGATCAAGTAAATCTCTCT 2732

RESULT 26
US-09-964-277-20
; Sequence 20, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucbe, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 3332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-20

Query Match 38.8%; Score 2117; DB 9; Length 3332;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2357; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
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Db 1395 GCGAGACGCGCTCTCAGTCACTCTGTGCCAGCTGTGCTACCTCAGAGGCAAGCAGAAA 1454
QY 1595 GGCCTGTGATCCCGCAGCGGTGCGCAAGCGTCCCAAGGTGAGCGCTGCTGTTAGAG 1654
Db 1455 GGCCTGTGATCCCGCAGCGGTGCGCAAGCGTCCCAAGGTGAGCGCTGCTGTTAGAG 1514

QY 1655 ACAGCCCGCTGTACAGGCGCTCAGTGGGCTGCACTTCGCGACAGCAGCTGGAGACA 1714
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QY 1775 TGGCAGCATCTCTTACATGAGCTTCTCTCTCAGATGAGTCTTGGAAATCTACAAACCTT 1834
DB 1655 TGGCAGCATCTCTTACATGAGCTTCTCTCTCAGATGAGTCTTGGAAATCTACAAACCTT 1694
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DB 1695 CCACTACTCTGAGTGGAGCAACCAAGCTATGCAAGTCTCTCTCTTTCAGAACTATCGG 1754
QY 1895 AGCAGATCTCCGAGAACCAAGTCTCTGATTAAGAGAGAACCAAGTCTCCCAAGAGCTGACA 1954
DB 1755 AGCAGATCTCCGAGAACCAAGTCTCTGATTAAGAGAGAACCAAGTCTCCCAAGAGCTGACA 1814
QY 1955 CCGCAGGCTCTTACAGACAGCCAGAGCAGATTCATTCGCTGAGAACCAAGCAGCTG 2014
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QY 2015 GCAACCGCCAGAGGTCCTTTTATCTCCACTGATCGAAGTGGAGCGCTGGAGACAATT 2074
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QY 2075 ACACACACAGCTTCTTTTCGAGCTTTCACACAGCAGACAGCCTCAAGAGTCTGCTG 2134
DB 1935 ACACACACAGCTTCTTTTCGAGCTTTCACACAGCAGACAGCCTCAAGAGTCTGCTG 1994
QY 2135 GCTGGGCTTAAAGGGCTGAGCTGAGATCTGGGCCCCGAGACCTTACCCCTTCC 2194
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QY 2195 TGACACAGCAGCTGTATTTTGCACAGAGTCTCACTCTCACTCTGCTCAGCATCT 2254
DB 2055 TGACACAGCAGCTGTATTTTGCACAGAGTCTCACTCTCACTCTGCTCAGCATCT 2114
QY 2255 ACGGAGGAGTGCAGATCTCTGCTCAAGTGCAGCAGCAGCTGCCACTTGGGAGACC 2314
DB 2115 ACGGAGGAGTGCAGATCTCTGCTCAAGTGCAGCAGCAGCTGCCACTTGGGAGACC 2174
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DB 2235 GGCATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGAGAACTGCCAAATGGAATTG 2294
QY 2435 GAGAGAGCATCATGTCAAGAAACAGTCAAGGAAAGCTGGGAAAAGTGGGAGTCACT 2494
DB 2295 GAGAGAGCATCATGTCAAGAAACAGTCAAGGAAAGCTGGGAAAAGTGGGAGTCACT 2354
QY 2495 CTACCTTTTCGGGAGAGTGAATCATTTAGAGTCTCTGAGAGAAAGACACTTGTAC 2554
DB 2355 CTACCTTTTCGGGAGAGTGAATCATTTAGAGTCTCTGAGAGAAAGACACTTGTAC 2414
QY 2555 TTCTATAGACAATTTTTTTCTGTTCACAAAAAAATTCCTGTAAATCTGAAATATA 2614
DB 2415 TTCTATAGACAATTTTTTTCTGTTCACAAAAAAATTCCTGTAAATCTGAAATATA 2473
QY 2615 TATATGTACATATATATTTTTTGAAGAAATGAGCTATGAGTGAAGCAACAGTGG 2674
DB 2474 TATATGTACATATATATTTTTTGAAGAAATGAGCTATGAGTGAAGCAACAGTGG 2533
QY 2675 ATCAACCAAGTTGTACTCTCTTAAACATCTGATTTGAAGATCACTGAATATCTCTTC 2734
DB 2534 ATCAACCAAGTTGTACTCTCTTAAACATCTGATTTGAAGATCACTGAATATCTCTTC 2593
QY 2735 AACAAAAATGAAAGGAGATGCTAGAAATCCCTTACAGGAGGAAAAACATTTTATTC 2794

DB 2594 AACAAAAATGAAAGGAGATGCTAGAAATCCCTTACAGGAGGAAAAACATTTTATTC 2653
QY 2795 AGTGAATTAACAATCTCTGTCTTAAAGAAAGAGTCTTGTGGTGGAGACAA 2854
DB 2654 AGTGAATTAACAATCTCTGTCTTAAAGAAAGAGTCTTGTGGTGGAGACAA 2713
QY 2855 ATCCCTTACCAATTTT-CAAGTGTGCTACTAAGAGATCTCAATATTAATGCTTTGCGG 2913
DB 2714 ATCCCTTACCAATTTTCAAGTGTGCTACTAAGAGATCTCAATATTAATGCTTTGCGG 2773
QY 2914 ACCCTTCAATGTAACCTTATGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTATGA 2973
DB 2774 ACCCTTCAATGTAACCTTATGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTATGA 2833
QY 2974 CCGTTTGAAGGAGAGGCTAGTGTAAATCCAGAGAAATGATCTTACCAAGCTAT 3033
DB 2834 CCGTTTGAAGGAGAGGCTAGTGTAAATCCAGAGAAATGATCTTACCAAGCTAT 2893
QY 3034 TCACAAACCCAGCTCACTGACAGCCGAGGAGACAGACATCACTGCTGAGACGACC 3093
DB 2894 TCACAAACCCAGCTCACTGACAGCCGAGGAGACAGACATCACTGCTGAGACGACC 2953
QY 3094 ATTAGGGGCTTTCGCAAGTCTTACCTTATGAGCAAAACCAATCTCAGACAGAAATCG 3153
DB 2954 ATTAGGGGCTTTCGCAAGTCTTACCTTATGAGCAAAACCAATCTCAGACAGAAATCG 3013
QY 3154 GGGCTTGAACCACTACCAATCTGTGTAGCCCAATTTTCTAGGCAATTTGTAATGTA 3213
DB 3014 GGGCTTGAACCACTACCAATCTGTGTAGCCCAATTTTCTAGGCAATTTGTAATGTA 3073
QY 3214 GCTAGTCACTTTTACAGCAATTCAACTGTCTATGCAAAATTCCTGGGCTAG 3273
DB 3074 GCTAGTCACTTTTACAGCAATTCAACTGTCTATGCAAAATTCCTGGGCTAG 3133
QY 3274 ATGAGATTAATTTTTTTCTTCACTTATGAGAGAGGAACTGTCTAGATTC 3333
DB 3134 ATGAGATTAATTTTTTTCTTCACTTATGAGAGAGGAACTGTCTAGATTC 3193
QY 3334 AGCTGAACCAACAGAACTGGCAACATCAAGATTTAAGCTTGAAGTGGAGGCTTAACA 3393
DB 3194 AGCTGAACCAACAGAACTGGCAACATCAAGATTTAAGCTTGAAGTGGAGGCTTAACA 3253
QY 3394 GTTACCTCCCTCTTGTGAATCAAGAAATGTTTAAATGGAATGTCAATCTTTAA 3453
DB 3254 GTTACCTCCCTCTTGTGAATCAAGAAATGTTTAAATGGAATGTCAATCTTTAA 3313
QY 3454 TAAAGATGAACCTGTTC 3472
DB 3314 TAAAGATGAACCTGTTC 3332

RESULT 27
US-10-104-047-1750
; Sequence 1750, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1e1 full length cdna
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1750
; LENGTH: 2558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1750

Query Match 38.5%, Score 2098; DB 17; Length 2558;

Qy 4732 CAGCCTTATGCTGCTTCACTAGTGTGATTAATCACTTCTGGAATCGAGACTGCCGT 4791
Db 2161 CAGCCTTATGCTGCTTCACTAGTGTGATTAATCACTTCTGGAATCGAGACTGCCGT 2220
Qy 4792 GCGGAGGGGCTGCTCGAGAGCGAGCTCTGAGCTGCTTGAAGTCTTTAGTGGGGTG 4851
Db 2221 GCGGAGGGGCTGCTCGAGAGCGAGCTCTGAGCTGCTTGAAGTCTTTAGTGGGGTG 2280
Qy 4852 GTGCTGCTCTCTTCAAGCATGTAATTGGGAAAACCTCGCTCACTAGAGGGGATACA 4911
Db 2281 GTGCTGCTCTCTTCAAGCATGTAATTGGGAAAACCTCGCTCACTAGAGGGGATACA 2340
Qy 4912 GATGCTGATTTTAAAGACAAACTAGACTTCTAGTGAAGTCTGGAATGATTTA 4971
Db 2341 GATGCTGATTTTAAAGACAAACTAGACTTCTAGTGAAGTCTGGAATGATTTA 2400
Qy 4972 GGAC 4975
Db 2401 GGAC 2404

RESULT 28
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyer8, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-03002
CURRENT APPLICATION NUMBER: US/09/816,494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3.

Query Match 34.8%; Score 1896; DB 9; Length 1998;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1996; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 538 ATGCCCATGAGATGATTTGAACTCAATTTGTACTGAGAGTTGGTCTCTGCGAA 597
Db 1 ATGCCCATGAGATGATTTGAACTCAATTTGTACTGAGAGTTGGTCTCTGCGAA 60
Qy 598 AGTGGAAAGGAAAAGTCTGCTTAATGATAGCCGGCCATTGTTGGAATACATACATCC 657
Db 61 AGTGGAAAGGAAAAGTCTGCTTAATGATAGCCGGCCATTGTTGGAATACATACATCC 120
Qy 658 CACATTTTGAAGCATTAATATCACTGCTCAAGCTTATGAAGCGAAGTTGCCAAG 717
Db 121 CACATTTTGAAGCATTAATATCACTGCTCAAGCTTATGAAGCGAAGTTGCCAAG 180
Qy 718 GACAAAGTATTAATTAACAGAGCTCATCCAGATTCAAGGAAACATTAAGTTGACATTGAT 777
Db 181 GACAAAGTATTAATTAACAGAGCTCATCCAGATTCAAGGAAACATTAAGTTGACATTGAT 240
Qy 778 TGCACTGAGAAAGTTGATGATTAAGATCAAAAGCTCCCAAGATGTTGCTCTCTTCA 837
Db 241 TGCACTGAGAAAGTTGATGATTAAGATCAAAAGCTCCCAAGATGTTGCTCTCTTCA 300
Qy 838 GACCTTTTCTCACTGATCTTCTGGGTAACTGAGAGAGAGCTTCACTCTGCTCACTG 897
Db 301 GACCTTTTCTCACTGATCTTCTGGGTAACTGAGAGAGAGCTTCACTCTGCTCACTG 360
Qy 898 CTTCAGAGTGGATTGCTGATGCTCTGCTGTTTCCCTGAGCTCTGTAAGAGAAATCC 957

Db 361 CTTCAGAGTGGATTGCTGATGCTCTGCTGTTTCCCTGAGCTCTGTAAGAGAAATCC 420
Qy 958 ACTCAAGCCCTACCTGATTTCTCAGCCTGCTTACCTGTTGCAACATTTGGGCAAC 1017
Db 421 ACTCAAGCCCTACCTGATTTCTCAGCCTGCTTACCTGTTGCAACATTTGGGCAAC 480
Qy 1018 CGAATTTCTCCCAATCTTTATCTTGGCTGCCAGAGATGCTCAACAGAGAGCTGATA 1077
Db 481 CGAATTTCTCCCAATCTTTATCTTGGCTGCCAGAGATGCTCAACAGAGAGCTGATA 540
Qy 1078 CAGCAAGATGGAGTTGTTATGTTAAATGCCAGCTATACCTGTCAAAGCTGACTTT 1137
Db 541 CAGCAAGATGGAGTTGTTATGTTAAATGCCAGCTATACCTGTCAAAGCTGACTTT 600
Qy 1138 ATCCCGAGTCAATTTCTGCGGTGCTGCTGTAATGACCTTTTGAGAAAATTTTG 1197
Db 601 ATCCCGAGTCAATTTCTGCGGTGCTGCTGTAATGACCTTTTGAGAAAATTTTG 660
Qy 1198 CCGTGTGGAACAATGATGATTTCAATGAGAAAGCAAAAGCTCCCAATGATGTT 1257
Db 661 CCGTGTGGAACAATGATGATTTCAATGAGAAAGCAAAAGCTCCCAATGATGTT 720
Qy 1258 CTAGTCACTGTTTAACTGGGATCTCCGCTCCGCAACATGCTATGCTTACATCAG 1317
Db 721 CTAGTCACTGTTTAACTGGGATCTCCGCTCCGCAACATGCTATGCTTACATCAG 780
Qy 1318 AAGAGATGACATGCTTTTAAAGAGCTTACAGATTTTGAAAGAAAAGCTTCT 1377
Db 781 AAGAGATGACATGCTTTTAAAGAGCTTACAGATTTTGAAAGAAAAGCTTCT 840
Qy 1378 ATATCTCCAACTCAATTTTCTGGGCAACTCTGCACTATGAGAAAGATTAAGAAC 1437
Db 841 ATATCTCCAACTCAATTTTCTGGGCAACTCTGCACTATGAGAAAGATTAAGAAC 900
Qy 1438 CAGACTGAGATCAGAGGCGCAAGAGCAAACTCAAGCTGCTGCACTGAGAGCAAAAT 1497
Db 901 CAGACTGAGATCAGAGGCGCAAGAGCAAACTCAAGCTGCTGCACTGAGAGCAAAAT 960
Qy 1498 GAACCTGCTCCTGCTGCTCAAGAGGTGAGACAGAAAGCGGCTTCAATGCCACC 1557
Db 961 GAACCTGCTCCTGCTGCTCAAGAGGTGAGACAGAAAGCGGCTTCAATGCCACC 1020
Qy 1558 TGTGCGCACTCTGCTTACCTCGAGAGCAGAGCAAAAGCGGCTGATCCGCGCAGCTG 1617
Db 1021 TGTGCGCACTCTGCTTACCTCGAGAGCAGAGCAAAAGCGGCTGATCCGCGCAGCTG 1080
Qy 1618 CCGAGCGTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1677
Db 1081 CCGAGCGTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1678 AGTGGCTGCACTGCTCCGAGACAGAGCTGGAAGACAGCAATTAAGCTCAAGCTTCTTC 1737
Db 1141 AGTGGCTGCACTGCTCCGAGACAGAGCTGGAAGACAGCAATTAAGCTCAAGCTTCTTC 1200
Qy 1738 TCTCTGATTAATCAATAGTTTCAATTTCAAGCCAGATGAGAGATCTTCAATGAGCTTC 1797
Db 1201 TCTCTGATTAATCAATAGTTTCAATTTCAAGCCAGATGAGAGATCTTCAATGAGCTTC 1260
Qy 1798 TCTCTCATCAAGAGATGCTTTGGAATACTACAACTTCACTACTGATGAGAGCAAC 1857
Db 1261 TCTCTCATCAAGAGATGCTTTGGAATACTACAACTTCACTACTGATGAGAGCAAC 1320
Qy 1858 AAGCTATGCAATTTCTCCCTGTTCAAGAACTATGAGAGAGATCTCCGAAACCAATCT 1917
Db 1321 AAGCTATGCAATTTCTCCCTGTTCAAGAACTATGAGAGAGATCTCCGAAACCAATCT 1380
Qy 1918 GATTAAGAGAGAGCAGATCCCAAGAGCTGAGACCGGAGGCTTGAAGAGCAG 1977
Db 1381 GATTAAGAGAGAGCAGATCCCAAGAGCTGAGACCGGAGGCTTGAAGAGCAG 1440
Qy 1978 AGCAAGGATTTGATTCGATCAGAAACAGAGCAGAGTGGCAACCGCCAGAGGCTCCCTTTA 2037
Db 1441 AGCAAGGATTTGATTCGATCAGAAACAGAGCAGAGTGGCAACCGCCAGAGGCTCCCTTTA 1500

QY	2038	TCGCCATCGATCGAAGTGGGAGGCTGGAGGACAATTACACACCAAGCTCTTTTCGGC	2097
Db	1501	TCGCCATCGATCGAAGTGGGAGGCTGGAGGACAATTACACACCAAGCTCTTTTCGGC	1560
QY	2098	CTTCCACACGCGCAGCAGCACTCAGCAAGTCTGTGGCCCTTAAAGGCTGGAC	2157
Db	1561	CTTCCACACGCGCAGCAGCACTCAGCAAGTCTGTGGCCCTTAAAGGCTGGAC	1620
QY	2158	TGCGAATCTTGGGCCCCCAAGACTCTAACCCCTTCCCTGACACAGCTGTATTTGGC	2217
Db	1621	TGCGAATCTTGGGCCCCCAAGACTCTAACCCCTTCCCTGACACAGCTGTATTTGGC	1680
QY	2218	ACAGAGTCCTCAACTTCTACTCTGCTCCAGCCATCTACGAGGCACTGCGCACTTACTCT	2277
Db	1681	ACAGAGTCCTCAACTTCTACTCTGCTCCAGCCATCTACGAGGCACTGCGCACTTACTCT	1740
QY	2278	GCTTACAGCTGCAGCCAGCTGCCACTTGGCGAGACAAGTCTATTCTGTGCGCAGCGG	2337
Db	1741	GCTTACAGCTGCAGCCAGCTGCCACTTGGCGAGACAAGTCTATTCTGTGCGCAGCGG	1800
QY	2338	CAGAGCCCAAGTACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAAGACCCCTTTGAA	2397
Db	1801	CAGAGCCCAAGTACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAAGACCCCTTTGAA	1860
QY	2398	AAGCAGTTTAAACGAGAGCTGCCAAATGGATTTTGGAGAGGACATCATGTCAAGAAC	2457
Db	1861	AAGCAGTTTAAACGAGAGCTGCCAAATGGATTTTGGAGAGGACATCATGTCAAGAAC	1920
QY	2458	AGGTCACGGGAAGAGCTGGGGAAGTGGGCACTGACTGACTGCTTTTCGGCAGCATGGA	2517
Db	1921	AGGTCACGGGAAGAGCTGGGGAAGTGGGCACTGACTGACTGCTTTTCGGCAGCATGGA	1980
QY	2518	ATCATTGAGGCTCTCTGCA	2535
Db	1981	ATCATTGAGGCTCTCTGCA	1998
RESULT 29			
US-10-377-072-27			
; Sequence 27, Application US/10377072			
; Publication No. US2004009501A1			
GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals Inc.			
; APPLICANT: Curtis, Rory A.J.			
; APPLICANT: Logan, Thomas Joseph			
; APPLICANT: Glucksmann, Maria A.			
; APPLICANT: Meyers, Rachel E.			
; APPLICANT: Williamson, Mark J.			
; APPLICANT: Rudolph-Owen, Laura A.			
; APPLICANT: Chun, Miyoung			
; APPLICANT: Tsai, Fong-Ying			
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,			
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES			
FILE REFERENCE: MP103-0180MINI			
CURRENT APPLICATION NUMBER: US/10/377, 072			
CURRENT FILING DATE: 2003-02-27			
PRIOR APPLICATION NUMBER: US 09/895, 860			
PRIOR FILING DATE: 2001-06-29			
PRIOR APPLICATION NUMBER: US 60/215, 370			
PRIOR FILING DATE: 2000-06-29			
PRIOR APPLICATION NUMBER: US 09/723, 806			
PRIOR FILING DATE: 2000-11-28			
PRIOR APPLICATION NUMBER: US 60/187, 455			
PRIOR FILING DATE: 2000-03-07			
PRIOR APPLICATION NUMBER: US 09/843, 297			
PRIOR FILING DATE: 2001-04-25			
PRIOR APPLICATION NUMBER: US 60/199, 801			
PRIOR FILING DATE: 2000-04-26			
PRIOR APPLICATION NUMBER: US 09/861, 801			
PRIOR FILING DATE: 2001-05-21			
PRIOR APPLICATION NUMBER: US 60/205, 508			

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? PRIOR FILING DATE: 2000-05-19
? PRIOR APPLICATION NUMBER: US 09/816,494
? PRIOR FILING DATE: 2001-03-23
? PRIOR APPLICATION NUMBER: US 09/815,419
? PRIOR FILING DATE: 2001-03-22
? Remaining Prior Application data removed - See File Wrapper or PALM
? NUMBER OF SEQ ID NOS: 114
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 1998
? TYPE: DNA
? ORGANISM: Homo Sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(1998)
US-10-377-072-27

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Query Match	34.8%	Score 1896;	DB 17;	Length 1998;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1996; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	538	ATGGGCCCAAGAGATGATTTGAACTCAAAATTTGTATCTGAAGATGGTGGCTCTGCTGGAA	597
Db	1	ATGGGCCCAAGAGATGATTTGAACTCAAAATTTGTATCTGAAGATGGTGGCTCTGCTGGAA	60
QY	598	AGTGGAAACGGAAAAAGTGTGCTAAATTGATATAGCCGGCCATTGTGGAAATACATATCATCC	657
Db	61	AGTGGAAACGGAAAAAGTGTGCTAAATTGATATAGCCGGCCATTGTGGAAATACATATCATCC	120
QY	658	CACATTTTGGAAAGCCATTATATCAACTGTCTCAAGCTTATGAGCGAAGTGGCAACG	717
Db	121	CACATTTTGGAAAGCCATTATATCAACTGTCTCAAGCTTATGAGCGAAGTGGCAACG	180
QY	718	GACAAAGTTAAATTAACAGAGCTATCCAGCATTAAGGAAACATTAAGCTTGACATTTAT	777
Db	181	GACAAAGTTAAATTAACAGAGCTATCCAGCATTAAGGAAACATTAAGCTTGACATTTAT	240
QY	778	TGCAGTCAGAAAGTTGTAGTTTACATCAAAAGCTCCCAAGATGTGGCTCTCTCTCA	837
Db	241	TGCAGTCAGAAAGTTGTAGTTTACATCAAAAGCTCCCAAGATGTGGCTCTCTCTCTCA	300
QY	838	GACTGTTTTCTCACTGTACTTCTGGGTAACCTGAGAAAGACTTCAACTGTTCACCTG	897
Db	301	GACTGTTTTCTCACTGTACTTCTGGGTAACCTGAGAAAGACTTCAACTGTTCACCTG	360
QY	898	CTTGAGAGTGGGTTTGCTGAGTGTCTCTGGTGTTCCTGGCCTCTGTGAAGAAAAATCC	957
Db	361	CTTGAGAGTGGGTTTGCTGAGTGTCTCTGGTGTTCCTGGCCTCTGTGAAGAAAAATCC	420
QY	958	ACTCTAGTCCCTACCTGCAATTTCTCAGGCTTGCTTAACTGTGGCAATTTGGGGAAC	1017
Db	421	ACTCTAGTCCCTACCTGCAATTTCTCAGGCTTGCTTAACTGTGGCAATTTGGGGAAC	480
QY	1018	CGAATTTCTTCCCAATCTTTTATCTTGCGCTGCCAGCGAATGTCCTCAACMAAGAGCTGATA	1077
Db	481	CGAATTTCTTCCCAATCTTTTATCTTGCGCTGCCAGCGAATGTCCTCAACMAAGAGCTGATA	540
QY	1078	CAGAGAAATGGGAATTTGTATATGTGTAAATGCGACGTATACCTGTCCAAAGCTGACTTT	1137
Db	541	CAGAGAAATGGGAATTTGTATATGTGTAAATGCGACGTATACCTGTCCAAAGCTGACTTT	600
QY	1138	ATCCCCGAGTCTCATTTCTGCGCGTGCCTGTGAATACAGCTTTTGTGAGAAAATTTTG	1197
Db	601	ATCCCCGAGTCTCATTTCTGCGCGTGCCTGTGTGAATACAGCTTTTGTGAGAAAATTTTG	660
QY	1198	CCGTGTGTGGAACAATCAGTAGATTTCAATTGAGAAAACAAAGCCTCAATGATGTGTT	1257
Db	661	CCGTGTGTGGAACAATCAGTAGATTTCAATTGAGAAAACAAAGCCTCAATGATGTGTT	720
QY	1258	CTAGTGCACGTGTTTAGCTGGGAATCTCCGCTCCGCAACATCGCTATCGCTTACATCATG	1317
Db	721	CTAGTGCACGTGTTTAGCTGGGAATCTCCGCTCCGCAACATCGCTATCGCTTACATCATG	780

Qy 1318 AAGAGATGACATGCTTTAGATGAGCTTACAGATTGTGMAAGAAAAAGACTACT 1377
Db 781 AAGAGATGACATGCTTTAGATGAGCTTACAGATTGTGMAAGAAAAAGACTACT 840
Qy 1378 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTCTGACCTATGAGAAAGATTAAAGAC 1437
Db 841 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTCTGACCTATGAGAAAGATTAAAGAC 900
Qy 1438 CAGACTGAGATCAGAGGCGCAAGAGCAAACTCAAGCTGTGACCTTGAGAGGCAAAAT 1497
Db 901 CAGACTGAGATCAGAGGCGCAAGAGCAAACTCAAGCTGTGACCTTGAGAGGCAAAAT 960
Qy 1498 GAACCTGTCCCTGTCTGTCTAGAGGGTGAAGAGAAACGAGAGCGCCCTCAGTCAACC 1557
Db 961 GAACCTGTCCCTGTCTGTCTAGAGGGTGAAGAGAAACGAGAGCGCCCTCAGTCAACC 1020
Qy 1558 TGTGCTGACCTGTCTGTCTAGAGGGTGAAGAGAAACGAGAGCGCCCTCAGTCAACC 1617
Db 1021 TGTGCTGACCTGTCTGTCTAGAGGGTGAAGAGAAACGAGAGCGCCCTCAGTCAACC 1080
Qy 1618 CCCAGCGTGGCCAGCGTGCAGCGCGTGTGTTAGAGAGCAGCGCGTGTGACAGGCGCTC 1677
Db 1081 CCCAGCGTGGCCAGCGTGCAGCGCGTGTGTTAGAGAGCAGCGCGTGTGACAGGCGCTC 1140
Qy 1678 AGTGGGCTGCACTGTCCGAGAGAGGCTGGAAGAGCAATTAAGCTCAAGCTTCTTC 1737
Db 1141 AGTGGGCTGCACTGTCCGAGAGAGGCTGGAAGAGCAATTAAGCTCAAGCTTCTTC 1200
Qy 1738 TCTCTGATCAATCAATCAGTTTCATATTACCGACGATGAGAGCATCTTACATGGCTTC 1797
Db 1201 TCTCTGATCAATCAATCAGTTTCATATTACCGACGATGAGAGCATCTTACATGGCTTC 1260
Qy 1798 TCTCTGATCAATCAATCAGTTTCATATTACCGACGATGAGAGCATCTTACATGGCTTC 1857
Db 1261 TCTCTGATCAATCAATCAGTTTCATATTACCGACGATGAGAGCATCTTACATGGCTTC 1320
Qy 1858 AAGCTATGCGAGTTCTCCCTGTTCAGAGAACTATCGAGAGCACTCCGAAACAGTCTCT 1917
Db 1321 AAGCTATGCGAGTTCTCCCTGTTCAGAGAACTATCGAGAGCACTCCGAAACAGTCTCT 1380
Qy 1918 GATTAAGAGAGAGCGAGATCCCAAGAGCTGAGAGCGCGAGGCTTTCAGAGAGCCAG 1977
Db 1381 GATTAAGAGAGAGCGAGATCCCAAGAGCTGAGAGCGCGAGGCTTTCAGAGAGCCAG 1440
Qy 1978 AGCAAGGATGTCATTTGGGTGAGAAACGAGAGCACTGAGAGCGCGAGGCTTTCAGAGAGCCAG 2037
Db 1441 AGCAAGGATGTCATTTGGGTGAGAAACGAGAGCACTGAGAGCGCGAGGCTTTCAGAGAGCCAG 1500
Qy 2038 TCTCCACTGATCGAAGTGGAGGAGTGGAGAGCAATTAACACAGAGCTTCTTTCGAGC 2097
Db 1501 TCTCCACTGATCGAAGTGGAGGAGTGGAGAGCAATTAACACAGAGCTTCTTTCGAGC 1560
Qy 2098 CTTTTCACAGCGACAGAGCACTTCAAGAGTCTGTGGCTGTGGCTTTAAGGGCTGGAGC 2157
Db 1561 CTTTTCACAGCGACAGAGCACTTCAAGAGTCTGTGGCTGTGGCTTTAAGGGCTGGAGC 1620
Qy 2158 TCGGATATCTTGGGCCCCCAGAACTCTTACCCCTTCCCTGACAGAGAGTGTATTTGGC 2217
Db 1621 TCGGATATCTTGGGCCCCCAGAACTCTTACCCCTTCCCTGACAGAGAGTGTATTTGGC 1680
Qy 2218 ACAGAGTCTTCACTTCTTCTGCTCAGAGCTTCAAGAGAGGAGGAGGAGTAACTCT 2277
Db 1681 ACAGAGTCTTCACTTCTTCTGCTCAGAGCTTCAAGAGAGGAGGAGGAGTAACTCT 1740
Qy 2278 GCCTACAGCTGACAGCTGCTCCCACTTTCGAGAGCAAGTCTATTCTGTGCGAGGCGG 2337
Db 1741 GCCTACAGCTGACAGCTGCTCCCACTTTCGAGAGCAAGTCTATTCTGTGCGAGGCGG 1800
Qy 2338 CAGAGGCAAGTGAAGAGTGAATCTGGGCGGAGCTGGAGCTGAAGAGAGCCCTTTGAA 2397
Db 1801 CAGAGGCAAGTGAAGAGTGAATCTGGGCGGAGCTGGAGCTGAAGAGAGCCCTTTGAA 1860
Qy 2398 AAGAGTTTAAACGAGAGCTGCCAAATGGAATTTGAGAGAGATCATGTCAAGAAC 2457

Db 1861 AAGCAGTTTAAACGAGAGCTGCCAAATGGAATTTGAGAGAGATCATGTCAAGAAC 1920
Qy 2458 AGCTCAGGGAAGAGCTGGGGAAGTGGGCGAGCTGAGCTTTTGGGAGAGATGGA 2517
Db 1921 AGCTCAGGGAAGAGCTGGGGAAGTGGGCGAGCTGAGCTTTTGGGAGAGATGGA 1980
Qy 2518 ATCATGAGGTCTCTGA 2535
Db 1981 ATCATGAGGTCTCTGA 1998

RESULT 30
US-10-377-072-27
Sequence 27, Application US/10377072
Publication No. US20040157221A9
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Miyoung
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MP103-0180NMIM
CURRENT APPLICATION NUMBER: US/10/377, 072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895, 860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723, 806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187, 455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843, 297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199, 801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861, 801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205, 508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816, 494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815, 419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27

Query Match 34.8%; Score 1896; DB 18; Length 1998;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1996; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 538 ATGGCCCATGAGATGATGGAATCAATTTGTTACTAGAGAGTGTGGCTCTCTCTGAA 597
Db 1 ATGGCCCATGAGATGATGGAATCAATTTGTTACTAGAGAGTGTGGCTCTCTCTGAA 60
Qy 598 AGTGAACGGAAGAGTGTCTAATGATAGCGGCGCATTTGTGAAATCAATATCATCC 657

Db 61 AGTGAACGGAAGGCTGCTAATGATAGCCGGCAATTTGGAAATACATATC 120
Qy 658 CACATTTTGGAAACCATTTATATCACTGCTCCAGCTTATGAAGGAAAGTTGCAACG 717
Db 121 CACATTTTGGAAACCATTTATATCACTGCTCCAGCTTATGAAGGAAAGTTGCAACG 180
Qy 718 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGCAACATTAAGGTTGACATGAT 777
Db 181 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGCAACATTAAGGTTGACATGAT 240
Qy 778 TGCAGTCAAGAGGTTGATGTTAAGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 837
Db 241 TGCAGTCAAGAGGTTGATGTTAAGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
Qy 838 GACTGTTTCTCACTGATCTTCGCGGTAACAGGAAAGAGCTTCAACTCTGTTCACTG 897
Db 301 GACTGTTTCTCACTGATCTTCGCGGTAACAGGAAAGAGCTTCAACTCTGTTCACTG 360
Qy 898 CTTCAGAGTGGGTTTGTGCTAGTCTCTGTTGTTTCTGAGCTCTGTGAAGAAATCC 957
Db 361 CTTCAGAGTGGGTTTGTGCTAGTCTCTGTTGTTTCTGAGCTCTGTGAAGAAATCC 420
Qy 958 ACTCTAGTCCCTACCTGCACTTCTCAGCTTGTCTTACCTGTTCCAAACATTTGGCAAC 1017
Db 421 ACTCTAGTCCCTACCTGCACTTCTCAGCTTGTCTTACCTGTTCCAAACATTTGGCAAC 480
Qy 1018 CGAAATCTTCCCAATCTTTATCTGCGTGCAGCGAGATGCTCTCAAGAGAGCTGTATA 1077
Db 481 CGAAATCTTCCCAATCTTTATCTGCGTGCAGCGAGATGCTCTCAAGAGAGCTGTATA 540
Qy 1078 CAGCAAGATGGAGATTGTTATGTATTAATGCCAGCTTACCTGTCCAAAGCTGACTT 1137
Db 541 CAGCAAGATGGAGATTGTTATGTATTAATGCCAGCTTACCTGTCCAAAGCTGACTT 600
Qy 1138 ATCCCCGAGTCTCATTTCTGCGTGTGCTGGAATGACAGCTTTTGTGAAGAAATTTTG 1197
Db 601 ATCCCCGAGTCTCATTTCTGCGTGTGCTGGAATGACAGCTTTTGTGAAGAAATTTTG 660
Qy 1198 CCGGTGTTGGAACAATCAGTATGATTTCAATTGGAAGCAAAAGCTCCATGAGATGTT 1257
Db 661 CCGGTGTTGGAACAATCAGTATGATTTCAATTGGAAGCAAAAGCTCCATGAGATGTT 720
Qy 1258 CTAGTGCACTGTTTAGTGGGATCTCCGCTCCGACCATGCTATGCTTACATCAG 1317
Db 721 CTAGTGCACTGTTTAGTGGGATCTCCGCTCCGACCATGCTATGCTTACATCAG 780
Qy 1318 AAGAGATGGAACATGCTTTTATGATGAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 1377
Db 781 AAGAGATGGAACATGCTTTTATGATGAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 840
Qy 1378 ATATCTCCAACTTCAATTTTCTGGGCAACTCTGCACTATGAGAAAGATTAAGAAC 1437
Db 841 ATATCTCCAACTTCAATTTTCTGGGCAACTCTGCACTATGAGAAAGATTAAGAAC 900
Qy 1438 CAGACTGGAAGATCAAGGCGCAAGAGCAAACTCAAGCTGTGCACTTGGAGAACCAAT 1497
Db 901 CAGACTGGAAGATCAAGGCGCAAGAGCAAACTCAAGCTGTGCACTTGGAGAACCAAT 960
Qy 1498 GAACCTGTCCCTGCTGCTCAGAGGTTGGAAGAAAGCGAGAGCCCTTCAGTCCACC 1557
Db 961 GAACCTGTCCCTGCTGCTCAGAGGTTGGAAGAAAGCGAGAGCCCTTCAGTCCACC 1020
Qy 1558 TGTGCGCACTGCTGCTCAGAGGCGCAAGAGCAAAAGCCGCTGCACTCCGCGAGG 1617
Db 1021 TGTGCGCACTGCTGCTCAGAGGCGCAAGAGCAAAAGCCGCTGCACTCCGCGAGG 1080
Qy 1618 CCCAGCGTCCGAGCGTGGAGCCCTCGCTTGAAGAGACAGCCGCTGTGTAAGCGGCTC 1677
Db 1081 CCCAGCGTCCGAGCGTGGAGCCCTCGCTTGAAGAGACAGCCGCTGTGTAAGCGGCTC 1140
Qy 1678 AGTGGGCTGCACTGTCCGAGACAGGCTGGAAGACAGCAATTAAGCTCAAGCCTTCTTC 1737

Db 1141 AGTGGGCTGCACTGTCCGAGACAGGCTGGAAGACAGCAATTAAGCTCAAGCCTTCTTC 1200
Qy 1738 TCTGTGATATCAATCAAGTTTCATATTTACGCGAGCATGGAGCAATCCTTACATGGCTTC 1797
Db 1201 TCTGTGATATCAATCAAGTTTCATATTTACGCGAGCATGGAGCAATCCTTACATGGCTTC 1260
Qy 1798 TCTGTGATGAAAGATGCTTTGGAATPACTACAAACCTTCCATCTTGTGATGGAAGCAAC 1857
Db 1261 TCTGTGATGAAAGATGCTTTGGAATPACTACAAACCTTCCATCTTGTGATGGAAGCAAC 1320
Qy 1858 AAGCTATGCGAGTCTCCCTGTTCAGGAATATTCGAGAGCAGACTCCGAAACAGTCTCT 1917
Db 1321 AAGCTATGCGAGTCTCCCTGTTCAGGAATATTCGAGAGCAGACTCCGAAACAGTCTCT 1380
Qy 1918 GATTAAGAGGAAGCCAGCATTCGAAAGAGTTCAGACCCGAGGCTTTCAGACAGCCAG 1977
Db 1381 GATTAAGAGGAAGCCAGCATTCGAAAGAGTTCAGACCCGAGGCTTTCAGACAGCCAG 1440
Qy 1978 AGCAAGGATTTGATGTTGGTTCAGAACAGAGAGGAGCCGCGCCAGAGGTCCTTTTA 2037
Db 1441 AGCAAGGATTTGATGTTGGTTCAGAACAGAGAGGAGCCGCGCCAGAGGTCCTTTTA 1500
Qy 2038 TCTCCACTGCAATCGAAGTGGAGGCGTGGAGAGCAATTAACCAACAAGCTTCTTTTGGC 2097
Db 1501 TCTCCACTGCAATCGAAGTGGAGGCGTGGAGAGCAATTAACCAACAAGCTTCTTTTGGC 1560
Qy 2098 CTTTCCACAGCCGAGGAGCACTTCAAGAAATCTGTGCTGGGCTTAAAGGCTGGCAC 2157
Db 1561 CTTTCCACAGCCGAGGAGCACTTCAAGAAATCTGTGCTGGGCTTAAAGGCTGGCAC 1620
Qy 2158 TCGGATATCTTTGGGCCCCGAGACCTTACCCCTTCCCTGACAGAGCTGGTATTTTGGC 2217
Db 1621 TCGGATATCTTTGGGCCCCGAGACCTTACCCCTTCCCTGACAGAGCTGGTATTTTGGC 1680
Qy 2218 ACAGAGTCTCAACATTTCTTCTGCTCAGCCATCTACGAGAGGAGGAGCTGCAATCTCT 2277
Db 1681 ACAGAGTCTCAACATTTCTTCTGCTCAGCCATCTACGAGAGGAGGAGCTGCAATCTCT 1740
Qy 2278 GCTTACAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2337
Db 1741 GCTTACAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
Qy 2338 CAGAGGCAAGTGAACAGAGCTGACTGCGGCGGAGCTGCAATGAAGAGAGCCCTTTGAA 2397
Db 1801 CAGAGGCAAGTGAACAGAGCTGACTGCGGCGGAGCTGCAATGAAGAGAGCCCTTTGAA 1860
Qy 2398 AAGCAATTTAAACGCAAGAGCTGCCAAATGGAATTTGAGAGAGCATGTTCAGAGAA 2457
Db 1861 AAGCAATTTAAACGCAAGAGCTGCCAAATGGAATTTGAGAGAGCATGTTCAGAGAA 1920
Qy 2458 AGGTCAAGGGAAGAGCTGGGGAAGAGGCGAGCTGCACTTCTTCCGCGAGCATGGA 2517
Db 1921 AGGTCAAGGGAAGAGCTGGGGAAGAGGCGAGCTGCACTTCTTCCGCGAGCATGGA 1980
Qy 2518 ATCATTTAGGTCCTGGA 2535
Db 1981 ATCATTTAGGTCCTGGA 1998

RESULT 31
US-10-094-749-673
; Sequence 673, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAT, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 673
LENGTH: 2102
TYPE: DNA
ORGANISM: Homo sapiens
US-10-094-749-673

Query Match 34.7%; Score 1889; DB 17; Length 2102;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 4; Indels 0; Gaps 0;

Matches 2089; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 483 TACATCATCGTGGCAATTAAGAAGAGAGTGGGAAAAGAGACTTATGTGTGTCATGCG 542
Db 1 TACATCATCGTGGCAATTAAGAAGAGAGTGGGAAAAGAGACTTATGTGTGTCATGCG 60
Qy 543 CCATGAGATGATTTGGAATCTCAATTTGTTACTGAGAGTTGGTGGCTCTGCTGGAAGTGG 602
Db 61 CCATGAGATGATTTGGAATCTCAATTTGTTACTGAGAGTTGGTGGCTCTGCTGGAAGTGG 120
Qy 603 AACGGAAAAGTGGCTGATTAATGATGAGCGGCAATTTGGAATCAATATCATCCCAT 662
Db 121 AACGGAAAAGTGGCTGATTAATGATGAGCGGCAATTTGGAATCAATATCATCCCAT 180
Qy 663 TTGGAAGCCATTAATCACTGCTCCAGCTTAATGAAGGAAAGTTGCAACAGAGCA 722
Db 181 TTGGAAGCCATTAATCACTGCTCCAGCTTAATGAAGGAAAGTTGCAACAGAGCA 240
Qy 723 AGTGTAAATACAGAGCTCATCCAGCAATTCAGCGAAATTAAGTTGATGATGAG 782
Db 241 AGTGTAAATACAGAGCTCATCCAGCAATTCAGCGAAATTAAGTTGATGATGAG 300
Qy 783 TCAGAAAGTGTAGTTTACGATCAAGAGTCCCAAGATTTGCTCTCTCTTCAAGATG 842
Db 301 TCAGAAAGTGTAGTTTACGATCAAGAGTCCCAAGATTTGCTCTCTCTTCAAGATG 360
Qy 843 TTTTCTCACTGATCTTGGGTTAACTGAGAGAGCTTCAACTGTGTTCACTGCTTGC 902
Db 361 TTTTCTCACTGATCTTGGGTTAACTGAGAGAGCTTCAACTGTGTTCACTGCTTGC 420
Qy 903 AGGTGGGTTGCTGAGATTTCTCTGTTGTTCCCTGAGCTCTGTGAAGAAAATCCACT 962
Db 421 AGGTGGGTTGCTGAGATTTCTCTGTTGTTCCCTGAGCTCTGTGAAGAAAATCCACT 480
Qy 963 AGTCCCACTGAGATTTCTGAGCGCTTGTACTGTTGCCCAACTGGGCCAACCCGAT 1022
Db 481 AGTCCCACTGAGATTTCTGAGCGCTTGTACTGTTGCCCAACTGGGCCAACCCGAT 540
Qy 1023 TCTTCCCAATCTTTATCTTGGCTGCGCAGAGATGCTCTCAACAAGAGCTGATACAGA 1082
Db 541 TCTTCCCAATCTTTATCTTGGCTGCGCAGAGATGCTCTCAACAAGAGCTGATACAGA 600
Qy 1083 GAATGGGATGATGATGATTAATGCAAGCTATACCTGTCCAAAAGCTGACTTATCC 1142
Db 601 GAATGGGATGATGATGATTAATGCAAGCTATACCTGTCCAAAAGCTGACTTATCC 660

Qy 1143 CGAGTCTCATTTCTGCGTGTGCTGAGATGACAGCTTTTGTGAGAAAATTTGCCGTG 1202
Db 661 CGAGTCTCATTTCTGCGTGTGCTGAGATGACAGCTTTTGTGAGAAAATTTGCCGTG 720
Qy 1203 GTTGGCAAAATCAGATGATTTTCAATTTGAGAAAGCAAAAGCTTCCAAATGATGTTCTAGT 1262
Db 721 GTTGGCAAAATCAGATGATTTTCAATTTGAGAAAGCAAAAGCTTCCAAATGATGTTCTAGT 780
Qy 1263 GCACGTTTACCTGGGATCTCCCGCTCCGCAACATGCTATGCTATCCCTTCACTAAGAAAG 1322
Db 781 GCACGTTTACCTGGGATCTCCCGCTCCGCAACATGCTATGCTATCCCTTCACTAAGAAAG 840
Qy 1323 GATGCAATGCTCTTATGATGAGCTTACAGATTTGTGAAAAGAAAAGACCTACTATATC 1382
Db 841 GATGCAATGCTCTTATGATGAGCTTACAGATTTGTGAAAAGAAAAGACCTACTATATC 900
Qy 1383 TCCAAACTTCAATTTTCTGGGCAACCTCTGAGCTATGAGAAAGATTAAGAACAGAC 1442
Db 901 TCCAAACTTCAATTTTCTGGGCAACCTCTGAGCTATGAGAAAGATTAAGAACAGAC 960
Qy 1443 TGGAGCATCAGAGGCGCAAGAGCAATCTACCTGCTGACCTGAGAGAGCCAAATGAAC 1502
Db 961 TGGAGCATCAGAGGCGCAAGAGCAATCTACCTGCTGACCTGAGAGAGCCAAATGAAC 1020
Qy 1503 TGTCCCTGCTGTCTCAGAGGCTGAGCAGAAAAGGAGAGGCGCCCTCACTCCACCTGTGC 1562
Db 1021 TGTCCCTGCTGTCTCAGAGGCTGAGCAGAAAAGGAGAGGCGCCCTCACTCCACCTGTGC 1080
Qy 1563 CGACTGTGCTACCTCAGAGGAGAGAGCAAAAGGCGCTGACCTCCGCAAGCTGCTCCAG 1622
Db 1081 CGACTGTGCTACCTCAGAGGAGAGAGCAAAAGGCGCTGACCTCCGCAAGCTGCTCCAG 1140
Qy 1623 CGTCCCAAGCTGAGAGCTGCTGTTAGAGACAGCCCGCTGTTAGAGAGGCTCAGTGG 1682
Db 1141 CGTCCCAAGCTGAGAGCTGCTGTTAGAGACAGCCCGCTGTTAGAGAGGCTCAGTGG 1200
Qy 1683 GCTGCACTGTCCGCAAGAGGCTGAGAGCAGCAATTAAGCTCAAGCGTTCTCTCTCT 1742
Db 1201 GCTGCACTGTCCGCAAGAGGCTGAGAGCAGCAATTAAGCTCAAGCGTTCTCTCTCT 1260
Qy 1743 GGATATCAATCAATTTCTATTTAGCCAGATGAGCAATCTTCACTGCTCTCTCT 1802
Db 1261 GGATATCAATCAATTTCTATTTAGCCAGATGAGCAATCTTCACTGCTCTCTCTCT 1320
Qy 1803 ATCAGAAAGTCTTTGGAATCTACAAACCTTCCACTACTTGTGATGAGACCAAGACT 1862
Db 1321 ATCAGAAAGTCTTTGGAATCTACAAACCTTCCACTACTTGTGATGAGACCAAGACT 1380
Qy 1863 ATGCGAGTTCCCTGCTGAGAACTATGGAAGAGACTCCGAAACAGTCCGATTA 1922
Db 1381 ATGCGAGTTCCCTGCTGAGAACTATGGAAGAGACTCCGAAACAGTCCGATTA 1440
Qy 1923 GGAAGAAAGCCAGATCTCCCAAGAGCTGAGAGCCGAGGCTTACAGACAGAGAGCA 1982
Db 1441 GGAAGAAAGCCAGATCTCCCAAGAGCTGAGAGCCGAGGCTTACAGACAGAGAGCA 1500
Qy 1983 GCGATTTGATTTGGTCAAGACAGAGAGAGTGGACCGCCAGAGTCTCTTTATCTCC 2042
Db 1501 GCGATTTGATTTGGTCAAGACAGAGAGAGTGGACCGCCAGAGTCTCTTTATCTCC 1560
Qy 2043 ACTGCATGAAAGTGGAGCGTGGAGCAATTAACACAGCGATCTCTTTTGGGCTTTC 2102
Db 1561 ACTGCATGAAAGTGGAGCGTGGAGCAATTAACACAGCGATCTCTTTTGGGCTTTC 1620
Qy 2103 CACCAAGCAGAGACCTCAAGAGTGTGCTGAGCTGAGGCTTAAAGGCTGAGCACTGGA 2162
Db 1621 CACCAAGCAGAGACCTCAAGAGTGTGCTGAGCTGAGGCTTAAAGGCTGAGCACTGGA 1680
Qy 2163 TATTTTGGCCCCCAGACCTTACCTCTTCCCTGACAGAGCTGTGATTTTGGCAAGA 2222
Db 1681 TATTTTGGCCCCCAGACCTTACCTCTTCCCTGACAGAGCTGTGATTTTGGCAAGA 1740
Qy 2223 GTCTCAACATTTCACTGTGCTCAGGCATCTAGAGGAGGTCAGTTACTGTGCTA 2282

Qy 3194 GCATTGCAATAGTAGTAGTACTAGTACACATTTTCAGACCAATTCAATGCTATGCA 3253
Db 1639 GCATTGCAATAGTAGTAGTACTAGTACACATTTTCAGACCAATTCAATGCTATGCA 1698
Qy 3254 CAAATTCCTCGTGGGCTAGATGAGATATTTTTTTCTTCTGAGCTTTATGAGAGA 3313
Db 1699 CAAATTCCTCGTGGGCTAGATGAGATATTTTTTTCTTCTGAGCTTTATGAGAGA 1757
Qy 3314 AGGGAACCTGCTAGTACGCTGACACACAGAACCTGGCAACATCAGATTAAAGC 3373
Db 1758 AGGGAACCTGCTAGTACGCTGACACACAGAACCTGGCAACATCAGATTAAAGC 1817
Qy 3374 TAAGTTGGAGGCTTAACGAGTCTACCTCCTTTGTAATCAAGAATTGTTAAAT 3433
Db 1818 TAAGTTGGAGGCTTAACGAGTCTACCTCCTTTGTAATCAAGAATTGTTAAAT 1877
Qy 3434 GGGATTGCAATCCTTTAAATTAAGATGAACCTGGTTTC 3472
Db 1878 GGGATTGCAATCCTTTAAATTAAGATGAACCTGGTTTC 1916

RESULT 33
US-10-072-012-257
; Sequence 257, Application US/10072012
; Publication No. US20040033493A1
GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zehrhusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkens, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Beba
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Raestelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier, Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072, 012
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-257

Query Match 24.2%; Score 1318; DB 17; Length 2071;
Best Local Similarity 99.4%; Pred.No. 0;
Matches 2068; Conservative 0; Mismatches 3; Indels 9; Gaps 1;

Qy 478 ACATTTACATCATGCTGGCAATTAAGAAGAGAGTGGGAAGAAGAGACTTATGTTGTC 537
Db 1 ACATTTACATCATGCTGGCAATTAAGAAGAGAGTGGGAAGAAGAGACTTATGTTGTC 60
Qy 538 ATGGCCCATGAGATGATGGAATCAATTTGTTACTGAGAGTTGGTGGCTCTGTGGA 597
Db 61 ATGGCCCATGAGATGATGGAATCAATTTGTTACTGAGAGTTGGTGGCTCTGTGGA 120
Qy 598 AGTGAACGAAAAGTCTCTAATGATGACCGGCGCATTTGGGAATACATATATCC 657
Db 121 AGTGAACGAAAAGTCTCTAATGATGACCGGCGCATTTGGGAATACATATATCC 180
Qy 658 CACATTTTGAAGCATTAATATCACTGCTCAAGCTTATGAAGCGAAGGTGGCAAG 717
Db 181 CACATTTTGAAGCATTAATATCACTGCTCAAGCTTATGAAGCGAAGGTGGCAAG 240
Qy 718 GACAAAGTGTAAATTACAGAGCTCATCAGATTCAGCGAAACATTAAGTTGACATTGAT 777
Db 241 GACAAAGTGTAAATTACAGAGCTCATCAGATTCAGCGAAACATTAAGTTGACATTGAT 300
Qy 778 TGCACTGCAAGGTTGATGTTAAGATGAAGTCTCCAAAGTGTGCTCTCTCTTCA 837
Db 301 TGCACTGCAAGGTTGATGTTAAGATGAAGTCTCCAAAGTGTGCTCTCTCTTCA 360
Qy 838 GACTGTTTTCACGTACTCTGAGTAACTGGAAGAGAGACTTCACTGTTCACTG 897
Db 361 GACTGTTTTCACGTACTCTGAGTAACTGGAAGAGAGACTTCACTGTTCACTG 420
Qy 898 CTTCAGAGTGGTGTGCTGAGTCTCTGTTGTTCCCTGAGCTCTGTGAAGAAATCC 957
Db 421 CTTCAGAGTGGTGTGCTGAGTCTCTGTTGTTCCCTGAGCTCTGTGTGAAGAAATCC 480
Qy 958 ACTCTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTTGCCACATTTGGCCAAACC 1017
Db 481 ACTCTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTTGCCACATTTGGCCAAACC 540
Qy 1018 CGAATTTCTCCCAATCTTTATCTTGGCTGCGAGGAGATGTCCTCAACAAGAGCTGATA 1077
Db 541 CGAATTTCTCCCAATCTTTATCTTGGCTGCGAGGAGATGTCCTCAACAAGAGCTGATA 600
Qy 1078 CAGCAGATGGAGTGTGTTATGTTAAATCCAGACTTACCTGTCCAAAGCTGACTTT 1137
Db 601 CAGCAGATGGAGTGTGTTATGTTAAATCCAGACTTACCTGTCCAAAGCTGACTTT 660
Qy 1138 ATCCCGAGTCTATTTCTGCTGCTGCTGCTGCTGATGACACCTTTTGTGAAGAAATTTTG 1197
Db 661 ATCCCGAGTCTATTTCTGCTGCTGCTGCTGCTGATGACACCTTTTGTGAAGAAATTTTG 720
Qy 1198 CCGTGTGGGCAAAATCAGTATGATTTCAATGAGAAAGAAAGCTCCAAATGAGTGT 1257
Db 721 CCGTGTGGGCAAAATCAGTATGATTTCAATGAGAAAGAAAGCTCCAAATGAGTGT 780
Qy 1258 CTAGTGCACTGTAGTGGGATCTCCGCTCCGCAACATGCTATGCTTACATCATG 1317
Db 781 CTAGTGCACTGTAGTGGGATCTCCGCTCCGCAACATGCTATGCTTACATCATG 840
Qy 1318 AAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 1377
Db 841 AAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 900

OY	1351	AGATTGGAGAAAGAAAAGACCTTACTATATCTCAAACTTCAATTTCTGGGCAACCTC	1410
Db	919	AGATTGGAGAAAGAAAAGACCTTACTATATCTCAAACTTCAATTTCTGGGCAACCTC	978
OY	1411	CTGCAGTATGAGAAAGATTAAAGACAGACTGGAGCATCAGGCGCAAGAGCAAACTC	1470
Db	979	CTGCAGTATGAGAAAGATTAAAGAACCAAGCTGAGGATCAGGCGCAAGAGCAAACTC	1038
OY	1471	AAGCTGCTGCACCTGGAGAAAGCAAAATGAACCTGTCCCTGCTGTCTCAGAGGCTGACAG	1533
Db	1039	AAGCTGCTGCACCTGGAGAAAGCAAAATGAACCTGTCCCTGCTGTCTCAGAGGCTGACAG	1098
OY	1531	AAAAGCGAGAGGCGCCCTGAGTCAACCCGTGCGGCACTGTGCTACTCTCAGAGGCAAGAGA	1590
Db	1099	AAAAGCGAGAGGCGCCCTGAGTCAACCCGTGCGGCACTGTGCTACTCTCAGAGGCAAGAGA	1155
OY	1591	CAAAAGCCCGCTGCAATCCCGCAGCGTGGCCAGCGTCCAGCGGTCAAGCCGCTGTTA	1655
Db	1159	CAAAAGCCCGCTGCAATCCCGCAGCGTGGCCAGCGTGGCCAGCGGTGGACACCGCTGTTA	1218
OY	1651	GAGGACAGCCCGCTGTGTACAGGCGCTCAGTGGCTTGCACTGTCCGACAGACGCTGAA	1710
Db	1219	GAGGACAGCCCGCTGTGTACAGGCGCTCAGTGGCTTGCACTGTCCGACAGACGCTGAA	1278
OY	1711	GACAGCAATTAAGCTCAACGCTTCTCTCTCTGTGATATCAATCAAGTTTCAATTTACACC	1770
Db	1279	GACAGCAATTAAGCTCAACGCTTCTCTCTCTGTGATATCAATCAAGTTTCAATTTACACC	1338
OY	1771	AGCATGGCAGCATCTTACATGAGCTTCTCTCTCATAGAAAGATGCTTGGAAATACACAA	1830
Db	1339	AGCATGGCAGCATCTTACATGAGCTTCTCTCTCATAGAAAGATGCTTGGAAATACACAA	1398
OY	1831	CCTTCCACTACTCTGGATGGAGCAACAAGCTATGCAAGTTCTCCCTGTTCAAGAACTA	1890
Db	1399	CCTTCCACTACTCTGGATGGAGCAACAAGCTATGCAAGTTCTCCCTGTTCAAGAACTA	1458
OY	1891	TCGGAGCAGCATCTCCGAAACCAGTCTCTATTAAGGAGAAAGCCAGATATCCCAAGAACTG	1955
Db	1459	TCGGAGCAGCATCTCCGAAACCAGTCTCTATTAAGGAGAAAGCCAGATATCCCAAGAACTG	1518
OY	1951	CAGACCGCGCAGGCTTTCAGACAGCCAGAGCAAGCAATGCAATTCGGTCAAGAACCGCAGAC	2010
Db	1519	CAGACCGCGCAGGCTTTCAGACAGCCAGAGCAAGCAATTCGGTCAAGAACCGCAGAC	1578
OY	2011	AGTGGCACCGCCAGAGGTCCTTTATCTCCATCGACATCGAAGTGGAGCGTGGAGAAC	2070
Db	1579	AGTGGCACCGCCAGAGGTCCTTTATCTCCATCGACATCGAAGTGGAGCGTGGAGAAC	1638
OY	2071	AATTACCAACACAGTTCTCTTTTGGGCTTTTCACACAGCAGCAGACCTTACGAACTCT	2130
Db	1639	AATTACCAACACAGTTCTCTTTTGGGCTTTTCACACAGCAGCAGACCTTACGAACTCT	1698
OY	2131	GCTGGCCCTGGGCTTAAAGGCGTGGGACCTCGATATCTTGGCCCCCACAACCTTACCCCT	2190
Db	1699	GCTGGCCCTGGGCTTAAAGGCGTGGGACCTCGATATCTTGGCCCCCACAACCTTACCCCT	1758
OY	2191	TCCCTGACCAAGCAGCTGTATTTTGGCACAAGTCTCTCACTTTTACTCTGTGCTCAACC	2250
Db	1759	TCCCTGACCAAGCAGCTGTATTTTGGCACAAGTCTCTCACTTTTACTCTGTGCTCAACC	1818
OY	2251	ATCTACGAGGAGGAGTGCAGATTACTTGTCTTACAGCTCAGCAGCAGCTGCCACTTGGCGA	2310
Db	1819	ATCTACGAGGAGGAGTGCAGATTACTTGTCTTACAGCTCAGCAGCAGCTGCCACTTGGCGA	1878
OY	2311	GACCAAGCTATTTCTGTGCGCAGGCGGCAAGGCCAAGTGAACAGGCTGACTCGCGGCGG	2370
Db	1879	GACCAAGCTATTTCTGTGCGCAGGCGGCAAGGCCAAGTGAACAGGCTGACTCGCGGCGG	1938
OY	2371	AGCTGGCATGAAGAGAGCCCTTTGAAAGCAGTTTAAACGACAGAACTGCGCAATGGAA	2430
Db	1939	AGCTGGCATGAAGAGAGCCCTTTGAAAGCAGTTTAAACGACAGAACTGCGCAATGGAA	1998
OY	2431	TTTGAGAGAGCATCATGTCAAGAGAACAGGTCAACGGAAGAGCTGGGAAAGTGGGCGAGT	2490

Db	1999	TTTGGAGAGGCAATCATGTGAGAGAA	CAGGTCACGGGAAAGCTGGGGGAAAGTGGGAGT	2058
Qy	2491	CAGCTTCAGCTTTTTCGGGACAGATGGAAATCATTTAGGCTCTCTGAGAAAGAAAGACACTTG		2550
Db	2059	CAGCTTCAGCTTTTTCGGGACAGATGGAAATCATTTAGGCTCTCTGAGAAAGAAAGACACTTG		2118
Qy	2551	TGACTTCATATGACAAATTTTTTTTTT		2575
Db	2119	TGACTTCATATGACAAATTTTTTTTTT		2143

RESULT 35
US-10-172-118-2599/c

; Sequence 2599, Application US/10172118
; Publication No. US20030224374A1
; Publication No. US20030224374A1

;
; GENERAL INFORMATION:
;
; APPLICANT: Dai, Hongyue
;
; ADDRESSEE: Mr. Wang

APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Linsley, Peter

! APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Roberts, Chris

APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc

APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

```

; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118

```

; CURRENT FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 60/380,770
 ; PRIOR FILING DATE: 2002-05-14

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; PRIOR FILING DATE: 2002-05
; NUMBER OF SEQ ID NOS: 26999

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; SEQ ID NO 259
; LENGTH: 940
;

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; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION

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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Contig55674
; DATABASE ENTRY DATE: 2001-06-18

```

US-10-172-118-2599 ; DATABASE ENTRY

Query Match	17.2%	Score 940;	DB 17;	Length 940;
Query Length	100.0%	Score 940;	DB 17;	Length 940;
Post Length	100.0%	Score 940;	DB 17;	Length 940;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 940; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4206 GTTTTCTCTGTTTTGAGAAATGACAGTTTTTGCACGAGATGACTTATGTTCC 4265

Db 940 GTTTTCTCTGTTTTGAGAAATGACAGTTTTTTCACAGATGTGACTTCATGTTCC 881

4266 TATGTTGACTTCTAAAACAGCACAGATGATATGACTCAACACAGACCGACTTGTAT 4325

Db 880 TATGTGACTTTAAACCAGACAGATGATATGACTCAACACAGACCGACTTGTAT 831

4326 GGGGATGATGAGCGCACAGACCTCACTAGTGTGCAAAATTAATGCTATGATGGGCT 4385

Db 820 GGGGATGATGAGCCGACAGACTCTACTAGTTGTGCACAAATATGCTATGATGGGT 761

4386 GTAAGTGAAGCGAAGAGGCTCAGCCGCAATTGTTATGATACCTGGAAAGTCTGTCA 4445

Db 760 GTAAAGTAAAGCGAAGAGGGTCAGCCGCAATTGTTATGATCTGGAAAGTCTGTCTCA 701

4446 ACGATTGAGTTAGTTTGTAGATATACATTGAATCTTTAATCAGACATTCGAGTTTC 4505

Db 700 ACGATTGAGTTAGTTTGTAGATATACATTGGAATCTTTAATCAGACATTCGAGTTTC 641

4506 ACACAGTAGTTTTTGATGTATGTACACACACACCAATGTGTAAACAGTTTCAACACTTCC 4565

Db 640 ACACAGTAGTTTGTAGTTATGACACACACACCAATGTGTACAGTTACCACTTCC 581

4566 AGAGTGTGCTCATGCCCCAAACATGTTTAAGAAAGGAAAGCATAGCTCCTTGCTAACGA 4625

Db 580 AGAGTGTGTCATGCCCAACATGTTTAAAGAAAGCAAGCAGTAGCTCCTTGCTAACGA 521

Qy	4626	TGTTTACAGAGCTTTGGGCACATTGGTTTTAATGAAGCTTCGTCACTTTTAGGGCTTCCTT	4685
Db	520	TGTTTACAGAGGTTTGCGGCACCTTGTTTTAAATGAGCTTCGTCACTTTTAGGGCTTCCTT	461
Qy	4686	GGCATGATGCCCTTCCTCTCTGGAACTGTGATGTAGTACAATCCATCAGACCCTTAGTACT	4745
Db	460	GGCATGATGCCCTTCCTCTCTGGAACTGTGATGTAGTACAATCCATCAGACCCTTAGTACT	401
Qy	4746	GGTTTCACTGTGTCAATATATCATGTTCTTTGAAATGAGA CTGCGGTGGCGAAGGGGTGGC	4805
Db	400	GGTTTCACTGTGTCAATATATCATGTTCTTTGAAATGAGA CTGCGGTGGCGAAGGGGTGGC	341
Qy	4806	CTCGAGGAGGAGGCTCTGAGAGCTGCTTGGATGTCCTTTAGGTGGGGGTGGGTGGCTCTCT	4865
Db	340	CTCGAGGAGGAGGCTCTGAGAGCTGCTTGGATGTCCTTTAGGTGGGGGTGGGTGGCTCTCT	281
Qy	4866	TCAGCATGTAAATTTGGGAAAACCTCGCGTCTACTAGGGGTGATA CAGATGCTGATTTTAA	4925
Db	280	TCAGCATGTAAATTTGGGAAAACCTCGCGTCTACTAGGGGTGATA CAGATGCTGATTTTAA	221
Qy	4926	AAGAGCAAACCTAGACTCTTAATGTGAAAGTGTCTGAAAATGATTTTAGACATGTGTAAAG	4985
Db	220	AAGAGCAAACCTAGACTCTTAATGTGAAAGTGTCTGAAAATGATTTTAGACATGTGTAAAG	161
Qy	4986	TTAGATGGAAGAACCTGTAAATTTTAAATATGAAATATAGTGTCTTTTGAAGTAAAGCACG	5045
Db	160	TTAGATGGAAGAACCTGTAAATTTTAAATATGAAATATAGTGTCTTTTGAAGTAAAGCACG	101
Qy	5046	CTGTTGAACGGTTAAACCTGTGATTTCTCATTTTGTGATGTGTCATGTATGTTAATGTATGA	5105
Db	100	CTGTTGAACGGTTAAACCTGTGATTTCTCATTTTGTGATGTGTCATGTATGTTAATGTATGA	41
Qy	5106	AATGATTAATTAATTAATCAAAAACCTGGTACCTGTATTAATCAT	5145
Db	40	AATGATTAATTAATTAATCAAAAACCTGGTACCTGTATTAATCAT	1
 RESULT 36 US-10-342-887-2599/c ; Sequence 2599, Application US/10342887 ; Publication No. US20040058340A1 GENERAL INFORMATION: APPLICANT: Dai, Hongyue APPLICANT: He, Yudong APPLICANT: Linsley, Peter S. APPLICANT: Mao, Mao APPLICANT: Roberts, Christopher J. APPLICANT: Van 't Veer, Laura Johanna APPLICANT: Van de Vijver, Marc J. APPLICANT: Bernards, Rene TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients FILE REFERENCE: 9301-188-999 CURRENT APPLICATION NUMBER: US/10/342,887 CURRENT FILING DATE: 2003-01-15 PRIORITY APPLICATION NUMBER: 60/289,918 PRIOR FILING DATE: 2001-06-18 PRIOR APPLICATION NUMBER: 60/380,710 PRIOR FILING DATE: 2002-05-14 PRIOR APPLICATION NUMBER: 10/172,118 PRIOR FILING DATE: 2002-06-14 NUMBER OF SEQ ID NOS: 2699 SEQ ID NO 2599 LENGTH: 940 TYPE: DNA ORGANISM: Homo sapiens US-10-342-887-2599			

Query Match	17.2%	Score 940	DB 17	Length 940
Best Local Similarity	100.0%	Pred. No. 0		
Matches 940	Conservative 0	Mismatches 0	Indels 0	Gaps 0

OY 4206 GTTTTTCCTCTTTTGGAAATGACAGTTTTTGGACAGATGTCACTTCATGTTCC 4265
|||||

Db	940	GTITTTCTCTGTTTTTGAGAAATGACAGTTTTTTTACAGAGATGTGACCTTACATGTTTTCC	861
QY	4266	TATGTGACTTTTAAACCAGACACAGATGATATGACTCAACACAGACCGACTTGGTAT	4322
Db	880	TATGTGACTTTTAAACCAGACACAGATGATGATCTCAACACAGACCGACTTGGTAT	821
QY	4326	GGGAGATGAGGCGGACAGACCTCACTGATGTGACAAATATATGTGCTATGATGAGGAT	438
Db	820	GGGAGATGAGGCGGACAGACCTCACTGATGTGACAAATATATGTGCTATGATGAGGAT	761
QY	4386	GTAAGTGAAGCAGAAAGGGTCAACCGCATTTGTTATGATATCTGGAAAGTCTGGTCA	4441
Db	760	GTAAGTGAAGCAGAAAGGGTCAACCGCATTTGTTATGATATCTGGAAAGTCTGGTCA	701
QY	4446	ACGATTTGAGTTAGTTTTTATGATATCATTTGAAATCTTTAATACAGACATTTCTCAAGTTTC	4507
Db	700	ACGATTTGAGTTAGTTTTTATGATATCATTTGAAATCTTTAATACAGACATTTCTCAAGTTTC	641
QY	4506	ACACAGTACTTTTGTGATGTTATGTACACACACACCAATATGTGTAAACAGTTACCCACTTCC	4566
Db	640	ACACAGTACTTTTGTGATGTTATGTACACACACACCAATATGTGTAAACAGTTACCACTTCC	581
QY	4566	AAGATGTGTCATGCCCAAACATGTTTAAAGAAAGAAAGCATGATGCTCTTGTCTAACGA	4622
Db	580	AAGATGTGTCATGCCCAAACATGTTTAAAGAAAGAAAGCATGATGCTCTTGTCTAACGA	521
QY	4626	TGTTTCAGAGGTTTTGGGGCACTTGATTTTAAATGAGCTTCTGATTAAGGGCTCTCTGT	4688
Db	520	TGTTTCAGAGGTTTTGGGGCACTTGATTTTAAATGAGCTTCTGATTAAGGGCTCTCTGT	461
QY	4686	GGCATGTCCTCCCTCTCTTCTGGAACGTGATGATGACATCTTACAGCCCTTAATGATGCT	4745
Db	460	GGCATGTCCTCCCTCTCTTCTGGAACGTGATGATGACATCTTACAGCCCTTAATGATGCT	401
QY	4746	GGTTCACTAGTGTGATATACAGTCTTGGAAATGGAACCTGCGGTGCGAAAGGGGTGGC	4800
Db	400	GGTTCACTAGTGTGATATACAGTCTTGGAAATGGAACCTGCGGTGCGAAAGGGGTGGC	341
QY	4806	CTCGAGGCGAGCTCTGAGCTGCTGGATGTCCTTAACTGGGGGTGATGCGTGGCTCTCT	4865
Db	340	CTCGAGGCGAGCTCTGAGCTGCTGGATGTCCTTAACTGGGGGTGATGCGTGGCTCTCT	281
QY	4866	TCAGATGTAATTTGGGGAAACCTTCGCGCTCATACAGGGGTATACAGATGTGCTATTTAA	4923
Db	280	TCAGATGTAATTTGGGGAAACCTTCGCGCTCATACAGGGGTATACAGATGTGCTATTTAA	221
QY	4926	AGAGCAAACTAGACTTCTATGTGAGAAAGTCTGGAAATGATTTAGACATGTGTAAAG	4985
Db	220	AGAGCAAACTAGACTTCTATGTGAGAAAGTCTGGAAATGATTTAGACATGTGTAAAG	161
QY	4986	TTAAGTGAAGAACTGTAATATGTTTAAATATGATATATGATGTTCTTTTGAAGTAAGCCAG	5045
Db	160	TTAAGTGAAGAACTGTAATATGTTTAAATATGATATATGATGTTCTTTTGAAGTAAGCCAG	101
QY	5046	CTGTTGAACGTTAACTGTGCACTTTCATCTTTTGAATGTGCATGTATGTTAAATGTAAGA	5105
Db	100	CTGTTGAACGTTAACTGTGCACTTTCATCTTTTGAATGTGCATGTATGTTAAATGTAAGA	41
QY	5106	AATGATTTAATTAATAATCAAACTGTATCTGTTTATATCAT	5145
Db	40	AATGATTTAATTAATAATCAAACTGTATCTGTTTATATCAT	1

```

RESULT 37
US-10-027-632-144266/c
: Sequence 144266, Application US/10027632
: Publication No. US20020198371A1
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotides
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027.632

```


|||||
Db 218 GTGGGGTGGTGGCTGCTCTTCACAGTAAATGCGGGAACCTCGGCTACTAGGG 159
Qy 4904 GTGATACAGATGGTATTTTAAAGACAAACCTAGCTTCTATGTGAGAGTCTGGAA 4963
Db 158 GTATACAGATGGTATTTTAAAGACAAACCTAGCTTCTATGTGAGAGTCTGGAA 99
Qy 4964 ATGATTTAGACATGTGTAAAGTATAGTGAAGAACTGTAAATGTTTATATGAAATAG 5023
Db 98 ATGATTTAGACATGTGTAAAGTATAGTGAAGAACTGTAAATGTTTATATGAAATAG 39
Qy 5024 TGTTCCTTTGAAGTAAGCCAG 5045
Db 38 TGTTCCTTTGAAGTAAGCCAG 17

RESULT 39
US-10-027-632-147620
; Sequence 147620, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147620
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-147620

Query Match 11.0%; Score 600; DB 13; Length 841;
Best Local Similarity 99.5%; Pred. No. 6.5e-310;
Matches 800; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4005 AACATAGAGGCTCGTGAAGATGATGCGATTTGCTTTCAAACTCCCTCGGC 4064
Db 1 AACATAGAGGCTCGTGAAGATGATGCGATTTGCTTTCAAACTCCCTCGGC 60
Qy 4065 TTGAGTTTATCAGTCAATATGCGGCTCTTTTGAAGCTTATTCACAGACGCT 4124
Db 61 TTGAGTTTATCAGTCAATATGCGGCTCTTTTGAAGCTTATTCACAGACGCT 120
Qy 4125 TTTTGGGGGTGGGCTGGGCGGGTGTGTCAATGTTCTTCCCTGTAAAGTGTGCT 4184
Db 121 TTTTGGGGGTGGGCTGGGCGGGTGTGTCAATGTTCTTCCCTGTAAAGTGTGCT 180
Qy 4185 AGTTGCTGCTCGTATCAGAGGTTTCTCTGTTTGAAGAAAGACAGTTTGTGACC 4244
Db 181 AGTTGCTGCTCGTATCAGAGGTTTCTCTGTTTGAAGAAAGACAGTTTGTGACC 240
Qy 4245 AGATGTGACTTCATGTTTCTATGTGATCTTAAACGACAGCAATGATGATGCTC 4304
Db 241 AGATGTGACTTCATGTTTCTATGTGATCTTAAACGACAGCAATGATGATGCTC 300

Qy 4305 AACACAGCCGACTTGGTTATGGGGATGATGAGCCGACAGACCTCACTAGTTGACA 4364
Db 301 AACACAGCCGACTTGGTTATGAGGATGATGAGCCGACAGACCTCACTAGTTGACA 360
Qy 4365 AATAATGTCTATGATGAGGAGTGTAAAGTGAAGACAGAGAGGCTCACCCGATTTGATG 4424
Db 361 AATAATGTCTATGATGAGGAGTGTAAAGTGAAGACAGAGAGGCTCACCCGATTTGATG 420
Qy 4425 ATACTGGGAAAGTGTGTGTCACCAATTTGAGTTATTTTATGATATACATTTGAAATCTTT 4484
Db 421 ATACTGGGAAAGTGTGTGTCACCAATTTGAGTTATTTTATGATATACATTTGAAATCTTT 480
Qy 4485 AATCAGACATTTCTCAAGTTTACACAGATGTTTGTATGTTTATGACACACCAAT 4544
Db 481 AATCAGACATTTCTCAAGTTTACACAGATGTTTGTATGTTTATGACACACCAAT 540
Qy 4545 GTGTACAGTTTACACCACTTCAGAGTGTGTATGATGCCAAACATGTTTAAAGAGAAA 4604
Db 541 GTGTACAGTTTACACCACTTCAGAGTGTGTATGATGCCAAACATGTTTAAAGAGAAA 600
Qy 4605 GCATGACTCTCTGCTTACAGATGTTTACAGAGTGTGGGCACTTGGTTTATGAGCTT 4664
Db 601 GCATGACTCTCTGCTTACAGATGTTTACAGAGTGTGGGCACTTGGTTTATGAGCTT 660
Qy 4665 CTGTCAATTTAGGGCTTCTTGTGGCCATGATGCCCTTCTCTGGAACGTGATGATGCTCA 4724
Db 661 CTGTCAATTTAGGGCTTCTTGTGGCCATGATGCCCTTCTCTGGAACGTGATGATGCTCA 720
Qy 4725 CATCTACAGCCTTTAGTGTGTGTTCACTAGTGTCAATATCATGTTTGAATGAGA 4784
Db 721 CATCTACAGCCTTTAGTGTGTGTTCACTAGTGTCAATATCATGTTTGAATGAGA 780
Qy 4785 CTGCGGTGGGGAAGGGGTGGCTTC 4808
Db 781 CTGCGGTGGGGAAGGGGTGGCTTC 804

RESULT 40
US-10-027-632-147620
; Sequence 147620, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147620
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-147620

Query Match 11.0%; Score 600; DB 17; Length 841;
Best Local Similarity 99.5%; Pred. No. 6.5e-310;
Matches 800; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 4005 AACATAGAGGTCACTGGAACAAGATAGTACAGATTGGCTTTCAAAATCTCTCTGGC 4064
DB 1 AACATAGAGGTCACTGGAACAAGATAGTACAGATTGGCTTTCAAAATCTCTCTGGC 60
QY 4065 TTGAGTTTATCAGCTTACATAGTGGGCTCTTTTGAAGCTTAAATTCACACAGAGCT 4124
DB 61 TTGAGTTTATCAGCTTACATAGTGGGCTCTTTTGAAGCTTAAATTCACACAGAGCT 120
QY 4125 TTTTGGGGGTGGGGCTGGGGGTGTGTGCAATTTCTTCCCTCTGTAGTGGCT 4184
DB 121 TTTTGGGGGTGGGGCTGGGGGTGTGTGCAATTTCTTCCCTCTGTAGTGGCT 180
QY 4185 AGTTCTGCTGCTGATCTCAGGTTTCTCTGTTTGAAGAAATGACAGTTTGGAC 4244
DB 181 AGTTCTGCTGCTGATCTCAGGTTTCTCTGTTTGAAGAAATGACAGTTTGGAC 240
QY 4245 AGGATGTGACTTCAATGTTTCTTATGATGATCTTAAACACAGACAGATGATGACTC 4304
DB 241 AGGATGTGACTTCAATGTTTCTTATGATGATCTTAAACACAGACAGATGATGACTC 300
QY 4305 AACACAGACCACTTGTGTTATGAGGATGATAGCCGACACACCTCCTACTAGTTGGACA 4364
DB 301 AACACAGACCACTTGTGTTATGAGGATGATAGCCGACACACCTCCTACTAGTTGGACA 360
QY 4365 AATAATGCTATGATGAGGAGGTAAAGTAAAGGACAGAAAGGGGTGACGCGCATTTGATG 4424
DB 361 AATAATGCTATGATGAGGAGGTAAAGTAAAGGACAGAAAGGGGTGACGCGCATTTGATG 420
QY 4425 ATACTGGGAAAGTGTGCTGATCAAGATTTGATGATTTTATGATATACATTTGAAATCTTT 4484
DB 421 ATACTGGGAAAGTGTGCTGATCAAGATTTGATGATTTTATGATATACATTTGAAATCTTT 480
QY 4485 AATCAGACATTTCTCAAGTTTCAACAGATGTTTGAATGTTATGATACACACACCAAT 4544
DB 481 AATCAGACATTTCTCAAGTTTCAACAGATGTTTGAATGTTATGATACACACACCAAT 540
QY 4545 GTGTAGAGTTTCAACACTTCCAGAGTGTGATGATGATGATGATGATGATGATGATGATG 4604
DB 541 GTGTAGAGTTTCAACACTTCCAGAGTGTGATGATGATGATGATGATGATGATGATGATG 600
QY 4605 GCAGTAGCTCTGCTGCTAAGATGTTTCAAGAGATTTGGGGCACTTGTTTAAATGAGCTT 4664
DB 601 GCAGTAGCTCTGCTGCTAAGATGTTTCAAGAGATTTGGGGCACTTGTTTAAATGAGCTT 660
QY 4665 CTGTCAATTTAGGGCTTCTTGTGCGATGCTCCCTTCTTGTGAACGTGTATGATCA 4724
DB 661 CTGTCAATTTAGGGCTTCTTGTGCGATGCTCCCTTCTTGTGAACGTGTATGATCA 720
QY 4725 CATCTTACAGCTTATAGTCTGTGCTCACTAGTCAATATCACTTCTTGAATTCGAGA 4784
DB 721 CATCTTACAGCTTATAGTCTGTGCTCACTAGTCAATATCACTTCTTGAATTCGAGA 780
QY 4785 CTGCGTGGCGAAGGGGTGGCGCTC 4808
DB 781 CTGCGTGGCGAAGGGGTGGCGCTC 804

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RESULT 41
US-10-027-632-24920/c
; Sequence 24920, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

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; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 24920
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24920

Query Match      9.9%; Score 541; DB 13; Length 803;
Best Local Similarity 99.7%; Pred. No. 2,8e-278;
Matches 641; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4389 AAGTGAAGCGAAGAGGGGTAGCCGCAATTTGATGATCTGGGAAAGTCTGTCAACG 4448
DB 643 AAGTGAAGCGAAGAGGGGTAGCCGCAATTTGATGATCTGGGAAAGTCTGTCAACG 584
QY 4449 AATTGAGTTATTTTATATATATATATATATATATATATATATATATATATATATAT 4508
DB 583 AATTGAGTTATTTTATATATATATATATATATATATATATATATATATATATATAT 524
QY 4509 CAGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4568
DB 523 CAGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 464
QY 4569 GTGTGATGATCCCAAAACATGTTTAAAGAAAGAGAGTCTCTTCTTAACGATGT 4628
DB 463 GTGTGATGATCCCAAAACATGTTTAAAGAAAGAGAGTCTCTTCTTAACGATGT 404
QY 4629 TTTCAAGAGTTTGGGGCACTTGTTTAAATGAGCTTCTGTATTTAGGGCTTCTTGGC 4688
DB 403 TTTCAAGAGTTTGGGGCACTTGTTTAAATGAGCTTCTGTATTTAGGGCTTCTTGGC 344
QY 4689 CATGATCCCTTCTTCTGGAACGTGATGATGATGATGATGATGATGATGATGATGATG 4748
DB 343 CATGATCCCTTCTTCTGGAACGTGATGATGATGATGATGATGATGATGATGATGATG 284
QY 4749 TCATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4808
DB 283 TCATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 224
QY 4809 GAGGCGAGGCTCTGAGCTGCTTGTGATGCTTTAGTGGGCTGCTGCTCTCTTCA 4868
DB 223 GAGGCGAGGCTCTGAGCTGCTTGTGATGCTTTAGTGGGCTGCTGCTCTCTTCA 164
QY 4869 GCATGTAATTTGGGGAACCTCGCGCTACTAGGGGGTATACAGATGATGATTTAAAGA 4928
DB 163 GCATGTAATTTGGGGAACCTCGCGCTACTAGGGGGTATACAGATGATGATTTAAAGA 104
QY 4929 GCAAAACTAGACTTCTATGATGAGAGTCTGGAATGATTTAGGACATGTTAAAGTTA 4988
DB 103 GCAAAACTAGACTTCTATGATGAGAGTCTGGAATGATTTAGGACATGTTAAAGTTA 44
QY 4989 GATGAAAGACTGTAATGTTTAAATGATGATGATGATGATGATGATGATGATGATG 5031
DB 43 GATGAAAGACTGTAATGTTTAAATGATGATGATGATGATGATGATGATGATGATG 1

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RESULT 42
US-10-027-632-24921/c
; Sequence 24921, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

```


Db 163 GCATGTAAATTGGGGAAACCTTCGYKTCYACAGGGGTATACAGATGTGATTTTAAAGA 104
Qy 4929 GCAAAACTAGACTTCTATGTGAGAGTGTGAAATGATTTAGACATGTGTAAGTTA 4988
Db 103 GCAAACTAGACTTCTATGTGAGAGTGTGAAATGATTTAGACATGTGTAAGTTA 44
Qy 4989 GATGAAAGACTGTAAATGTTTAAATATGATATAGTTCCTT 5031
Db 43 GATGAAAGACTGTAAATGTTTAAATATGATATAGTTCCTT 1

RESULT 44
US-10-027-632-24921/c
; Sequence 24921, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24921
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24921

Query Match 9.9%; Score 541; DB 17; Length 803;
Best Local Similarity 99.7%; Pred. No. 2.8e-278;
Matches 641; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4389 AAGTGAAGCGAAGAGGCGTACCGCATGTTTATGATACGCGAAAGTGCCTGCAACG 4448
Db 643 AAGTGAAGCGAAGAGGCGTACCGCATGTTTATGATACGCGAAAGTGCCTGCAACG 584
Qy 4449 ATTTGAGTTAGTTTATGATATACATGAAATCTTTAATCAGACATCTCAAGTTTCA 4508
Db 583 ATTTGAGTTAGTTTATGATATACATGAAATCTTTAATCAGACATCTCAAGTTTCA 524
Qy 4509 CAGTAGTTTGTGATGTATGACACACACACCAAAATGTGTAAAGTTTCAACATTTCCA 4568
Db 523 CAGTAGTTTGTGATGTATGACACACACCAAAATGTGTAAAGTTTCAACATTTCCA 464
Qy 4569 GTGTGTGATATGCCCAAAACATGTTTAAAGAAAGAAAGATGATGCTCCCTTGTAAAGAT 4628
Db 463 GTGTGTGATATGCCCAAAACATGTTTAAAGAAAGAAAGATGATGCTCCCTTGTAAAGAT 404
Qy 4629 TTCAGAGAGTTTGGGGCACTTGTTTATGAGCTTGTCAATTTAGGGCTTCTTGGC 4688
Db 403 TTCAGAGAGTTTGGGGCACTTGTTTATGAGCTTGTCAATTTAGGGCTTCTTGGC 344
Qy 4689 CATGGTCCCTTCTTCTTGGAACCTGTATGTATGATCCTCAAGCCTTTAGTGTGT 4748
Db 343 CATGGTCCCTTCTTCTTGGAACCTGTATGTATGATCCTCAAGCCTTTAGTGTGT 284

Qy 4749 TCACAGTGTGATATACATGATCTTGTGATTCGACACTCCGTGCGAAGGGGTGCTC 4808
Db 283 TCACAGTGTGATATACATGATCTTGTGATTCGACACTCCGTGCGAAGGGGTGCTC 224
Qy 4809 GGAGCAGGCTCTGAGAGTGTGTTGATGTCTTTAGGTGGGGTGTGCTGTCTCTTCA 4868
Db 223 GGAGCAGGCTCTGAGAGTGTGTTGATGTCTTTAGGTGGGGTGTGCTGTCTCTTCA 164
Qy 4869 GCATGTAAATTGGGGAAACCTTCGCGTCTACTAGGGGTGATACAGATGTGATTTAAAGA 4928
Db 163 GCATGTAAATTGGGGAAACCTTCGCGTCTACTAGGGGTGATACAGATGTGATTTAAAGA 104
Qy 4929 GCAAACTAGACTTCTATGTGAGAGTGTGAAATGATTTAGACATGTGTAAGTTA 4988
Db 103 GCAAACTAGACTTCTATGTGAGAGTGTGAAATGATTTAGACATGTGTAAGTTA 44
Qy 4989 GATGAAAGACTGTAAATGTTTAAATATGATATAGTTCCTT 5031
Db 43 GATGAAAGACTGTAAATGTTTAAATATGATATAGTTCCTT 1

RESULT 45
US-10-357-930-43560
; Sequence 43560, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43560
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-43560

Query Match 7.9%; Score 431; DB 18; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.6e-219;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4175 AAGTGTGCTAGTGTGCTGCTCGATATCTCAGATTTTCTCGTTTGTGAAATGGAAG 4234
Db 13 AAGTGTGCTAGTGTGCTGCTCGATATCTCAGATTTTCTCGTTTGTGAAATGGAAG 72
Qy 4235 TTTTGTGACAGAGTGTGACTTCAATGTTTCTATGTGAGACTTTAAACAGACAGAT 4294
Db 73 TTTTGTGACAGAGTGTGACTTCAATGTTTCTATGTGAGACTTTAAACAGACAGAT 132
Qy 4295 GATATGACTCAACACAGACGACTTGTGTTATGGGAGATGATGCGCACAGACTCACTA 4354
Db 133 GATATGACTCAACACAGACGACTTGTGTTATGGGAGATGATGCGCACAGACTCACTA 192

QY 4355 GTTGTGACAAATATATGTCTATGATGGGGTGTAAAGTAGAGCAGAGAGGCTCAGCCG 4414
|
|
|
Db 193 GTTGTGACAAATATATGTCTATGATGGGGTGTAAAGTAGAGCAGAGAGGCTCAGCCG 252
|
|
|
QY 4415 CATGTGTATGATCTCTGGGAAAGTGTCTCAACAGATTGAGTTTGTATATATACAT 4474
|
|
|
Db 253 CATGTGTATGATCTCTGGGAAAGTGTCTCAACAGATTGAGTTTGTATATATACAT 312
|
|
|
QY 4475 TGAATCTTAAATCAGACATCTCAAGTTTCACAGATGTTTGTATGTTATGACACA 4534
|
|
|
Db 313 TGAATCTTAAATCAGACATCTCAAGTTTCACAGATGTTTGTATGTTATGACACA 372
|
|
|
QY 4535 CACACCAATATGTATTAACAGTTCCACTTCAGAGTGTGTCATGCCCCAAACATGTTTA 4594
|
|
|
Db 373 CACACCAATATGTATTAACAGTTCCACTTCAGAGTGTGTCATGCCCCAAACATGTTTA 432
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|
QY 4595 AGAAGAGAAAG 4605
|
|
|
Db 433 AGAAGAGAAAG 443

RESULT 46
US-10-357-930-10717/c
; Sequence 10717, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT FILING DATE: 2003-02-04
; PRIOR FILING DATE: 2003-02-16
; PRIOR FILING DATE: 2003-02-17
; PRIOR FILING DATE: 2000-02-17
; PRIOR FILING DATE: 2000-03-16
; PRIOR FILING DATE: 2000-03-16
; PRIOR FILING DATE: 2000-03-16
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-09
; PRIOR FILING DATE: 2000-07-18
; PRIOR FILING DATE: 2000-07-18
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10717
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-10717

Query Match 7.6%; Score 416; DB 18; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.8e-211;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 TGTCTATGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATCGCTATCGCTACAT 1313
|
|
|
Db 424 TGTCTATGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATCGCTATCGCTACAT 365
|
|
|
QY 1314 CATGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTGTGAAAAGAAAAAACC 1373
|
|
|
Db 364 CATGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTGTGAAAAGAAAAAACC 305
|
|
|
QY 1374 TACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACTATGAGAAAGATTAA 1433
|
|
|
Db 304 TACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACTATGAGAAAGATTAA 245

QY 1434 GAACCAAGCTGAGCATGAGGCGCAAGAGCAAACTCAAGCTGCTGCACTTGAAGAGCC 1493
|
|
|
Db 244 GAACCAAGCTGAGCATGAGGCGCAAGAGCAAACTCAAGCTGCTGCACTTGAAGAGCC 185
|
|
|
QY 1494 AAATGAACCTGTCCCTGTCTCTCAAGAGGTGACAGAAAAAGCAGACGCCCTCAGTCC 1553
|
|
|
Db 184 AAATGAACCTGTCCCTGTCTCTCAAGAGGTGACAGAAAAAGCAGACGCCCTCAGTCC 125
|
|
|
QY 1554 ACCCTGCGGACATCTGTACTTCAAGAGCAGACGACAAAGGCCCTGTGATCCCCGAC 1613
|
|
|
Db 124 ACCCTGCGGACATCTGTACTTCAAGAGCAGACGACAAAGGCCCTGTGATCCCCGAC 65
|
|
|
QY 1614 CGTGCCAGCGTGCAGCGGTGACCGGTGCTGTGAGAGACAGCCCGCTGTAC 1669
|
|
|
Db 64 CGTGCCAGCGTGCAGCGGTGACCGGTGCTGTGAGAGACAGCCCGCTGTAC 9

RESULT 47
US-10-357-930-31909/c
; Sequence 31909, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT FILING DATE: 2003-02-04
; PRIOR FILING DATE: 2003-02-16
; PRIOR FILING DATE: 2003-02-17
; PRIOR FILING DATE: 2000-02-17
; PRIOR FILING DATE: 2000-03-16
; PRIOR FILING DATE: 2000-03-16
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-09
; PRIOR FILING DATE: 2000-07-18
; PRIOR FILING DATE: 2000-07-18
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31909
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-31909

Query Match 7.6%; Score 414; DB 18; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.4e-210;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1256 TTCTATGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATCGCTATCGCTACAT 1315
|
|
|
Db 467 TTCTATGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATCGCTATCGCTACAT 408
|
|
|
QY 1316 TGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTGTGAAAAGAAAAAAGACTTA 1375
|
|
|
Db 407 TGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTGTGAAAAGAAAAAAGACTTA 348
|
|
|
QY 1376 CTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACTATGAGAAAGATTAA 1435
|
|
|
Db 347 CTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACTATGAGAAAGATTAA 288
|
|
|
QY 1436 ACCAGCTGAGATCAGAGGCGCAAGAGCAAACTCAAGCTGTGACCTGTGAGAGAGCCAA 1495
|
|
|
Db 287 ACCAGCTGAGATCAGAGGCGCAAGAGCAAACTCAAGCTGTGACCTGTGAGAGAGCCAA 228

QY 1496 ATGAACCTGCTCTGCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 1555
DB 227 ATGAACCTGCTCTGCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 168
QY 1556 CCTGTGCCGACTCTGCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 1615
DB 167 CCTGTGCCGACTCTGCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 108
QY 1616 TGCCGAGGTGCGCCGAGGTGACAGCGCCCTGTTAGAGGACAGCGCCCTGTTAC 1669
DB 107 TGCCGAGGTGCGCCGAGGTGACAGCGCCCTGTTAGAGGACAGCGCCCTGTTAC 54

RESULT 48

US-10-357-930-40868/c
; Sequence 40868, Application US/10357930
; Publication No. US20040259086a1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40868
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-40868

Query Match 7.6%; Score 414; DB 18; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.4e-210; Indels 0; Gaps 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1256 TTCTAGTCACTGTTTCTGAGATCTCCGCTCCGACCATGCTATGCTTACATCA 1315
DB 467 TTCTAGTCACTGTTTCTGAGATCTCCGCTCCGACCATGCTATGCTTACATCA 408
QY 1316 TGAAGAGATGACATGCTCTTGAAGCTTACAGATTTGTGAAGAAAAAGACCTA 1375
DB 407 TGAAGAGATGACATGCTCTTGAAGCTTACAGATTTGTGAAGAAAAAGACCTA 348
QY 1376 CTATATCTCCAACTTCAATTTCTGAGGCAATCTCTGACATATGAGAAAGATTAGA 1435
DB 347 CTATATCTCCAACTTCAATTTCTGAGGCAATCTCTGACATATGAGAAAGATTAGA 288
QY 1436 ACCGAGCTGAGCATCAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGCCAA 1495
DB 287 ACCGAGCTGAGCATCAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGCCAA 228
QY 1496 ATGAACCTGCTCTGCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 1555
DB 227 ATGAACCTGCTCTGCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 168

QY 1556 CCTGTGCCGACTCTGCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 1615
DB 167 CCTGTGCCGACTCTGCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 108
QY 1616 TGCCGAGGTGCGCCGAGGTGACAGCGCCCTGTTAGAGGACAGCGCCCTGTTAC 1669
DB 107 TGCCGAGGTGCGCCGAGGTGACAGCGCCCTGTTAGAGGACAGCGCCCTGTTAC 54

RESULT 49

US-10-357-930-41017/c
; Sequence 41017, Application US/10357930
; Publication No. US20040259086a1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41017
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-41017

Query Match 7.6%; Score 414; DB 18; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.4e-210; Indels 0; Gaps 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1256 TTCTAGTCACTGTTTCTGAGATCTCCGCTCCGACCATGCTATGCTTACATCA 1315
DB 467 TTCTAGTCACTGTTTCTGAGATCTCCGCTCCGACCATGCTATGCTTACATCA 408
QY 1316 TGAAGAGATGACATGCTCTTGAAGCTTACAGATTTGTGAAGAAAAAGACCTA 1375
DB 407 TGAAGAGATGACATGCTCTTGAAGCTTACAGATTTGTGAAGAAAAAGACCTA 348
QY 1376 CTATATCTCCAACTTCAATTTCTGAGGCAATCTCTGACATATGAGAAAGATTAGA 1435
DB 347 CTATATCTCCAACTTCAATTTCTGAGGCAATCTCTGACATATGAGAAAGATTAGA 288
QY 1436 ACCGAGCTGAGCATCAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGCCAA 1495
DB 287 ACCGAGCTGAGCATCAGGCGCAAAAGCAAACTCAAGCTGCTGACCTGAGAGCCAA 228
QY 1496 ATGAACCTGCTCTGCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 1555
DB 227 ATGAACCTGCTCTGCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 168
QY 1556 CCTGTGCCGACTCTGCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 1615
DB 167 CCTGTGCCGACTCTGCTCTCTCTCTCTCAAGAGGTGACAGAAAAAGCGAGCGCCCTCACTGAC 108

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1616 TGCACGCGTGCACGCGTGCACGCGTGCCTGTAGAGGACAGCCCGCTGTAC 1669
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Db 107 TCCACGCGTGCACGCGTGCACGCGTGCCTGTAGAGGACAGCCCGCTGTAC 54
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RESULT 50
US-10-2220-891-86/c
; Sequence 86, Application US/10220891
; Publication No. US20030207286A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWARA, AKIRA
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED
; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS
; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE
; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
; FILE REFERENCE: 7388-73435
; CURRENT APPLICATION NUMBER: US/10/220,891
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000/140387
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/159195
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2)..(3)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(12)
; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
; LOCATION: (32)..(32)
; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
; LOCATION: (35)..(35)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (46)..(46)
; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
; LOCATION: (201)..(201)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (595)..(595)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (633)..(633)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (657)..(657)
; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
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; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:

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, NAME/KEY: modified base
, LOCATION: (666)..(666)
, OTHER INFORMATION: a, t, c, g, unknown or other
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, NAME/KEY: modified base
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, LOCATION: (766)..(766)
, OTHER INFORMATION: a, t, c, g, unknown or other
, FEATURE:
, NAME/KEY: modified base
, LOCATION: (783)..(783)
, OTHER INFORMATION: a, t, c, g, unknown or other
,
US-10-220-891-86

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Search completed: February 15, 2005, 22:17:30
Job time : 2782 secs

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OM protein - protein search, using sw model

Run on: February 9, 2005, 12:09:54 ; Search time 125.848 Seconds
(without alignments)
1721.062 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 3418

Sequence: 1 MAHEMIGQIVTERLVALL.....LGKVGSGSFGSGSMETIEVS 665

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3406	99.6	665	9 US-09-816-494-2	Sequence 2, Appl1
2	3406	99.6	665	15 US-09-964-277-2	Sequence 26, Appl1
3	3406	99.6	665	15 US-10-377-072-26	Sequence 680, App
4	3406	99.6	665	15 US-10-072-012-680	Sequence 14, Appl1
5	3406	99.6	665	15 US-10-168-506-14	Sequence 7, Appl1
6	3406	99.6	665	15 US-10-343-357-7	Sequence 2, Appl1
7	3406	99.6	665	15 US-10-257-026-2	Sequence 240, App
8	3406	99.6	665	15 US-10-648-593-240	Sequence 247, App
9	3406	99.6	665	16 US-10-648-593-247	Sequence 26, Appl1
10	3406	99.6	665	16 US-10-377-072-26	Sequence 679, App
11	3406	99.6	690	15 US-10-072-012-679	Sequence 703, App
12	3406	99.6	690	15 US-10-072-012-703	Sequence 54204, A
13	3406	99.6	690	15 US-10-425-114-54204	

14	3399	99.4	665	15 US-10-094-749-2312	Sequence 2312, App
15	3399	99.4	665	15 US-10-072-012-681	Sequence 681, App
16	3379.5	98.9	665	15 US-10-072-012-258	Sequence 258, App
17	3358.5	98.3	680	15 US-10-072-012-256	Sequence 256, App
18	3079.5	90.1	660	15 US-10-072-012-682	Sequence 682, App
19	2930	85.7	672	15 US-10-296-115-1259	Sequence 1259, App
20	2721.5	79.6	677	15 US-10-072-012-683	Sequence 683, App
21	2500	73.1	517	15 US-09-964-277-21	Sequence 21, Appl1
22	1326	38.8	665	15 US-10-072-012-699	Sequence 699, App
23	1302	38.1	665	15 US-10-072-012-700	Sequence 700, App
24	1297	37.9	253	15 US-10-108-260A-4872	Sequence 4872, App
25	1075.5	31.5	616	15 US-10-072-012-266	Sequence 266, App
26	917	26.8	501	15 US-10-072-012-702	Sequence 702, App
27	807	23.6	155	9 US-09-964-277-7	Sequence 701, App
28	732.5	21.4	461	15 US-10-072-012-701	Sequence 701, App
29	654.5	19.1	169	14 US-10-346-356-15	Sequence 15, Appl1
30	654.5	19.1	170	9 US-09-775-925-26	Sequence 26, Appl1
31	654.5	19.1	170	9 US-09-847-519A-11	Sequence 11, Appl1
32	654.5	19.1	170	14 US-10-314-058-14	Sequence 14, Appl1
33	654.5	19.1	170	14 US-10-405-808-16	Sequence 16, Appl1
34	654.5	19.1	170	15 US-10-655-073-16	Sequence 16, Appl1
35	619	18.1	155	9 US-09-964-277-6	Sequence 6, Appl1
36	619	18.1	155	9 US-09-955-732-6	Sequence 12, Appl1
37	566	16.6	140	17 US-10-803-728-12	Sequence 47, Appl1
38	469	13.7	444	9 US-09-964-899-47	Sequence 130, App
39	469	13.7	482	14 US-10-346-356-2	Sequence 164, App
40	469	13.7	482	15 US-10-058-270A-130	Sequence 2, Appl1
41	469	13.7	482	16 US-10-648-593-164	Sequence 805, App
42	466.5	13.6	381	14 US-10-184-832-2	Sequence 805, App
43	453	13.3	394	9 US-09-736-457-805	Sequence 805, App
44	453	13.3	394	9 US-09-902-941-805	Sequence 805, App
45	453	13.3	394	9 US-09-849-628-805	Sequence 805, App

ALIGNMENTS

RESULT 1
US-09-816-494-2
Sequence 2, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-09-816-494-2

Query Match	99.6%	Score 3406;	DB 9;	Length 665;
Best Local Similarity	99.7%	Pred. No. 98-238;		
Matches 663;	Conservative	1;	Mismatches 1;	Indels 0;
				Gaps 0;
QY	1	MAHEMIGQIVTERLVALL	ESTETVLLIDSPFPVNTSHLEAININCSKLMRRLOQ	60
DB	1	MAHEMIGQIVTERLVALL	ESTETVLLIDSPFPVNTSHLEAININCSKLMRRLOQ	60
QY	61	DKVLTTELIOHSAKRVVD	DOSSQDVASISDCFLTVLGLKLEKSFNSVHL	120
DB	61	DKVLTTELIOHSAKRVVD	DOSSQDVASISDCFLTVLGLKLEKSFNSVHL	120
QY	121	LAGGAFAFSRCPGICGK	STLVPTCISOPCLPVANIGPTRILPNLYGCGQDVANKELI	180
DB	121	LAGGAFAFSRCPGICGK	STLVPTCISOPCLPVANIGPTRILPNLYGCGQDVANKELI	180

QY 181 QONGIGYVLANASYTCPEKDPFI PESHFLRVVNDSECEKILPMLDKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLANASNTCPKDPFI PESHFLRVVNDSECEKILPMLDKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAYRFVEKERPTISPNFNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAYRFVEKERPTISPNFNFLGQLLDYEKKIKN 300
QY 301 QTGASGPKSKLKLHLKEKNEPVPVAVSGGQKSETPSPCADSATSBAAGRPVHPASV 360
DB 301 QTGASGPKSKLKLHLKEKNEPVPVAVSGGQKSETPSPCADSATSBAAGRPVHPASV 360
QY 361 PSVPVQPSLLEDSPLVQALSGHLISADRLSDNKLKRSFSLDIKSVYSASMAASLHGF 420
DB 361 PSVPVQPSLLEDSPLVQALSGHLISADRLSDNKLKRSFSLDIKSVYSASMAASLHGF 420
QY 421 SSSSDALEYKRPSTLLDGTNKLCOFSPVOELSEQTPETSPDKEBASIPKILQIARPSDQ 480
DB 421 SSSSDALEYKRPSTLLDGTNKLCOFSPVOELSEQTPETSPDKEBASIPKILQIARPSDQ 480
QY 481 SKRLHSVRTSSSGTAQRSLSPLRSGSVEDNHTSFLFGLSTSQOHLTKSAGLKGWH 540
DB 481 SKRLHSVRTSSSGTAQRSLSPLRSGSVEDNHTSFLFGLSTSQOHLTKSAGLKGWH 540
QY 541 SDIIAPOTSTPLTSSWYFATESHFSASAIYGGASYSYSCSOLPTCGDQVYVRRR 600
DB 541 SDIIAPOTSTPLTSSWYFATESHFSASAIYGGASYSYSCSOLPTCGDQVYVRRR 600
QY 601 QKPSDRADSRSRWSHESPFKQFRKRS COMEFGBSINSENRREELGKVSGSSFSGSME 660
DB 601 QKPSDRADSRSRWSHESPFKQFRKRS COMEFGBSINSENRREELGKVSGSSFSGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 2
US-09-964-277-2
Sequence 2, Application US/09964277
Patent No. US20020137170A1
GENERAL INFORMATION:
APPLICANT: Wei, Bo
APPLICANT: Wei, Ralf M.
TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.434
CURRENT APPLICATION NUMBER: US/09/964,277
NUMBER OF FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PaetSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-277-2

Query Match 99.6%; Score 3406; DB 9; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQVTERLVALLSEGTETKVLIDSRPFVENVTSHTLAININCKMKRRLOQ 60
DB 1 MAHEMIGTQVTERLVALLSEGTETKVLIDSRPFVENVTSHTLAININCKMKRRLOQ 60
QY 61 DKVLTIELIHSASAKKVIDIDCSQKVVVYDOSQDVASISDCFTVLILGKLEKSFNSVHL 120
DB 61 DKVLTIELIHSASAKKVIDIDCSQKVVVYDOSQDVASISDCFTVLILGKLEKSFNSVHL 120
QY 121 LAGGAESRCPGCEGKSTLVPCISQCLPVANIGFTILPNLYIGCGRDVANKELI 180
DB 121 LAGGAESRCPGCEGKSTLVPCISQCLPVANIGFTILPNLYIGCGRDVANKELI 180

QY 181 QONGIGYVLANASYTCPEKDPFI PESHFLRVVNDSECEKILPMLDKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLANASNTCPKDPFI PESHFLRVVNDSECEKILPMLDKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAYRFVEKERPTISPNFNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAYRFVEKERPTISPNFNFLGQLLDYEKKIKN 300
QY 301 QTGASGPKSKLKLHLKEKNEPVPVAVSGGQKSETPSPCADSATSBAAGRPVHPASV 360
DB 301 QTGASGPKSKLKLHLKEKNEPVPVAVSGGQKSETPSPCADSATSBAAGRPVHPASV 360
QY 361 PSVPVQPSLLEDSPLVQALSGHLISADRLSDNKLKRSFSLDIKSVYSASMAASLHGF 420
DB 361 PSVPVQPSLLEDSPLVQALSGHLISADRLSDNKLKRSFSLDIKSVYSASMAASLHGF 420
QY 421 SSSSDALEYKRPSTLLDGTNKLCOFSPVOELSEQTPETSPDKEBASIPKILQIARPSDQ 480
DB 421 SSSSDALEYKRPSTLLDGTNKLCOFSPVOELSEQTPETSPDKEBASIPKILQIARPSDQ 480
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DB 481 SKRLHSVRTSSSGTAQRSLSPLRSGSVEDNHTSFLFGLSTSQOHLTKSAGLKGWH 540
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DB 541 SDIIAPOTSTPLTSSWYFATESHFSASAIYGGASYSYSCSOLPTCGDQVYVRRR 600
QY 601 QKPSDRADSRSRWSHESPFKQFRKRS COMEFGBSINSENRREELGKVSGSSFSGSME 660
DB 601 QKPSDRADSRSRWSHESPFKQFRKRS COMEFGBSINSENRREELGKVSGSSFSGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 3
US-10-377-072-26
Sequence 26, Application US/10377072
Publication No. US20040009501A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceutical Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Miyoung
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117
TITLE OR INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
FILE REFERENCE: MEI03-0180NMIM
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19

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; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 26
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-377-072-26

Query Match      99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238; Indels 0; Gaps 0;
Matches 663; Conservative 1; Mismatches 1;

QY      1 MAHEMIGTQIVTERLVALLSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRLQQ 60
DB      1 MAHEMIGTQIVTERLVALLSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRLQQ 60

QY      61 DKVLTTELIOHSAKHKVDIDCSQKVVYVDQSQDVASLSDCFLLVLLGKLEKSNVYHL 120
DB      61 DKVLTTELIOHSAKHKVDIDCSQKVVYVDQSQDVASLSDCFLLVLLGKLEKSNVYHL 120

QY      121 LAGFAERSRCPFGCEGKSTLVPTCISOPCLPVANIGPTRILPVLNYGCGORDVANKELI 180
DB      121 LAGFAERSRCPFGCEGKSTLVPTCISOPCLPVANIGPTRILPVLNYGCGORDVANKELI 180

QY      181 QONGIGYVLNMSYTCPKDPFIPESHFLRPVNDSPCEKILPWLKDSVDFIERAKASNGCV 240
DB      181 QONGIGYVLNMSYTCPKDPFIPESHFLRPVNDSPCEKILPWLKDSVDFIERAKASNGCV 240

QY      241 LVHCLAGISRSATIAIAYIMKMDMSLDBAYRFVKEKPTISPNNFLGQLLDYEKKIKN 300
DB      241 LVHCLAGISRSATIAIAYIMKMDMSLDBAYRFVKEKPTISPNNFLGQLLDYEKKIKN 300

QY      301 QTGASGPKSKLKLHLKKNBPVPAVSEGGKSETPPLSPCADSATSEAGORPVHPASV 360
DB      301 QTGASGPKSKLKLHLKKNBPVPAVSEGGKSETPPLSPCADSATSEAGORPVHPASV 360

QY      361 PSVPVQSPLELSDSPVQALSGHLGADRLSDSNKLKRSFSLDIKSVSASMAASLHGF 420
DB      361 PSVPVQSPLELSDSPVQALSGHLGADRLSDSNKLKRSFSLDIKSVSASMAASLHGF 420

QY      421 SSSDALLEYKSTLIDGTNKLCOFSPVOELSEQTPETSPDXEASIPKCLQTAPPSDQ 480
DB      421 SSSDALLEYKSTLIDGTNKLCOFSPVOELSEQTPETSPDXEASIPKCLQTAPPSDQ 480

QY      481 SKRLHSVTSSTSGTQORSLSPHRSAGVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 540
DB      481 SKRLHSVTSSTSGTQORSLSPHRSAGVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 540

QY      541 SDILAPQTSPLTSSWYFATESSHFYASAIYGSASAYSAYSCQLPTCGDQVYSVRR 600
DB      541 SDILAPQTSPLTSSWYFATESSHFYASAIYGSASAYSAYSCQLPTCGDQVYSVRR 600

QY      601 QKPSRADSRSRWHEESPPEKQFKRRSCQMEFGESIMSENRRREELGKVGSSFSGSME 660
DB      601 QKPSRADSRSRWHEESPPEKQFKRRSCQMEFGESIMSENRRREELGKVGSSFSGSME 660

QY      661 IIEVS 665
DB      661 IIEVS 665

```

```

; APPLICANT: Zehnusen, Bryan
; APPLICANT: Patutajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esba
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 680
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-680

Query Match      99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238; Indels 0; Gaps 0;
Matches 663; Conservative 1; Mismatches 1;

QY      1 MAHEMIGTQIVTERLVALLSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRLQQ 60
DB      1 MAHEMIGTQIVTERLVALLSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRLQQ 60

QY      61 DKVLTTELIOHSAKHKVDIDCSQKVVYVDQSQDVASLSDCFLLVLLGKLEKSNVYHL 120
DB      61 DKVLTTELIOHSAKHKVDIDCSQKVVYVDQSQDVASLSDCFLLVLLGKLEKSNVYHL 120

QY      121 LAGFAERSRCPFGCEGKSTLVPTCISOPCLPVANIGPTRILPVLNYGCGORDVANKELI 180
DB      121 LAGFAERSRCPFGCEGKSTLVPTCISOPCLPVANIGPTRILPVLNYGCGORDVANKELI 180

QY      181 QONGIGYVLNMSYTCPKDPFIPESHFLRPVNDSPCEKILPWLKDSVDFIERAKASNGCV 240
DB      181 QONGIGYVLNMSYTCPKDPFIPESHFLRPVNDSPCEKILPWLKDSVDFIERAKASNGCV 240

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QY 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAYRFVKEKPTTSPNPNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAYRFVKEKPTTSPNPNFLGQLLDYEKKIKN 300
QY 301 QTGASGPKSKLKLHLKRNBPVPAVSEGGQKSETPPLSPCADSATSEAAQRPVHPASV 360
DB 301 QTGASGPKSKLKLHLKRNBPVPAVSEGGQKSETPPLSPCADSATSEAAQRPVHPASV 360
QY 361 PSVPSVQPSLLEDSPLVQALSGHLMSADRLSDNKLKRSFSLDIKSYVSASMAASLHGF 420
DB 361 PSVPSVQPSLLEDSPLVQALSGHLMSADRLSDNKLKRSFSLDIKSYVSASMAASLHGF 420
QY 421 SSSDALBYKRPSTTLDTGNTKLCQFSPVQELSEOTPETSPDKEASIPKQLQTARPSDSQ 480
DB 421 SSSDALBYKRPSTTLDTGNTKLCQFSPVQELSEOTPETSPDKEASIPKQLQTARPSDSQ 480
QY 481 SKRLHSVRTSSSGTRQORSLSPLRSGSVEDNHTSTFLFGISTSQOHLTYSAGLKGWH 540
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QY 541 SDILAPQTSPTSLTSSWYFATESHFFYSASAIYGGASYSAYSCSQLPTCGDQVYSVRR 600
DB 541 SDILAPQTSPTSLTSSWYFATESHFFYSASAIYGGASYSAYSCSQLPTCGDQVYSVRR 600
QY 601 QKPSDRADSRSMHEESPFEKQFRRSCOMEFGESIMSENRREELGKVGSQSSFFSGSME 660
DB 601 QKPSDRADSRSMHEESPFEKQFRRSCOMEFGESIMSENRREELGKVGSQSSFFSGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 5
US-10-168-506-14
; Sequence 14, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDASANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168,506
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-506-14

Query Match 99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERIVALLESGETEKVLLIDSRPFVEYNTSHLEAININCKLMKRRRIQQ 60
DB 1 MAHEMIGTQIVTERIVALLESGETEKVLLIDSRPFVEYNTSHLEAININCKLMKRRRIQQ 60
QY 61 DKVLTLEIHSAAKKVDIDSOQKVVYVDDSSQVDAISSQCFITVLILGKLEKSPNSVHL 120
DB 61 DKVLTLEIHSAAKKVDIDSOQKVVYVDDSSQVDAISSQCFITVLILGKLEKSPNSVHL 120
QY 121 LAGFAEFSRCFPGLCBGKSTLVPTCISQPCLPVANIIGPTRILPMLYLGCQDVLNKLKI 180

DB 121 LAGFAEFSRCFPGLCBGKSTLVPTCISQPCLPVANIIGPTRILPMLYLGCQDVLNKLKI 180
QY 181 QONGIYVANAATYCPKPFIPESHPLRYPVNDSCBKILPMLDKSVPIEKAKXSNVCV 240
DB 181 QONGIYVANAATYCPKPFIPESHPLRYPVNDSCBKILPMLDKSVPIEKAKXSNVCV 240
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DB 301 QTGASGPKSKLKLHLKRNBPVPAVSEGGQKSETPPLSPCADSATSEAAQRPVHPASV 360
QY 361 PSVPSVQPSLLEDSPLVQALSGHLMSADRLSDNKLKRSFSLDIKSYVSASMAASLHGF 420
DB 361 PSVPSVQPSLLEDSPLVQALSGHLMSADRLSDNKLKRSFSLDIKSYVSASMAASLHGF 420
QY 421 SSSDALBYKRPSTTLDTGNTKLCQFSPVQELSEOTPETSPDKEASIPKQLQTARPSDSQ 480
DB 421 SSSDALBYKRPSTTLDTGNTKLCQFSPVQELSEOTPETSPDKEASIPKQLQTARPSDSQ 480
QY 481 SKRLHSVRTSSSGTRQORSLSPLRSGSVEDNHTSTFLFGISTSQOHLTYSAGLKGWH 540
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QY 541 SDILAPQTSPTSLTSSWYFATESHFFYSASAIYGGASYSAYSCSQLPTCGDQVYSVRR 600
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QY 601 QKPSDRADSRSMHEESPFEKQFRRSCOMEFGESIMSENRREELGKVGSQSSFFSGSME 660
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QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 6
US-10-343-357-7
; Sequence 7, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y.Tom
; APPLICANT: ELIOTT, VICKI S.; RANKOWAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HAWALTA, April J.A.
; APPLICANT: LU, Dyrung Alina M.; TRIBOUREY, Catherine M.
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Damien B.; CHAWLA, Narinder K.
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: US/10/343,357
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366

PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CD1
US-10-343-357-7

Query Match 99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERVALLIESGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOO 60
DB 1 MAHEMIGTQIVTERVALLIESGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOO 60
QY 61 DKVLTTELQHSKAKKVDIDCSQKVVVYDQSSODVASLSDCFEVLTLGKLEKSFNSVHL 120
DB 61 DKVLTTELQHSKAKKVDIDCSQKVVVYDQSSODVASLSDCFEVLTLGKLEKSFNSVHL 120
QY 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
DB 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
QY 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
DB 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
QY 181 QONGIGYVLNASTYCKPDPFIPESHFLRPVNDSPCEKILPMWLDKSVDFIEKAKANGCV 240
DB 181 QONGIGYVLNASTYCKPDPFIPESHFLRPVNDSPCEKILPMWLDKSVDFIEKAKANGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPNEFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPNEFLGQLLDYEKKIKN 300
QY 301 QTGAAGPKSKLKLHLKEKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
DB 301 QTGAAGPKSKLKLHLKEKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
QY 361 PSVPVQPSLLEDSPLVQALSGHLHSAADRLSDNSKLRKSFSLDIKSVSYASMAASLHGF 420
DB 361 PSVPVQPSLLEDSPLVQALSGHLHSAADRLSDNSKLRKSFSLDIKSVSYASMAASLHGF 420
QY 421 SSSSEDALEYKSTLLDGNKLCQPSVQELSEQPTETSPDKBEASIPKKLQTAARPSDQ 480
DB 421 SSSSEDALEYKSTLLDGNKLCQPSVQELSEQPTETSPDKBEASIPKKLQTAARPSDQ 480
QY 481 SKRLHSVTRSSSGTAQRSLSPLRHSGSVEDNYHTSFLGSLSTSOOHLTKSAGLGKGM 540
DB 481 SKRLHSVTRSSSGTAQRSLSPLRHSGSVEDNYHTSFLGSLSTSOOHLTKSAGLGKGM 540
QY 541 SDILAPQSTPSTPLTSSWTFATESHFFYSASAIYGGASAYSAYSCQLPTCGQOVYSVRR 600
DB 541 SDILAPQSTPSTPLTSSWTFATESHFFYSASAIYGGASAYSAYSCQLPTCGQOVYSVRR 600
QY 601 QKPSRADSRMRHESPEKQFKRRSCOMERGEISMSNRREELGKVGSSSFGSME 660
DB 601 QKPSRADSRMRHESPEKQFKRRSCOMERGEISMSNRREELGKVGSSSFGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 7
US-10-257-026-2
Sequence 2, Application US/10257026
Publication No. US20040086659A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
TITLE OF INVENTION: New dual specificity phosphatase
FILE REFERENCE: DUSP10KOWS

CURRENT APPLICATION NUMBER: US/10/257,026
CURRENT FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-10-257-026-2

Query Match 99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERVALLIESGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOO 60
DB 1 MAHEMIGTQIVTERVALLIESGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOO 60
QY 61 DKVLTTELQHSKAKKVDIDCSQKVVVYDQSSODVASLSDCFEVLTLGKLEKSFNSVHL 120
DB 61 DKVLTTELQHSKAKKVDIDCSQKVVVYDQSSODVASLSDCFEVLTLGKLEKSFNSVHL 120
QY 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
DB 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
QY 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
DB 121 LAGFAEFRCRPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCORVDLNKELI 180
QY 181 QONGIGYVLNASTYCKPDPFIPESHFLRPVNDSPCEKILPMWLDKSVDFIEKAKANGCV 240
DB 181 QONGIGYVLNASTYCKPDPFIPESHFLRPVNDSPCEKILPMWLDKSVDFIEKAKANGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPNEFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPNEFLGQLLDYEKKIKN 300
QY 301 QTGAAGPKSKLKLHLKEKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
DB 301 QTGAAGPKSKLKLHLKEKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
QY 361 PSVPVQPSLLEDSPLVQALSGHLHSAADRLSDNSKLRKSFSLDIKSVSYASMAASLHGF 420
DB 361 PSVPVQPSLLEDSPLVQALSGHLHSAADRLSDNSKLRKSFSLDIKSVSYASMAASLHGF 420
QY 421 SSSSEDALEYKSTLLDGNKLCQPSVQELSEQPTETSPDKBEASIPKKLQTAARPSDQ 480
DB 421 SSSSEDALEYKSTLLDGNKLCQPSVQELSEQPTETSPDKBEASIPKKLQTAARPSDQ 480
QY 481 SKRLHSVTRSSSGTAQRSLSPLRHSGSVEDNYHTSFLGSLSTSOOHLTKSAGLGKGM 540
DB 481 SKRLHSVTRSSSGTAQRSLSPLRHSGSVEDNYHTSFLGSLSTSOOHLTKSAGLGKGM 540
QY 541 SDILAPQSTPSTPLTSSWTFATESHFFYSASAIYGGASAYSAYSCQLPTCGQOVYSVRR 600
DB 541 SDILAPQSTPSTPLTSSWTFATESHFFYSASAIYGGASAYSAYSCQLPTCGQOVYSVRR 600
QY 601 QKPSRADSRMRHESPEKQFKRRSCOMERGEISMSNRREELGKVGSSSFGSME 660
DB 601 QKPSRADSRMRHESPEKQFKRRSCOMERGEISMSNRREELGKVGSSSFGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 8
US-10-648-593-240
Sequence 240, Application US/10648593
Publication No. US20040106132A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP

```

; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 240
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-240
```

```

Query Match      99.6%; Score 3406; DB 16; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MAHEMIGTQIVTERLVALLESGETEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
DB 1 MAHEMIGTQIVTERLVALLESGETEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
QY 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSDVASLSDCFLTVLLGKLEKSFNSVHL 120
DB 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSDVASLSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGGFAEFSRCFPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
DB 121 LAGGFAEFSRCFPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
QY 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKANGCV 240
DB 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKANGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKERRPTISPENFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKERRPTISPENFLGQLLDYEKKIKN 300
QY 301 QTGASGPKSKLKLHLEKPNRPVAVSEGQKSETPLSPCADSATSEAAQRPVHPASV 360
DB 301 QTGASGPKSKLKLHLEKPNRPVAVSEGQKSETPLSPCADSATSEAAQRPVHPASV 360
QY 361 PSVPSVQPSLLEDSPLVOALSGHLISADRLSDNKLKRSFSLDIKSYSSASMAASLHGF 420
DB 361 PSVPSVQPSLLEDSPLVOALSGHLISADRLSDNKLKRSFSLDIKSYSSASMAASLHGF 420
QY 421 SSSSDALEYKPESTTLDTGNKLCQFSVQELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
DB 421 SSSSDALEYKPESTTLDTGNKLCQFSVQELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
QY 481 SKRLHSVRTSSGTAQRSLISPLHRSVSVDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
DB 481 SKRLHSVRTSSGTAQRSLISPLHRSVSVDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
QY 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSACSLPTCGQOYVSRRR 600
DB 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSACSLPTCGQOYVSRRR 600
QY 601 QKPSDRADSRSRWHEESPFEKQPKRRSCQMEFGESIMSENRSREELGKVGSSFSGSM 660
DB 601 QKPSDRADSRSRWHEESPFEKQPKRRSCQMEFGESIMSENRSREELGKVGSSFSGSM 660
QY 661 IIEVS 665
DB 661 IIEVS 665
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RESULT 9
US-10-648-593-247
; Sequence 247, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
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; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
```

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; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 247
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-247
```

```

Query Match      99.6%; Score 3406; DB 16; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MAHEMIGTQIVTERLVALLESGETEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
DB 1 MAHEMIGTQIVTERLVALLESGETEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
QY 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSDVASLSDCFLTVLLGKLEKSFNSVHL 120
DB 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSDVASLSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGGFAEFSRCFPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
DB 121 LAGGFAEFSRCFPGICEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
QY 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKANGCV 240
DB 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKANGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKERRPTISPENFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKERRPTISPENFLGQLLDYEKKIKN 300
QY 301 QTGASGPKSKLKLHLEKPNRPVAVSEGQKSETPLSPCADSATSEAAQRPVHPASV 360
DB 301 QTGASGPKSKLKLHLEKPNRPVAVSEGQKSETPLSPCADSATSEAAQRPVHPASV 360
QY 361 PSVPSVQPSLLEDSPLVOALSGHLISADRLSDNKLKRSFSLDIKSYSSASMAASLHGF 420
DB 361 PSVPSVQPSLLEDSPLVOALSGHLISADRLSDNKLKRSFSLDIKSYSSASMAASLHGF 420
QY 421 SSSSDALEYKPESTTLDTGNKLCQFSVQELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
DB 421 SSSSDALEYKPESTTLDTGNKLCQFSVQELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
QY 481 SKRLHSVRTSSGTAQRSLISPLHRSVSVDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
DB 481 SKRLHSVRTSSGTAQRSLISPLHRSVSVDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
QY 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSACSLPTCGQOYVSRRR 600
DB 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSACSLPTCGQOYVSRRR 600
QY 601 QKPSDRADSRSRWHEESPFEKQPKRRSCQMEFGESIMSENRSREELGKVGSSFSGSM 660
DB 601 QKPSDRADSRSRWHEESPFEKQPKRRSCQMEFGESIMSENRSREELGKVGSSFSGSM 660
QY 661 IIEVS 665
DB 661 IIEVS 665
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RESULT 10
US-10-377-072-26
; Sequence 26, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
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; APPLICANT: Millennium Pharmaceuticals Inc.
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```
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamsen, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Myoung
; APPLICANT: Teal, Peng-Yung
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP103-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-377-072-26

Query Match      99.6%; Score 3406; DB 16; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches .1; Indels 0; Gaps 0;
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Db
361 PSVPSVQPSLLEDSPLVQALSGHLSDADLEDSNKLKRSFSLDIKSVSASAMAASLHGF 420
Qy
421 SSSDALERYKSTTLDDGNKLCQSPVQELSEQTPETSPDKEBASIPKQLGTARPSDQ 480
Db
422 SSSDALERYKSTTLDDGNKLCQSPVQELSEQTPETSPDKEBASIPKQLGTARPSDQ 480
Qy
481 SKRLHSVTRSSSGTQQRSLSPHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 540
Db
481 SKRLHSVTRSSSGTQQRSLSPHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 540
Qy
541 SDILAPQSTPSTLSSWTFATESHFPYSASAIYGSASAYSQSLPTCGDQVSVRR 600
Db
541 SDILAPQSTPSTLSSWTFATESHFPYSASAIYGSASAYSQSLPTCGDQVSVRR 600
Qy
601 QKPSRDRSRKRWHESSPEKQPKRSCQMEGESIMSNRRRELGRKGSQSSPFGSM 660
Db
601 QKPSRDRSRKRWHESSPEKQPKRSCQMEGESIMSNRRRELGRKGSQSSPFGSM 660
Qy
661 IIEVS 665
Db
661 IIEVS 665

RESULT 11
US-10-072-012-679
; Sequence 679, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esba
; APPLICANT: Padigaru, Muradithara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Groesse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acid Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
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; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentm Ver. 2.1
; SEQ ID NO 679
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-679

Query Match      99.6%; Score 3406; DB 15; Length 690;
Best Local Similarity 99.7%; Pred. No. 9.5e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTOIVTELVALLSGTEKVLIDSRPVEVNTSHILEAININSKIMKRLQ 60
DB 26 MAHEMIGTOIVTELVALLSGTEKVLIDSRPVEVNTSHILEAININSKIMKRLQ 85
QY 61 DKVLITELIHSANHKVDIDCSQKVVYDDSDVASLSSDCFLTVLLGLKLEKSFNSVHL 120
DB 86 DKVLITELIHSANHKVDIDCSQKVVYDDSDVASLSSDCFLTVLLGLKLEKSFNSVHL 145
QY 121 LAGGFAFRCFPGCLCGKSTLVPCTISQCLPVANIGPTRLIPNLYLGGQRDVLNKELI 180
DB 146 LAGGFAFRCFPGCLCGKSTLVPCTISQCLPVANIGPTRLIPNLYLGGQRDVLNKELI 205
QY 181 QONGIGVYLNASTYCPKDFIPESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 240
DB 206 QONGIGVYLNASTYCPKDFIPESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 265
QY 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVKEKRPPTISPNFNLGQLDYEKKIKN 300
DB 266 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVKEKRPPTISPNFNLGQLDYEKKIKN 325
QY 301 QTCASGPKSKLKLHLEKNEPVPANVSEGGQSETLSPPCADSAATSEAAQRPVHPASV 360
DB 326 QTCASGPKSKLKLHLEKNEPVPANVSEGGQSETLSPPCADSAATSEAAQRPVHPASV 385
QY 361 PSVPSVQPSLLEDSPLVQALSGHLNADRLSDNKLKRSPLDIKVSASMAASLHGF 420
DB 386 PSVPSVQPSLLEDSPLVQALSGHLNADRLSDNKLKRSPLDIKVSASMAASLHGF 445
QY 421 SSSSEDALEYKQSTLLDGTNKLCOFSPVQELSEQTBETSPOKREASIPKCLQTARPSDQ 480
DB 446 SSSSEDALEYKQSTLLDGTNKLCOFSPVQELSEQTBETSPOKREASIPKCLQTARPSDQ 505
QY 481 SKRIHSVRTSSSGTAQRSLPLHRSQVEDNYHTSFLGLSTSQOHLTKSAGLKGWH 540
DB 506 SKRIHSVRTSSSGTAQRSLPLHRSQVEDNYHTSFLGLSTSQOHLTKSAGLKGWH 565
QY 541 SDILAPQSTPSLTSSWYFATESHFPYSASAIYGSASAYSAYSCSOLPTCGDQVYSVRR 600
DB 566 SDILAPQSTPSLTSSWYFATESHFPYSASAIYGSASAYSAYSCSOLPTCGDQVYSVRR 625
QY 601 QXPSPRADSRKWHESPEKOPKRRSCOMEFGEISMSNRSREELGKVGSGSFGSWE 660
DB 626 QXPSPRADSRKWHESPEKOPKRRSCOMEFGEISMSNRSREELGKVGSGSFGSWE 685
QY 661 IIEVS 665
DB 666 IIEVS 690

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RESULT 12
US-10-072-012-703

; Sequence 703, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patcurajan, Meera

```

; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esba
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie E.
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Furtak, Karayna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentm Ver. 2.1
; SEQ ID NO 703
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-703

Query Match      99.6%; Score 3406; DB 15; Length 690;
Best Local Similarity 99.7%; Pred. No. 9.5e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTOIVTELVALLSGTEKVLIDSRPVEVNTSHILEAININSKIMKRLQ 60
DB 26 MAHEMIGTOIVTELVALLSGTEKVLIDSRPVEVNTSHILEAININSKIMKRLQ 85
QY 61 DKVLITELIHSANHKVDIDCSQKVVYDDSDVASLSSDCFLTVLLGLKLEKSFNSVHL 120
DB 86 DKVLITELIHSANHKVDIDCSQKVVYDDSDVASLSSDCFLTVLLGLKLEKSFNSVHL 145
QY 121 LAGGFAFRCFPGCLCGKSTLVPCTISQCLPVANIGPTRLIPNLYLGGQRDVLNKELI 180
DB 146 LAGGFAFRCFPGCLCGKSTLVPCTISQCLPVANIGPTRLIPNLYLGGQRDVLNKELI 205
QY 181 QONGIGVYLNASTYCPKDFIPESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 240
DB 206 QONGIGVYLNASTYCPKDFIPESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 265
QY 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVKEKRPPTISPNFNLGQLDYEKKIKN 300

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Db 266 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITISPNFNLQQLDYEKKIKX 325
Qy 301 QTGASGPFSKTLKHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 360
Db 326 QTGASGPFSKTLKHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 385
Qy 361 PSVPSVQPSLLEDSPLVQALSGHLHLSADRLSDNSKLSFSLDIKVSYSASMAASLHGF 420
Db 386 PSVPSVQPSLLEDSPLVQALSGHLHLSADRLSDNSKLSFSLDIKVSYSASMAASLHGF 445
Qy 421 SSSSDALEYKPSSTLLDGTNKLCOFSVQELSEQTPETSPDXKEASIPKKLQTARPSDQ 480
Db 446 SSSSDALEYKPSSTLLDGTNKLCOFSVQELSEQTPETSPDXKEASIPKKLQTARPSDQ 505
Qy 481 SKRLHSVRTSSSGTARSLSLPLHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
Db 506 SKRLHSVRTSSSGTARSLSLPLHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 565
Qy 541 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGQOVYSVRRR 600
Db 566 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGQOVYSVRRR 625
Qy 601 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENREBELGKVGQSSPFGSME 660
Db 626 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENREBELGKVGQSSPFGSME 685
Qy 661 IIEVS 665
Db 686 IIEVS 690
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RESULT 13

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US-10-425-114-54204
; Sequence 54204, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54204
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI.pep
US-10-425-114-54204
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Query Match 99.6%; Score 3406; DB 15; Length 690;
Best Local Similarity 99.7%; Pred. No. 9,5e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MAHEMIGTOIVTERVALLESGETEKVLLDSRPVYVNSHILEANINCSKLMKRRLOO 60
Db 26 MAHEMIGTOIVTERVALLESGETEKVLLDSRPVYVNSHILEANINCSKLMKRRLOO 85
Qy 61 DKVLTITELIQHSAXHKVDIDCSQKVVVYDQSSQDVASLSDFLTVLLGKLEKSFNSVYL 120
Db 86 DKVLTITELIQHSAXHKVDIDCSQKVVVYDQSSQDVASLSDFLTVLLGKLEKSFNSVYL 145
Qy 121 LAGGFABSRCPGLCEGUSTLVPTGISQPCLPVANIGTRILIPNLYLGCQDVLNKEIL 180
Db 146 LAGGFABSRCPGLCEGUSTLVPTGISQPCLPVANIGTRILIPNLYLGCQDVLNKEIL 205
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Qy 181 QONGIGVYLNASVTCPKPDFIPESHFLRPVNDSPFCEKILPWLDKSVDFIERAKANGCV 240
Db 206 QONGIGVYLNASVTCPKPDFIPESHFLRPVNDSPFCEKILPWLDKSVDFIERAKANGCV 265
Qy 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITISPNFNLQQLDYEKKIKX 300
Db 266 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITISPNFNLQQLDYEKKIKX 325
Qy 301 QTGASGPFSKTLKHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 360
Db 326 QTGASGPFSKTLKHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 385
Qy 361 PSVPSVQPSLLEDSPLVQALSGHLHLSADRLSDNSKLSFSLDIKVSYSASMAASLHGF 420
Db 386 PSVPSVQPSLLEDSPLVQALSGHLHLSADRLSDNSKLSFSLDIKVSYSASMAASLHGF 445
Qy 421 SSSSDALEYKPSSTLLDGTNKLCOFSVQELSEQTPETSPDXKEASIPKKLQTARPSDQ 480
Db 446 SSSSDALEYKPSSTLLDGTNKLCOFSVQELSEQTPETSPDXKEASIPKKLQTARPSDQ 505
Qy 481 SKRLHSVRTSSSGTARSLSLPLHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
Db 506 SKRLHSVRTSSSGTARSLSLPLHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 565
Qy 541 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGQOVYSVRRR 600
Db 566 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGQOVYSVRRR 625
Qy 601 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENREBELGKVGQSSPFGSME 660
Db 626 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENREBELGKVGQSSPFGSME 685
Qy 661 IIEVS 665
Db 686 IIEVS 690
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RESULT 14

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US-10-094-749-2312
; Sequence 2312, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYOKU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2312
; LENGTH: 665
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-094-749-2312
Query Match      99.4%; Score 3399; DB 15; Length 665;
Best Local Similarity 99.5%; Pred. No. 2.9e-237;
Matches 662; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MAHEMIGQVTERLVALLBSGTEKVLIDSRPVEYNTSHLEAININCSKLMKRRLQ 60
DB      1 MAHEMIGQVTERLVALLBSGTEKVLIDSRPVEYNTSHLEAININCSKLMKRRLQ 60
QY      61 DKVLITELIOHSAGKXVDIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
DB      61 DKVLITELIOHSAGKXVDIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
QY      121 LAGGFAFRSRCFPLCGKSTLVPTCISQCLPVANIGPRLIIPNVLGQDVLNKEIM 180
DB      121 LAGGFAFRSRCFPLCGKSTLVPTCISQCLPVANIGPRLIIPNVLGQDVLNKEIM 180
QY      181 QONGIGVLANASYCPRKDFIPESHFLRPVNDSPCEKILPMIDKSVDFTEKKAANGCV 240
DB      181 QONGIGVLANASYCPRKDFIPESHFLRPVNDSPCEKILPMIDKSVDFTEKKAANGCV 240
QY      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
DB      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
QY      301 QTASGPKSKLKLHLKEKNEPVPAYSEGQKSETPLSPCADSATSEAGORPVHPASV 360
DB      301 QTASGPKSKLKLHLKEKNEPVPAYSEGQKSETPLSPCADSATSEAGORPVHPASV 360
QY      361 PSVPSVQPSLLEDSPLVQALSGHLISADRLSDSNKLKRSPLDIKSVSYSASMAASIHGF 420
DB      361 PSVPSVQPSLLEDSPLVQALSGHLISADRLSDSNKLKRSPLDIKSVSYSASMAASIHGF 420
QY      421 SSSDALERYKPESTTLDGNTKLCOFSPVQELSEQTPETSPDKKASIPKLTQTARPSDQ 480
DB      421 SSSDALERYKPESTTLDGNTKLCOFSPVQELSEQTPETSPDKKASIPKLTQTARPSDQ 480
QY      481 SKRLHSVRRSSSGTARSLSLPLHRSGSVEDNHTSTFLGLSTSQOHLTKSAGLGKGMH 540
DB      481 SKRLHSVRRSSSGTARSLSLPLHRSGSVEDNHTSTFLGLSTSQOHLTKSAGLGKGMH 540
QY      541 SDILAPQTSPLTSSMYFATESSHFYASAIYGSASAYASCQLPCTGPOVYVRRR 600
DB      541 SDILAPQTSPLTSSMYFATESSHFYASAIYGSASAYASCQLPCTGPOVYVRRR 600
QY      601 QKPSDPAISRHSWHEESPKEQPKRRSCQMEFGESIMSNRSREELGKVGQSFPQSGME 660
DB      601 QKPSDPAISRHSWHEESPKEQPKRRSCQMEFGESIMSNRSREELGKVGQSFPQSGME 660
QY      661 IIEVS 665
DB      661 IIEVS 665

RESULT 15
US-10-072-012-681
; Sequence 681, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patnurejan, Meera
; APPLICANT: Shimke, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Bsha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
```

```

; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Wolman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Groose, William M.
; APPLICANT: Alsdorok II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 681
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-681
Query Match      99.4%; Score 3399; DB 15; Length 665;
Best Local Similarity 99.5%; Pred. No. 2.9e-237;
Matches 662; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MAHEMIGQVTERLVALLBSGTEKVLIDSRPVEYNTSHLEAININCSKLMKRRLQ 60
DB      1 MAHEMIGQVTERLVALLBSGTEKVLIDSRPVEYNTSHLEAININCSKLMKRRLQ 60
QY      61 DKVLITELIOHSAGKXVDIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
DB      61 DKVLITELIOHSAGKXVDIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
QY      121 LAGGFAFRSRCFPLCGKSTLVPTCISQCLPVANIGPRLIIPNVLGQDVLNKEIM 180
DB      121 LAGGFAFRSRCFPLCGKSTLVPTCISQCLPVANIGPRLIIPNVLGQDVLNKEIM 180
QY      181 QONGIGVLANASYCPRKDFIPESHFLRPVNDSPCEKILPMIDKSVDFTEKKAANGCV 240
DB      181 QONGIGVLANASYCPRKDFIPESHFLRPVNDSPCEKILPMIDKSVDFTEKKAANGCV 240
QY      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
DB      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
QY      301 QTASGPKSKLKLHLKEKNEPVPAYSEGQKSETPLSPCADSATSEAGORPVHPASV 360
DB      301 QTASGPKSKLKLHLKEKNEPVPAYSEGQKSETPLSPCADSATSEAGORPVHPASV 360
QY      361 PSVPSVQPSLLEDSPLVQALSGHLISADRLSDSNKLKRSPLDIKSVSYSASMAASIHGF 420
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Db	361	PSVPSVOPSLLEDSPVVOALSGIHL	SADRLLEDNKLKRSFSLDIKSVSYSA	MAASLHGF	420
Qy	421	SSSEDALEYKPESTTLIDGTNKL	CQSPVOELSEQTPETSPDKEAS	IPKLOQARPSDQ	480
Db	421	SSSEDALEYKPESTTLIDGTNKL	CQSPVOELSEQTPETSPDKEAS	IPKLOQARPSDQ	480
Qy	481	SKRLHSVRTSSSGTAORSL	PLHRSGSVEDNYHTSFLGLSTSOOHL	TKSAGLGLKGMH	540
Db	481	SKRLHSVRTSSSGTAORSL	PLHRSGSVEDNYHTSFLGLSTSOOHL	TKSAGLGLKGMH	540
Qy	541	SDILAPQSTPSTPLTSSWYFATES	SHFYSAAIYGSASAYSAYSCS	QLPTCGDQVYSVRR	600
Db	541	SDILAPQSTPSTPLTSSWYFATES	SHFYSAAIYGSASAYSAYSCS	QLPTCGDQVYSVRR	600
Qy	601	QKPSRADSRKRWHEESPPEKOF	KRRSCOMFGEBSIMSENREBEL	GKVGSQSSFTSGSME	660
Db	601	QKPSRADSRKRWHEESPPEKOF	KRRSCOMFGEBSIMSENREBEL	GKVGSQSSFTSGSME	660
Qy	661	IIIEVS	665		
Db	661	IIIEVS	665		

Search completed: February 9, 2005, 12:28:41
 Job time : 128.848 secs

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Db 421 SSEDALERYKSTTLDGNTKLCQFSVVOELSEQTPETSPDKESAPIPKKLQTAAPSDQ 480
Qy 481 SKLHSAVTRSSSGTAORSLSPHRSQSVEDNHTSPGLSTSQOHLTKSAGLKGWH 540
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Qy 541 SDILAQOTSTPSLTSSWYFATESSHFYASAIYGSASYSAYVSCQLPCTGDOVYSVRR 600
Db 541 SDILAQOTSTPSLTSSWYFATESSHFYASAIYGSASYSAYVSCQLPCTGDOVYSVRR 600
Qy 601 OKPSDADSRSRHSESPPEKOPKRRSCOMEFESIMSENRSEBELGKVGSGSPFSGME 660
Db 601 OKPSDADSRSRHSESPPEKOPKRRSCOMEFESIMSENRSEBELGKVGSGSPFSGME 660
Qy 661 IIEVS 665
Db 661 IIEVS 665
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RESULT 2
US-09-949-016-9121
; Sequence 9121, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9121
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9121
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Query Match 38.7%; Score 1324; DB 4; Length 661;
Best Local Similarity 45.1%; Pred. No. 2,4e-106;
Matches 314; Conservative 93; Mismatches 186; Indels 104; Gaps 21;

Qy 1 MAHEHIGIOIV-TEHLVALLBSGTEKVLIDRPFVEVNTSTITLAININSGKMKRLQ 59
Db 37 MAGDLPKRVMDAKLASLIRGGPGPLVIDSRSFVEHNSWHLVSSVNICSKYKRLIQ 96
Qy 60 QDKVLITELIHSAGKHYDIDCSQKVVYVYDOSOPVASISDPCFTLVLLIGLKESFNSVH 119
Db 97 QGKVTIALILIPANASQVEATERPOVVYVYDOSSTRASVLAADSFISILSKIDGCFDVA 156
Qy 120 LLAGFAFSSRCFPLGCEGK-STLVPTCISQPCLEFVANIGPTRLIPNLVYLCQORDVLNKE 178
Db 157 ILTGFAFSSCFPLGCEGKPAALLPMSLSQCLFVPSVGLTRILPHLYLGSQKDVANKD 216
Qy 179 LIOONGIGVYNASVTCCKPDPFIPESHFLRVVNDSPCEKILPMLDKSVDFTEKAKASNG 238
Db 217 LMTQNGISVYNASVTCCKPDPFIPESHFLRVVNDSPCEKILPMLDKSVDFTEKAKASNG 276
Qy 239 CVLVHCLAGISRSATIALAYIMKMDMSLDEAYRFVKEKRTTISPENFLGQLLDYEKKI 298
Db 277 QVIVHCLAGISRSATIALAYIMKMDMSLDEAYRFVKEKRTTISPENFLGQLLDYEKKI 336
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Qy 299 KNQTASGPKSKTLKHLKEPN---EPYAVSEGGQKSETPSPPCADSAT--SEAAQR 353
Db 337 KLLAALQGGPG-----TSGTEPPSPPAAGPLPRLP--PPTSSAATGNAABRG 386
Qy 354 PVHPASVSVSPVQPSLLEDSPLVQALSGHLSDRLIEDSNKLRSFLDIKVSYSASM 413
Db 387 GLSAGEBPAPPTPPA---TSALQOGLRGHLHSSRLQDTRLKRSFSLDIKSA----- 437
Qy 414 AASLHGFSSSEDALERYKSTTLDGNT-----KLCQF-SP--VOELSEQTPETSPD 461
Db 438 -----YAPSKMPDGPDPDEKAPKCLKLSPSGAALGLSPPIPD--SPD 480
Qy 462 KEESAPIPKKLQTAAPSDQSKRLHSAVTRSSSGTAORSLSPHRSQSVEDNHTSPGL- 520
Db 481 AAPDARPPRRRRPRP-----PASPAR--SPHSLG-----LNFQD 514
Qy 521 --LSTSQOHLTKSAGLKG-----WHSILAQOTSTPSLTSSWYFATESSHFYSA 569
Db 515 AARQTPRHGLSLASAPGLPFGQQPAQAGAMAPLDSP--GTPSPDPGWCFSPE----- 565
Qy 570 SAHYGSASYSAYVSCQLPCTGDOVYSVRRQKPSDRADSRHSESPPEKOPKRRSCQ 629
Db 566 GAQAGAGVLFAPFGRAAPGPGGSDLRREARAPAPDARTGWPPEBPAPETOPKRRSCQ 625
Qy 630 MEFGESIMSENRSR-BELGKVGSGSPFSGSMEIIEVS 665
Db 626 MEFEFG-MVEGRAGEHIALGKAQASFGSVEVIEVS 661
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RESULT 3
US-09-544-716-14
; Sequence 14, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: LucHE, Ralf M.
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125,415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-14
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Query Match 19.1%; Score 654.5; DB 4; Length 170;
Best Local Similarity 72.5%; Pred. No. 5.6e-49;
Matches 121; Conservative 27; Mismatches 18; Indels 1; Gaps 1;

Qy 134 GLCEGK-STLVPTCISQPCLEFVANIGPTRLIPNLVYLCQORDVLNKELIIONGIGVYNAS 192
Db 1 GLCEKPAALLPMSLSQCLFVPSVGLTRILPHLYLGSQKDVANKDLMQNGISVYNAS 60
Qy 193 YTCCKPDPFIPESHFLRVVNDSPCEKILPMLDKSVDFTEKAKASNGCVLVHCLAGISRSA 252
Db 61 NSCKPDPFIPESHFLRVVNDSPCEKILPMLDKSVDFTEKAKASNGCVLVHCLAGISRSA 120
Qy 253 TIALAYIMKMDMSLDEAYRFVKEKRTTISPENFLGQLLDYEKKIK 299
Db 121 TIALAYIMKMDMSLDEAYRFVKEKRTTISPENFLGQLLDYEKKIK 167
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RESULT 4
US-09-557-921-15
; Sequence 15, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: LucHE, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
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/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6486
/ LENGTH: 491
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-8486
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Best Local Similarity 34.0%; Pred. No. 3.4e-32;
Matches 113; Conservative 63; Mismatches 107; Indels 49; Gaps 8;
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QY 19 LESGTEKVLIDSRPVEYNTSHILBAININCSKLMKRLOQDKVLITELIQHSA-KHKY 77
DB 137 LELGNERRLLMDCRQPELYESSHIESAINVAIGIMLRLOQKNLTVRALFTRGEDRDF 196
QY 78 DIDC-SQKVVYDQSSOD-VASISDCFLTVLLGKLEKSPNSVHLLAGPAEFSRCFPG 135
DB 197 TRRCGDTVVLVDESSDNMENTGESVLGLLKLKDEGCRAFYLEGGFSKQAEFFSLH 256
QY 136 CEKSTLVPTG-ISOCLPVANIG----- 158
DB 257 CE--TVUDSCSSSPPLVVLGIGRISDSSDIESLDNDPNSATDSDSPLSNSQP 314
QY 159 --PTRLPMLYIGCORVDLANKELIQONGIGVYVNASYTPKP-DPIESHPLRPVNDSP 215
DB 315 SEFVEILPFLYIGACADSTNLDVLEBFGIKYILNVTPLNPLFENAGFEKYQIPSDHM 374
QY 216 CEKILPMLDKSVDFLEKAKASNGCTVHCLAGISRSATITAIYIMKMDMSIDEAYRPV 275
DB 375 SGNLSQFPPEALSFIDEARGKCGVLAHCLAGISRSVTVAYVLMQKMLSMNDAYDIYK 434
QY 276 EKRPITSPNFNLGOLLDEYKKIKQGTGASGP 307
DB 435 MKKSNISPFNFMGQLDPERLT-----GLSSP 462
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RESULT 9
US-09-557-921-2
/ Sequence 2, Application US/09557921
/ Patent No. 6551810
/ GENERAL INFORMATION:
/ APPLICANT: Lucne, Ralf M.
/ TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
/ FILE REFERENCE: 200125.416
/ CURRENT APPLICATION NUMBER: US/09/557,921
/ CURRENT FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 482
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-557-921-2
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Best Local Similarity 35.9%; Pred. No. 4.5e-32;
Matches 107; Conservative 65; Mismatches 96; Indels 30; Gaps 7;
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QY 27 LLIDSRPVEYNTSHILBAININCS-KLMKRLOQDKVLITELIQ-HSAKHKVIDISGQK 84
DB 173 VILDRPMEYNTSHILBAININCS-KLMKRLOQDKVLITELIQ-HSAKHKVIDISGQK 232
QY 85 VVVYDQSSODVASISDCFLTVLLGKLEKSPNSVHLLAGPAEFSRCFPG-CEBK----- 139
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DB 233 IIVYDENTNPSRVMSPQPLHIVLESIKREKEPLVLKGGSLFFKQNHENLQDNLQOE 292
QY 140 -----STVPTCISQPCLP-VANIGETRLPMLYIGCORVDLANKELIQONGIGY 187
DB 293 CREVGGSASASGLPQPI--PTPDINAEILTPILPFLIGNEQDADQDLDMQNLNIGY 350
QY 188 VNAS-----YTCPPDPFPESHFLRPVNDSPFCKILPMLDKSVDFLEKAKASNGCTV 242
DB 351 VINVTTPLHYEKGFLF---NYKRLPATDSNNKONLQYFEAEFLEBAQCCKGLIT 406
QY 243 HCLAGISRSATITAIYIMKMDMSIDEAYRPVKEKRPITSPNFMGOLLDEYKKIRN 300
DB 407 HCOAGVSRSATIVIAVLMKHTMTWTDAYKFFYKGRPITSPNFMGOLLDEYEDLN 464
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RESULT 10
US-09-702-705-805
/ Sequence 805, Application US/09702705
/ Patent No. 6504010
/ GENERAL INFORMATION:
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/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ CURRENT FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 805
/ LENGTH: 394
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-702-705-805
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Query Match      13.3%; Score 453; DB 4; Length 394;
Best Local Similarity 31.4%; Pred. No. 8e-31;
Matches 120; Conservative 73; Mismatches 143; Indels 46; Gaps 13;
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DB 39 LPSG-GKCLLDCCRPFLAHSAGYILGSVNVRCNTIVRR-AKGSVLEQILPAEEVRAR 96
QY 77 VDIDCSQKVVYDQSSODVASISDCFLTVLLGKLEKSF--NSVHLLAGPAEFSRCFPG 134
DB 97 LRSGLYANVIVYDERSRASLRDSTVSLVQALRNARRTDICLKGYERFSSEYPE 156
QY 135 LCEGKSTL-----VPTCISQPCLPVA-----NIGETRLPMLYIGCORVDLANKEL 179
DB 157 FCSKTALAAIPRPVPSATEPLDLDSCSCGTPALHDGVEILPFLYLSAVHAARDM 216
QY 180 IQONGIGVYVNASYTPCKPFPESHFLRPVNDSPFCKILPMLDKSVDFLEKAKASNGC 239
DB 217 LDALGITALLNVSSDCN-HFEGHYQKCIPEVDNHRADISSWMEIEIXIDAVKOCGR 275
QY 240 VLVHCLAGISRSATITAIYIMKMDMSIDEAYRPVKEKRPITSPNFMGOLLDEYKKIR 299
DB 276 VLVHCGAGISRSATITAIYIMKMRVRLAEAFVQKRSITIPNNSFMQLOLFESQVL 335
QY 300 NQTAGSGPKSKLKLHLEKPNFPAVSEGGQKSETPPLSPPCASITSEAAGORPVHPAS 359
DB 336 ATSCAAEAS-----PSGPL-----GERGKTPTATP-----TSQVFSEFPV-SVG 373
QY 360 VPVPSVQPSLSDPLVQALS 381
DB 374 VHSAPSSLPYL--HSPITTSPS 393
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QY 300 NOTGASGGRKXKLLHLEKNEPVPVAVSGGGKSETPPLSPCADSATSEAGRPVHPAS 359
Db 336 ATSCAAEAS-----PSCPL-----GGRKTPATP-----TSQFVPSFV-SVG 373
QY 360 VPSVSVQPSLIEDSPVOALS 381
Db 374 VHSAPSSLPYL--HSPITTSPS 393

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 14, 2005, 09:42:14 / Search time 293.645 Seconds
(without alignments)
3705.573 Million cell updates/sec

Title: US-10-029-345A-109
Perfect score: 3418
Sequence: 1 MAHEMIGQIVTERLVALL.....LGKVGSGSFGSGMEIIEVS 665

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 81813359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3406	99.6	3544	4	US-09-816-494-1
3	1326	38.8	2377	4	US-09-920-668-3
4	1324	38.7	2351	4	US-09-949-016-3450
5	799.5	23.4	1378	4	US-09-949-016-14992
6	480	11.0	2109	4	US-09-016-434-1135
7	480	11.0	2109	4	US-09-023-655-946
8	475	11.0	2475	4	US-09-949-016-2615
9	475	11.9	333	4	US-09-513-999C-2877
10	469	13.7	1830	4	US-09-557-921-1
11	453	13.3	1238	4	US-09-702-705-803
12	453	13.3	1238	4	US-09-736-457-803

13	453	13.3	1238	4	US-09-614-124B-803	Sequence 803, App
14	453	13.3	1238	4	US-09-671-325-803	Sequence 803, App
15	453	13.3	1238	4	US-09-589-184-803	Sequence 803, App
16	453	13.3	1238	4	US-09-658-824-803	Sequence 803, App
17	451.5	13.2	2240	4	US-09-016-434-1100	Sequence 1100, App
18	450.5	13.2	2064	4	US-09-702-705-825	Sequence 825, App
19	450.5	13.2	2064	4	US-09-736-457-825	Sequence 825, App
20	450.5	13.2	2064	4	US-09-614-124B-825	Sequence 825, App
21	450.5	13.2	2064	4	US-09-671-325-825	Sequence 825, App
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26	450.5	13.2	2109	4	US-09-614-124B-826	Sequence 826, App
27	450.5	13.2	2109	4	US-09-671-325-826	Sequence 826, App
28	450.5	13.2	2109	4	US-09-589-184-826	Sequence 826, App
29	450.5	13.2	2109	4	US-09-658-824-826	Sequence 826, App
30	450.5	13.2	2263	4	US-09-949-016-2210	Sequence 2210, App
31	447	13.1	1993	2	US-08-990-379-2	Sequence 2, App1
32	445	13.0	1238	2	US-08-530-290-11	Sequence 11, App1
33	428.5	12.5	2000	4	US-09-016-434-1291	Sequence 1291, App
34	428.5	12.5	2000	4	US-09-919-497-10	Sequence 10, App1
35	428.5	12.5	2015	4	US-09-949-016-4369	Sequence 4369, App
36	427.5	12.5	2283	4	US-09-949-016-4617	Sequence 4617, App
37	427.5	12.5	2303	4	US-09-922-146-3	Sequence 3, App1
38	425	12.4	944	4	US-09-371-671B-10	Sequence 10, App1
39	405.5	11.9	1987	2	US-08-990-379-1	Sequence 1, App1
40	384	11.2	2473	4	US-09-949-016-623	Sequence 623, App
41	382.5	11.2	1619	4	US-09-702-705-801	Sequence 801, App
42	382.5	11.2	1619	4	US-09-736-457-801	Sequence 801, App
43	382.5	11.2	1619	4	US-09-614-124B-801	Sequence 801, App
44	382.5	11.2	1619	4	US-09-671-325-801	Sequence 801, App
45	382.5	11.2	1619	4	US-09-589-184-801	Sequence 801, App

ALIGNMENTS

RESULT 1
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117. NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT FILING DATE: 2001-03-23
PRIORITY APPLICATION NUMBER: 2001-03-23
PRIORITY FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:
Pred. No.: 0
Score: 3406.00
Percent Similarity: 99.85%
Best Local Similarity: 99.70%
Query Match: 99.65%
DB: 4
Gaps: 0

US-10-029-345A-109 (1-665) x US-09-816-494-3 (1-1998)

QY 1 MetAAHhEGUMeTILGLYThrGInLleValThrGUAGLeuValAlaIleuLengU 20
DB 1 ATGGCCCTATGAGATGATTGGAACCTCAATTGTACTGAGAGGTGGTGGCTCTGGAA 60
QY 21 SerGlyThrGUlueValIleuLeuIleAsperArpPropheValGUlueYrAnthrSer 40

Db 61 AGTGAACGGAAAAAGTGTCTAATTGATAGCCGGCAATTGTGGAAATACATATACCTC 120
Qy 41 HisGileuGluuAlaIleuNIleuNCysSerIleuMetIlyAspArgIleuGlnGln 60
Db 121 CACATTTTGGAAAGCCATTAATATCACTGCTCCAACTTAATGAAGGAAAGTTGGCAACG 180
Qy 61 AspIlyValIleuIleThrGluIleuIleGlnHisSerAlaIlyHisIlyValAspIleAsp 80
Db 181 GCAAAAGTGTATTTACAGAGCTCATCCAGCATTCAGCCAAACATTAAGTTGACATTTGAT 240
Qy 81 CysSerGlnIlyValIlyValIlyAspGlnSerSerGlnAspValAlaSerIleuSerSer 100
Db 241 TGCAGTGCAGAAAGTGTAGTTAGATCAAAAGCTCCCAAGATGTCTCTCTCTTCA 300
Qy 101 AspCysPheIleuThrValIleuIleuGlyIlyIleuGlnIlySerPheIleuSerValHisIleu 120
Db 301 GACGTGTTTCTCATCTACTCTGAGGTAAACGTGGAGAAAGCTTCAACTCTGTTCACCTG 360
Qy 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyIleuCysGlnGlyIlySer 140
Db 361 CTTGACAGGTGGGTTTCTGATGTTCTCTCGTTGTTTCCCTGGCTCTGTGAAGAAATCC 420
Qy 141 ThrIleuValProThrCysIleSerGlnProCysIleuProValAlaAsnIleGlyProThr 160
Db 421 ACTCTAGTCCCTAACCTGCAATTTCTCAGCCTTGCTTACTGTTGCCAACATGGGCCAAC 480
Qy 161 ArgGileuProAsnIleuIlyIleuGlyCysGlnArgAspValIleuAsnIleGlyIleuIle 180
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Db 541 CAGCAAGAAAGGAGTTGTTATGTGTTAAATGCCAGCAATCTGTCCAAAGCTGACTTT 600
Qy 201 IleProGlnSerHisPheIleuArgValProValAsnAspSerPheCysGlnIlyIleu 220
Db 601 ATCCCCGAGTCTCATTTCTCGCTGTGCTGAGATGACAGCTTTGTGAGAAATTTTGG 660
Qy 221 ProTProIleuAspIlySerValAspPheIleGlnIlyValAlaIleSerAsnIlyCysVal 240
Db 661 CCGTGTGTGACAAATCACTAATTTTCTAGGACCACTCTCGAGACTATGAGAAAGATTAAAGAC 720
Qy 241 IleuValHisCysIleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIlyIleMet 260
Db 721 CTAGTGCACATGTTTGTAGCTGATCTCCGCTCCGCAACATGCTATGSCCTACATCATG 780
Qy 261 LysArgMetAspMetSerIleuAspGlnAlaIlyArgPheValIlyGlnIlyArgProThr 280
Db 781 AAGAGATGACATGTCTTTAGATGACAGCTTACAGATTTGTGAAAGAAAGAAAGACCTTACT 840
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Qy 321 GluProValProAlaValSerIleuGlyIlyGlnIlySerGlnThrProIleuSerProPro 340
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Qy 341 CysAlaAspSerAlaThrSerGlnAlaIleuGlnArgProValHisProAlaSerVal 360
Db 1021 TGTGCCGACTGTCTACTCAGAGGCAAGCAAGCAAAAGCCCGTGCATCCGCGCAGCGTG 1080
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Qy 381 SerGlyIleuHisIleuSerAlaAspArgIleuGlnAspSerAsnIlyIleuIlyArgSerPhe 400

Db 1141 AGTGGGCTGACCTGTCCGACAGACAGCTGGAAGACAGCAATTAAGCTCAAGGTTCTTCC 1200
Qy 401 SerIleuAspIleIlySerValSerIlySerAlaSerMetAlaAlaSerIleuHisGlyPhe 420
Db 1201 TCTCTGGATATCAATCAATCAATGTTTCAATTCACAGCCAGCAAGGACATCTCTACATGCTTC 1260
Qy 421 SerSerSerGlnAspAlaIleuGlnIlyThrIlyIlyProSerThrThrIleuAspGlyIlyThrAsn 440
Db 1261 TCTCTATCAGAAAGATGCTTTGGATACTACAAACCTTCACTACTCTGATGGAGCCAAAC 1320
Qy 441 IlyIleuCysGlnPheSerProValGlnIleuSerGlnGlnThrProGlnThrSerPro 460
Db 1321 AAGCTATCCAGATTTCTCCCTGTTTCAAGAACTATGAGAGAGACTCCGAAACAGTCTCT 1380
Qy 461 AspIlyGlnGlnAlaSerIleProIlyIlyIleuGlnThrAlaArgProSerAspSerGln 480
Db 1381 GATTAAGAGAGAAAGCCAGATCCCAAGAGCTGCAGACCGGACAGCTTCCAGACAGCCAG 1440
Qy 481 SerIlyAspIleuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerIleu 500
Db 1441 AGCAAGCATTTGCATTCGTGTGAGAACAGAGCAAGTGGCACTCCGCAAGAGTCCCTTTTA 1500
Qy 501 SerProIleuHisArgSerGlySerValGlnAspAsnIlyHisIlySerPheIleuPheGly 520
Db 1501 TCTCCACTGCATTCGAAGTGGAGCGTGGAGGACATTAACACAGCTTCTTTTGGGC 1560
Qy 521 LeuSerThrSerGlnGlnHisIleuThrIlySerAlaGlyIleuGlyIleuIlyGlyIlyThrHis 540
Db 1561 CTYTCCACAGCCAGACAGACCTCAGCAAGTCTGCTGCTGAGCTTTAAAGGGCTGGCAC 1620
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Qy 561 ThrGlnSerSerHisPheIlySerAlaSerAlaIleIlyGlyIlySerAlaSerIlySer 580
Db 1681 ACAGAGTCTTCACTTACTGCTGCTCAGCCATCTTAACGAGGACAGTCCAGATTACTCT 1740
Qy 581 AlaIlySerCysSerGlnIleuProThrCysGlyIlyAspGlnAlaIlySerValArgArg 600
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Qy 601 GlnIlyProSerAspArgAlaAspSerArgArgSerThrHisGlnIlySerProPheGln 620
Db 1801 CAGAAAGCAAGTGCAGAGCTGACTCGCGGAGAGCTGGATGAAGAGGCCCTTTGAA 1860
Qy 621 LysGlnPheIlyArgArgSerCysGlnMetGlnPheGlyIlySerIleMetSerGlnAsn 640
Db 1861 AAGCAGTTTAAACGACAGAGCTGCCAATGGAATTTGAGAGGACATCATGTCCAGAGAAC 1920
Qy 641 ArgSerArgGlnIlyIleuGlyIlyValGlySerGlnSerSerPheSerGlySerMetGln 660
Db 1921 AGGTCAAGGAGAGCTGGGGAAGTGGGAGTCAAGTCTTGTGGGAGAGATGAAA 1980

RESULT 2

US-09-816-494-1
; Sequence 1, Application us/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: us/09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0


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/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (589) ... (2583)
US-09-816-494-1

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Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 4 Gaps: 0

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DB AGTGGAAAGGAAAAGTGTCTCTAATTGATAGCCGGCAATTTGTGGAAATACAAATCATCC 708
QY 41 HisIleLeuGluAlaIleAsnIleAsnCySerIleValMetLeuArgArgLeuGlnGln 60
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QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaValHisIleValAspIleAsp 80
DB GACAAAGGTATATACAGAGCTCATCCAGCAATTCAGCAACAAATAGGTTGACATATAT 828
QY 81 CysSerGlnIleValIleValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB TGCACATCAGAAAGTGTAGTTTACATCAAAAGCTCCCAAGATGTTGCCCTCTCTCTCA 888
QY 101 AspCyPheLeuThrValLeuLeuGluIleValLeuGluIleValSerPheAsnSerValHisLeu 120
DB GACTTTTCTTCCACTGTACTCTCTGGGTAAACTGAGAAAGAGCTTCAACTCTGTCACTG 948
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuCyGlnGlyIleYrSer 140
DB CTGGAGGTGGGTGTGCTGAGTCTCTCTGTGTCTCTGCTGCTGTAAGAAAGAAATCC 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB ACTCTAGTCCCTACCTGCACTTCTCAAGCTTCTTACCTGTGGCCAACTTGGGCCAAC 1068
QY 161 ArgIleLeuProAsnLeuTyrLeuGluIleCysGlnArgAspValLeuAsnIleGluLeuIle 180
DB CGAATTTCTTCCCAATCTTATCTTGTGGTGGCCAGAGATGTCTCTCAACAGAGAGCTGAT 1128
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProIleProAspPhe 200
DB CAGCAAGATGGGATTTGTTATGTGTTAAATGCAACAAATACCTGTGCCAAAGCTTACTT 1188
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluIleValIleLeu 220
DB ATCCCGAGTCTCATTTCTGGGTGGTGGCTGTGGAATGACAGCTTTTGGAAATTTTGG 1248
QY 221 ProTyrLeuAspIleValSerValAspPheIleGluValAlaValAlaSerAsnIleCysVal 240
DB CCGTGTGTGACAAATCAGTATGATTTCAATTGGAAGCAAAAGCTCCCAATGATGATGTT 1308
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrTyrIleMet 260
DB CTAGTGCACTGTTTAGTGGATCTCCGCTCCGCAACCATGCTATGGCTTACATCATG 1368
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluIleYrArgProThr 280
DB LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluIleYrArgProThr 280
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DB 1369 AAGAGATGACATGTCTTATGATGAGCTTACAGATTTGTGAAGAAAAAGACCTACT 1428
QY 281 IleSerProAsnPheAsnPheLeuGluIleLeuLeuAspTyrGluIleValIleLysAsn 300
DB ATATCTCCAACTTAAATTTTCTGGGCCAACTCTGCACTATGAAAGAAAGTTAAGAAC 1488
QY 301 GlnThrGlyAlaSerGlyProIleSerIleValLeuLeuHisLeuGluIleValProAsn 320
DB CAGACTGAGATCAAGGAGCCAAAGCAAACTCAAGCTGTCTGACTGAGAAAGCCAAAT 1548
QY 321 GluProValProAlaValSerGluGlyIleGlnIleYrSerGluThrProLeuSerProPro 340
DB GAACCTGTCTCCGTGTCTCAGAGGGGTGAGCAAGAAAGAGAGACCCCTCAGTCCACCC 1608
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyIleValArgProValHisProAlaSerVal 360
DB TGTGCCACTGTCTGCTTCACTCAGAGGAGCAAGCAAGAGCCCGCTCATCTCCGACGCGG 1668
QY 361 ProSerValProSerValGlnProSerLeuGluAspSerProLeuValGlnAlaLeu 380
DB CCCAGCTGTCCAGGCTGACGCTGTCTGTATAGAGACAGCCCGCTGTACAGGCGCTC 1728
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnIleValYrArgSerPhe 400
DB AGTGGCTGCACTGTCTGCGCAGACAGGCTGGAAAGACAAATTAAGCTCAAGGCTTCTTC 1788
QY 401 SerLeuAspIleValSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
DB TCTCTGATATCAATCAATCAGTTTCAATTCAGCAGCAATGCGCATCTTATATGAGCTTC 1848
QY 421 SerSerSerGluAspAlaLeuGluTyrTyrIlePyrProSerThrThrLeuAspGluThrAsn 440
DB TCTCATATCAAGATGCTTTTGAATATCAAACTTCACTCACTGTGATGGAGCCAAAC 1908
QY 441 LysLeuCyGlnPheSerProValGlnIleLeuSerGlnGlnThrProGluThrSerPro 460
DB AAGCTATCCAGTCTTCTCCCTGTTCAGGAATATGAGAGACATCCCGAAACCAAGTCT 1968
QY 461 AspIleGluGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSerGln 480
DB GATAAGGAGAAAGCCAGCATCCCAAGAGCTGCAAGCCGCGCATTCAGACAGCCAG 2028
QY 481 SerIleValGluHisSerValArgThrSerSerSerGlyThrAlaArgSerLeuLeu 500
DB AGCAAGCAATTCATCTCGGTCAAGACAGCAAGTGGCAAGCCCAAGAGTCCCTTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
DB TCTCATGCAATCGAAGTGGAGGCTGGAGGACATTAACAACACAGCTTCTTTTCCGC 2148
QY 521 LeuSerThrSerGlnGlnHisLeuThrIleYrSerAlaGlyLeuGlyLeuIleGlyTyrHis 540
DB CTTTCCACACAGCCAGCAACCTCAAGAGTCTGTGCTGAGCTTAAAGGGCTGGCAC 2208
QY 541 SerAspIleValAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
DB TGGATATCTTGGCCCCCAAGCCCTTACCTTCCCTGACCAAGAGCTGTGATTTTGGC 2268
QY 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIleYrSerAlaSerTyrSer 580
DB ACAAGTCTCACTCACTTACTTCTGCTCCTCAGCAATCAAGAGGAGGAGGCAAGTACT 2328
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGluAspGlnValTyrSerValArgArgArg 600
DB GCTTACAGCTCAGCAGCTCCCACTTGGCGAGACCAAGTCTATTTCTGTGCGCGCGGG 2388
QY 601 GlnIlePyrProSerAspArgAlaAspSerArgArgSerTyrHisGluGluSerProPheGlu 620
DB CAGAAAGCCAAAGTGAAGAGTGAATCTCGGCGGAGAGCTGGCATGAAGAGAGCCCTTTAA 2448
QY 621 LysGlnPheLysArgTyrSerCysGlnMetGluPheGlyIleSerIleMetSerGluAsn 640
DB AAGCAGTTTAAACGAGAGAGCTGCCAAATGGAATTTGGAGAGAGATCATGTCAAGAAC 2508
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[illegible]

DB 1536 CCCGCGCAGAGCTCCGCG-----CTGAAGTTCGGCGAT 1568
QY 521 -----LeuserThserGlnGlnHisLeuThrySerAlaGlyLeuGlyLeuGly 538
DB 1569 GCGGCGCGGAGACTCCGGGACGCGGCTCTCGGCTTCGGCGCGCGGCTGCGCGG 1628
QY 539 -----TPrHAserAAsp1LeuAlaProGlnThrs 549
DB 1629 CCTGGCAGACCG 1682
QY 550 ThrProSerLeuThrsSerSerTrpTyPheAlaThrGlySerSerHisPheTySerAla 569
DB 1683 ACGCGCTCG 1721
QY 570 SerAlaIleTyGlyGlySerAlaSerTyPheAlaTySerCySerGlnLeuProThr 589
DB 1722 GCGCGCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1781
QY 590 CySerGlyAspGlnValTySerValArgArgGlnTyPheSerAspArgAlaAspSer 609
DB 1782 CCAAGCG 1841
QY 610 ArgArgSerTrpHisGlnLeuSerProPheGlnTyGlnPheLeuArgArgSerGln 629
DB 1842 CGGACCGGCTGGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1901
QY 630 MetGluPheGlyGlySerIleMetSerGluAsnArgSerArg---GluGluLeuGlyLys 648
DB 1902 ATGGAGTTGAGAGAGGCG---ATGGTGAGAGGCGCGCGCGCGCGCGCGCGCG 1958
QY 649 ValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 665
DB 1959 CTGGCGACAGACGCGAGCTTCTCGGCGACGCGAGCGTCAAGGATGCC 2009
RESULT 4
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250
Alignment Scores:
Pred. No.: 2,18e-126 Length: 2351
Score: 1324.00 Matches: 314
Percent Similarity: 58.398 Conservative: 93
Best Local Similarity: 45.054 Mismatches: 186
Query Match: 38.744 Indels: 104
Gaps: 21
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QY 1 MetAlaHisLeuMetIleGlyThyrGlnIleVal---ThrGluArgLeuValAlaLeuLeu 19
DB 109 ATGGCTGGGAGACGGCTCCCGAGAAAGTATGATGATGCCAAGAGCTGGCCAGCTGCTG 168

QY 20 GluSerGlyThyrGluValLeuLeuIleAspSerArgProPheValGluTyraEnthr 39
DB 169 CGGCG 228
QY 40 SerHisIleLeuGlnAlaIleAsnIleAsnCySerTyLeuMetIleArgArgLeuGln 59
DB 229 TGGCATGTCTCAGCTCCGCTCAACATCTCTCTCCAGCTGATGAAGCGCGCTGCGAG 288
QY 60 GlnAspIleValLeuIleThyrGluLeuIleGlnHisSerAlaIleHisValAspIle 79
DB 289 CAGGCGAAGTACCATTCGAGCATTCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 348
QY 80 AspCySerGlnTyValValValTyraAspGlnSerSerGlnAspValAlaSerLeuSer 99
DB 349 ACGAGACCAAGAGAGTGTGTGTCTTATGACAGAGACCGCGGAGCCAGCCGCTGCGCC 408
QY 409 GAGAGACGCTTCTCTCCATCTCTGAGCAAGCTGACGCGCTTTCGACAGCGTGGCC 468
QY 120 LeuLeuAlaGlyValPheAlaGluPheSerArgCyPheProGlyLeuCySerGlyLys 139
DB 469 ATCTTCACCTGGGAGGCTTCGCCACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 528
QY 140 ---SerThrLeuValProThrCyIleSerGlnProCyLeuProValAlaAsnIleGly 158
DB 529 CTGCTGCT 588
QY 159 ProThrArgIleLeuProAsnLeuTyIleGlyCySerGlnArgAspValLeuAsnIleGly 178
DB 589 CTGACCGGATCTGCTGCTCACTCACTGAGGCTGCGCAAGAGACGCTTAAACAGAT 648
QY 179 IleuIleGlnHisArgIleGlyTyValLeuAsnAlaSerTyThrCyProLysPro 198
DB 649 CTGATGACGCAAAATGAGATAGCTACGCTTCAACGCGAGACGCTGCGCGCGCT 708
QY 199 AspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCySerGlyLys 218
DB 709 GACTTCATCTGCGAAGCGCGCTTCTGCGGAGTCCCATGAGACACACTACTGTGAAA 768
QY 219 IleLeuProTrpLeuAspIleSerValAspPheIleGluTyLeuAlaIleAsnIleGly 238
DB 769 CTGCGCGCTGCTGCGAGCAAGTCACTGAGTTCATGATGAAGCCAGCTCTCCAGCTCG 828
QY 239 CyValLeuValHisCyLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTy 258
DB 829 CAAGTATCGTCACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
QY 259 IleMetIleArgMetAspMetSerLeuAspGluAlaTyArgPheValLysGlyLysArg 278
DB 889 ATCATGAGACCATGGCATGTCTCTCCGACGAGCTTACAGGTTCTGTGAAGACAGCGCC 948
QY 279 ProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyGluTyLysIle 298
DB 949 CGCTCATCTGCGCCCACTTCACTTCTGCGCGAGCTCTGAGTACAGAGCGCGCTG 1008
QY 299 LysAsnGlnThyrGlyAlaSerGlyProLysSerTyLeuLysLeuLeuHisLeuGlyLys 318
DB 1009 AAGCTGCTGGCGCGCTGCGAGCGGCGAGCCCGCGC-----ACC 1044
QY 319 ProAsn-----GluProValProAlaValSerGluGlyGlnLysSerGluThr 335
DB 1045 CCTCTAGGAGCGCGGAGGCTCGCGCGAGTCTGCGCGCGCGCGCGCGCGCGCGCG 1104
QY 336 ProLeuSerProProCyAlaAspSerAlaThr-----SerGluAlaIleGlyLysArg 353
DB 1105 CCA-----CACTACCTCAAGAGCGCTGCGACAGGAGATGCGGCTGCCAGGAGGCG 1158
QY 354 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuAsp 373
DB 1159 GCGCTGAGCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1209
QY 374 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 393

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Db      1210 AGGCACTGACAGAGGCGCTGCGGCTGCACCTCTCCGACCGCCCTGCAGAGACT 1269
Qy      394 AsnlybLeuLybArgSerPheSerLeuAspIleYbSerValSerYbSerAlaSerMet 413
Db      1270 AACCGCTCTAAGGCGCTCTCTCTCTCTGACATCAAGCTCC----- 1311
Qy      414 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluIuYbYbYbProSer 433
Db      1312 -----TACGCCCTTAGC 1323
Qy      434 ThrThrLeuAspGlyThrAsn-----LysLeuCySGlnPhe 445
Db      1324 ATCGGCGCCGACGCGCCCGGCGCCCGGACCGCGCGAGGCGCCGGAAGCTCTCAAGCTG 1383
Qy      446 ---SerPro-----ValGlnGluLeuSerGlnGlnThrProGluThrSerProAsp 461
Db      1384 GACAGCCCTGTCGGGGCGCGCGCTGCGGCTGTCTCGCCCATCCCGGAC--ACCCCGGAC 1440
Qy      462 LysGluGluAlaSerIleProLybLybLeuGlnThrAlaArgProSerAspSerGlnSer 481
Db      1441 GCGCGCCCTGATGCGCGCCGACGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1485
Qy      482 LysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSer 501
Db      1486 -----CCGCGCGGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1509
Qy      502 ProLeuHisArgSerGlySerValGluAspAsnYbHisThrSerPheLeuPheGly--- 520
Db      1510 CCGCGCCGACGCTCGCG-----CTGAACCTTCGCGCGAT 1542
Qy      521 -----LeuSerThrSerGlnGlnHisLeuThrLybSerAlaGlyLeuGlyLeuLybGly 538
Db      1543 GCGCGCCGCGAGACTCGCGCGGACGCGGCTCTCGGCGCTGTGCGCGCGCGCGCGCGCGCG 1602
Qy      539 -----TrpHisSerAspIleLeuAlaProGlnThrSer 549
Db      1603 CTTGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1656
Qy      550 ThrProSerLeuThrSerSerTrpYbPheAlaThrGluSerSerHisPheYbSerAla 569
Db      1657 AGCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1695
Qy      570 SerAlaIleTybGlySerAlaSerYbSerAlaTybSerCybSerGlnLeuProThr 589
Db      1696 GCGCGACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1755
Qy      590 CybGlyAspGlnValTybSerValArgArgArgGlnLybProSerAspArgAlaAspSer 609
Db      1756 CCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1815
Qy      610 ArgArgSerTrpHisGluGluSerProPheGluLybGlnPheLybArgArgSerCybGln 629
Db      1816 CCGAGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1875
Qy      630 MetGluPheGlyLeuSerIleMetSerGluAsnArgSerArg---GluGluLeuGlyLyb 648
Db      1876 ATGAGATTGAGAGAGGCG---ATGGTGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1932
Qy      649 ValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 665
Db      1933 CTGGCGAAGAGCGAGCTTCTCTCGGCGACGTCGAGAGTCATCGAGGTGTCC 1983

RESULT 5
US-09-949-016-14992
; Sequence 14992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14992
; LENGTH: 13782
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14992

Alignment Scores:
Pred. No.: 1,36e-70 Length: 13782
Score: 799.50 Matches: 254
Percent Similarity: 34.53% Conservative: 63
Best Local Similarity: 27.67% Mismatches: 154
Query Match: 23.39% Indels: 449
DB: Gaps: 23

US-10-029-345A-109 (1-665) x US-09-949-016-14992 (1-13782)
Qy      123 GLyGlyPheAlaGluPheSerArgCybPheProGlyLeuCybGlnGlyb---SerThr 141
Db      8879 GGGGGCTTCGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8938
Qy      142 LeuValProThrCybIleSerGlnProCybLeuProValAlaAsnIleGlyProThrArg 161
Db      8939 CTGTACCATGAGCTCTCCAGCGCTGCGCTGTGCGCAGAGTGCGGCGCTGACCGCGC 8998
Qy      162 IleLeuProAsnLeuTybLeuGlyCybGlnArgArgValIleAsnIleGlyb--- 178
Db      8999 ATCTGCTTCACTTACTTACTGCTGCGCTGCGAGAGAGCGTCTTAACAGAGT-GTGTGTCA 9057
Qy      178 ----- 178
Db      9058 GTGAGTTCGGGGGGGTGTCATGTGGAAAGGGGCAAGAGCTCCAGAGCAGCTTGGCAGC 9117
Qy      178 ----- 178
Db      9118 GAGAGCGGGGATGAGAGGAGAAAGAGCTGAAGCAGTGAAGCTGTGTGGAGAA 9177
Qy      178 ----- 178
Db      9178 GCATGTGGGGGCCAGAGAGAGACCCAGGCTCCCAACCATGTCCCTGAAGAGACCA 9237
Qy      178 ----- 178
Db      9238 GCAAGGCTTGGGGAGAGGCGCGGAGGCTGCGGGGAGAGAGCGGGAGCTGGCATGCCAA 9297
Qy      178 ----- 178
Db      9298 GCTGCGATGTCACTGGGCTCTGGCCAGCTCTGAAGAAATCCATGTTTAAAAATGGT 9357
Qy      178 ----- 178
Db      9358 GACGAGGAAAAAGGTAAAGCAACCAACGAGCAATCAATAAATTCCTAGAGCCCAAC 9417
Qy      178 ----- 178
Db      9418 ACCAGCGTGGGTGGGGCTGCGAGTCGAGAGCCAGCCGTGCCCAACCCCGCGACGGGCC 9477
Qy      178 ----- 178
Db      9478 CAGGTGCAAGGTGAGACAGAGAGGCTCTGTGGGCTCTCCCTGTGATACATCGAGATCT 9537
Qy      178 ----- 178
Db      9538 GGGACAAATTCCAAGCTCCAGAGATTCTAAAGGCTCTGTACGCGGAGGCGAGGAGAAAG 9597
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1135:
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91418933
US-09-016-434-1135

Alignment Scores:
Pred. No.: 5,67e-39 Length: 2109
Score: 480.00 Matches: 121
Percent Similarity: 51.62% Conservative: 70
Best Local Similarity: 32.70% Mismatches: 126
Query Match: 14.04% Indels: 53
Gaps: 9
DB: 4

US-10-029-345A-109 (1-665) x US-09-016-434-1135 (1-2109)
QY 19 LeugluserGlyThrglulysValleuLeuileaspSerArpProPhyValgluTyraAn 38
DB 430 CTGGAGCTGGCGAAGAGCGGCTGCTGATGAGCTGCCGCCGAGAGCTATACGAG 489
QY 39 ThrSerHisIleleuGlulAlaIleasnIleasnCySerIysleuMetIysArgIleu 58
DB 430 TCGTGCACATGAGTCCGCTCAACGTCGATCCCGGATCATGCTCGGCGCTCG 549
QY 59 GlnGlnApIysValleuIleThrgluleuIleGlnHisSerAla---IyHisIysVal 77
DB 550 CAGAAAGGTACCTGCGGCTGGCGGCTCTTCACGCGCGGAGAGCCGGAGCCGCTTC 609
QY 78 AspIleaspCyS---SerGlnIysValIValIYrAspGlnSerSerGlnasp---Val 95
DB 610 ACCCGGCGCTGGGACGACACAGTGTGTCTACGACGACGACGACGACGACGAC 669
QY 96 AlaSerIleuSerSeraspCySPhleuThrValIleuLeuGlyIysleuGlnIysSerPhe 115
DB 670 GAGAAATACGGGCGGAGTCTGCTCGGCTGCTGCTCAAGAACTCAAGACGAGGAG 729
QY 116 AanserValHisIleuLeuAlaIleGlyPheAlaGlnPheSerArpCySPhProGlyIleu 135
DB 730 TCCCGGCGCTTACCTGAGAGGTGCTTCAAGTAAAGTTCACAAAGGCTTCCTGCAT 789
QY 136 CysGlnGlyIysSerThrIleuValProThrCyS---IleSerGlnProCysleuProVal 154

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DB 790 TCGGAG-----ACCAATCTAGACGGCTCGTGTACAGACAGCTGCCCGCTTGCATGTG 843
QY 155 AlaasnIleGly----- 158
DB 844 CTGGGGGCTCGGGGGCGCTGGGATCTGACTCTGACTCTTCCTCGGACATGAGTGTGACTT 903
QY 158 ----- 158
DB 904 GACCGAGACCCCAATAGTGAACAGACTCGATGTGTGCTCGCTGTCACAGCAGGCT 963
QY 159 -----ProThrArgIleleuProAsnleuThryleuGlyCySglnIysValleuAn 176
DB 964 TCCCTTCCAGTGGAGATCTTGCGCTTCTCTACTTGCTGGCTGTGCCAAGATCCACCAAC 1023
QY 177 IysGlnleuIleGlnIleasnGlyIleGlyTyrrValleuAnAlaSerTyrrThrcySPro 196
DB 1024 TTGAGAGTGTGGAGGAATTCGGCATCAAGTACATCTTGAAGCTCAACCCCAATTGCGG 1083
QY 197 LysPro---AspPheIleProGlnSerHisPheIleuAlaGValProValAsnAspSerPhe 215
DB 1084 AATCTCTTGAAGACGACGAGAGTTTAATACAGCAAAATCCCATCTCGGATCACTGG 1143
QY 216 CysGlnIysIleleuProThrIleuAspIysSerValaAspPheIleGlyValaIlysAla 235
DB 1144 AGCCAAACCTGTGCCAGTCTTTCCTGAGGCCATTTCTTTCATATGATGAAGCCGGGCG 1203
QY 236 SerAsnGlyCySValleuValHisCysleuAlaGlyIleSerArgSerAlaThrIleAla 255
DB 1204 AAGAACTGTGTGTCTGTGATCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
QY 256 IleAlaTyrrIleMetIysArgMetAspSerIleuAsnGlnAlaTyrrAspPhyValIys 275
DB 1264 GTGGCTTACCTTAGCAAGACCTCATCTGTGATGAAGATGCTATGACATTTGTCAA 1323
QY 276 GlnIysArgProThrIleSerProAsnPhenAsnPhenleuGlyGlnleuLeuAspTyrrGlu 295
DB 1324 ATGAAATAATCCAACTATCCCTTCACTTCACTTCACTGCTGCTGCTGCTGCTGCTG 1383
QY 296 LysIysIleIysAsnGlnThrglyAlaSerGlyPro-----LysSerIysleuIys 312
DB 1384 AGGACGCTG-----GAGCTCGACGAGCCCATGTGACAAAGGTTTCACGACG 1431
QY 313 LeuIleuIleuGlnIysProAsnGlnIleProAlaValaIleSerGlnGlyGlnIys 332
DB 1432 CAGCTGTATTTTACACCCCTTCCAAACGATGTATACAGGTGACTCTGTGATCT 1491
QY 333 Ser-GlnThrProleuSerProProCyS 341
DB 1492 ACGTGAAGACCCCAACCCCTCTTGC 1519

RESULT 7
US-09-023-655-946
/ Sequence 946, Application US/09023655
/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS

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Qy 31 rArgProPheValGluTyr-AsnThrSerHisIleuGluAlaIleAsnCyse 51
Db 59 CCGGCATTTGTGGAATCCAAATACATCCACATTTTGGAGCCATTATATACCTGCT 118
Qy 51 etIlyLeuWetIyAgaIgleuGlnAspIyValIuIethrGluLeuIleGln 71
Db 119 CCAGCTTATGAGCCAGAGGTGCAACAGCAAGGTTATTAACAGAGCTCATCAGC 178
Qy 71 fAserAlaIyHisIyValAspIleAspCySerGlnIyValIValIYrAspGln 91
Db 179 ATTACGCGAATTAAGTTAGATTGATGACGACGAGGTTGATTACGATCAMA 238
Qy 91 eSerGlnAspValAlaSerLeuSerSerAspCySphLeuThrValIleuGluIyVal 111
Db 239 GCTCCCAAGATGTGCTCTCTCTCTTCCAGACGTTTCTCATCTGACTTCTGGTAAAC 298
Qy 111 euGluIySerPheAsnSerValHisIleuAla 122
Db 299 TGGAGAAAGCTTCAACTCTGTTCACTGCTTCA 333

RESULT 10
US-09-557-921-1
/ Sequence 1, Application US/09557921
/ Patent No. 6551810
/ GENERAL INFORMATION:
/ APPLICANT: Lucbe, Ralf M.
/ APPLICANT: Wei, Bo
/ TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
/ FILE REFERENCE: 200125.416
/ CURRENT APPLICATION NUMBER: US/09/557,921
/ CURRENT FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1830
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-557-921-1

Alignment Scores:
Pred. No.: 6,04e-38 Length: 1830
Score: 469.00 Matches: 107
Percent Similarity: 57.72% Conservative: 65
Best Local Similarity: 35.91% Mismatches: 96
Query Match: 13.72% Indels: 30
Gaps: 7
DB: 4

US-10-029-345A-109 (1-665) x US-09-557-921-1 (1-1830)
Qy 27 LeuLeuIleAspSerArgProPheValGluTyrAsnThrSerHisIleuGluAlaIle 46
Db 603 GTCATCATTTGATGACGAGCCCTTCATGAGTACACAAAGATGATCCAGAGGCTGTC 662
Qy 47 AsnIleAsnCyseSer---IySleuWetIyAgaIrgLeuGlnIAspIySValIleuIle 65
Db 663 CACATTAATGTCGCGATTAAGATCAACGCGCGAGACTCAGAGAGGCAAGATCACTGTC 722
Qy 66 ThrGluLeuIleGln---HisSerAlaIyHisIyValAspIleAspCySerGlnIyS 84
Db 723 CTAGACTTGATTTCTGTAGGAGGAGCAAGCACTCTTCAAGAGATCTTTTCCAAAGAA 782
Qy 85 ValIValIValIYrAspGlnSerGlnAspValAlaSerLeuSerSerAspCySphLeu 104
Db 783 ATTATATGTTTATGATGAGATACCAATGATACCAAGCCAGATGATGCTCCCAAGCCACTT 842
Qy 105 ThrValIleuGluIySleuGluIySerPheAsnSerValHisIleuAlaIyGlyIy 124
Db 843 CACATAGCTCTCGAGTCCCTGAAAGAGAAAGCAACCTCTGCTGTGTTGAAGGTGA 902
Qy 125 PheAlaGluPheSerArgCySphProGluIyLeuCyGluGluIyS----- 139
Db 903 CTTAGTAGTTTAAAGCAGAAACATGAAACCTCTGTGACAACTCCCTCCAGCTCCAAAG 962
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Qy 140 -----SerThrLeuValProThrCySileSer 148
Db 963 TGGCGGAGAGTGGGGGGCGGCGCATCCGGGCTGAGGCTGTGACTGTACAGCCCATC--- 1019
Qy 149 GlnProCyLeuPro---ValAlaAsnIleGlyProThrArgIleLeuProAsnLeuTyr 167
Db 1020 ---CCACACACCCCTGACATCGAGAACGCTGAGCTCACCCCTCTTGGCCCTTCGTTCC 1076
Qy 168 LeuGluIyCySerAlaArgAspValLeuAsnIySgluLeuIleGlnIleAsnGluIyIleGlyTyr 187
Db 1077 CTGGATATGAGAGGATGCTGACGACCTGACACCATGCGAGGCTGAACATGGACTAC 1136
Qy 188 ValIleuAsnAlaSer-----TyrThrCyProIySProAspPheIlePro 202
Db 1137 GTCATACAGTACACCATCATCTTCCCTCTACCATAGAGAAAGCCCTGTC----- 1190
Qy 203 GluSerHisPheLeuArgValProValAsnAspSerPheCySgluIySileuProTyr 222
Db 1191 -----ACTACAAAGCGCTGCGACGACCTGACAGCAGCAAGAGAACTGCGGCAGTAC 1244
Qy 223 LeuAspIySerValAspPheIleGluIySAlaIyAlaSerAsnIyCySValIleuVal 242
Db 1245 TTGAAAGAGCTTTGAGTTCAITGAGAGACTCACAGCTGCGAGAGGCTTCTCATC 1304
Qy 243 HisCySleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleWetIySArg 262
Db 1305 CACTGCGAGGCTGGGGTGTCCGCTCCGACCATGTGATCGCTTACTTGAAGAGCAC 1364
Qy 263 MetAspMetSerLeuAspGluAlaTyrArgPheValIySgluIySArgProThrIleSer 282
Db 1365 ACTCGGATGACCATGATGATGCTTAAATTGTCAAAGGCAAGCAACCAATTATCTCC 1424
Qy 283 ProAsnPheAspPheLeuGluIyGlnIleuAspTyrGluIySAlaIySAsn 300
Db 1425 CCAACCTTAACCTCATGGGCGAGTTGCTAGAGTTGAGAGAAAGCACTAAACAC 1478

RESULT 11
US-09-702-705-803
/ Sequence 803, Application US/09702705
/ Patent No. 6504010
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Lidun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ CURRENT FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 803
/ LENGTH: 1238
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-702-705-803

Alignment Scores:
Pred. No.: 1.34e-36 Length: 1238
Score: 453.00 Matches: 120
Percent Similarity: 50.52% Conservative: 73
Best Local Similarity: 31.41% Mismatches: 143
Query Match: 13.25% Indels: 46
DB: 4 Gaps: 13

US-10-029-345A-109 (1-665) x US-09-702-705-803 (1-1238)
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Qy      300 AaenGlnThrGlyValAserGlyProlySserLyLeuLybLeuLeuHsiLeuGlnLySPro 319
Db      1059 GCCACGCTCTGCTGCTCGAGAGCTGTAGC-----CC 1091
Qy      320 AaenGlnProValProAlaValSserGlnGlyGlnLySserGlnThrProLeuSserPro 339
Db      1092 TCGGACCCCTG-----GGGAGCGGGCGAAGACCCTCGCACCC 1133
Qy      340 ProCyAlaAspSerAlaThrSserGlnAlaAlaGlyGlnArgProValHsiProAlaSer 359
Db      1134 -----ACCTCGCAGTTCTGCTTCAAGCTTTCCGGTC--TCGCGGCG 1172
Qy      360 ValProSerValProSerValGlnProSserLeuLeuGlnAspSerProLeuValGlnAla 379
Db      1173 GTGCACTCGGCCCCCGACGAGCTGCTTACTTG-----CACAGCCCATCACCACCTCT 1226
Qy      380 LeuSer 381
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RESULT 14
US-09-671-325-803
; Sequence 803, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannon, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-803

Alignment Scores:
Pred. No.: 1.34e-36 Length: 1238
Score: 453.00 Matches: 120
Percent Similarity: 50.52% Conservatve: 73
Best Local Similarity: 31.41% Mismatches: 143
Query Match: 13.25% Indels: 46
Db: 4 Gaps: 13

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Qy      19 LeuGlnSerGlyThrGlnLyValLeuLeuHsiLeuAspSerArgProPheValGlnLySPro 38
Db      158 CTGCCGAGGCGC--GGCAAGTGCCTGCTGCTGCACTGCAGACCGTTCCTGGCGACAGC 224
Qy      39 ThrSerHsiLeuGlnAlaLeuLeuHsiLeuAsnCySserLyLeuMetLySArgLyLeu 58
Db      225 GCGGCTCATCTCTAGTTCGCTTCAACGCGCTGAACCACTGCTGCGGCGCGG--- 281
Qy      59 GlnGlnAspLyValLeuLeuThrGlnLeuLeu-----GlnHsiSerAlaLySArgLyS 76
Db      282 GCTAAGGCTCGGTGAGCTGAGAGATCTGCCCGCGAGAGAGAGATAGCGCCCGC 341
Qy      77 ValAspLeuAspCySserGlnLySValValValLyTrArgGlnSserGlnAspValAla 96
Db      1227 CCCAGC 1232
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Db      342 TTGCGCTCGGCTCTACTCGAGGCTCATGCTTCAAGACGAGCGAGCCCGCGCGAG 401
Qy      97 SerLeuSserSerAspCybPheLeuThrValLeuLeuGlyLybLeuGlnLySserPhe--- 115
Db      402 AACCTCCGAGAGACAGCAGCGTGTGGTGGGACAGGCGCTGCGCGAAGCGCGAG 461
Qy      116 ---AaenSerValHsiLeuLeuAlaGlyGlyPheAlaGlnPheSserArgCybPheProGly 134
Db      462 CGCAGCGACATGCTGCTGTCAAGCGGCTATAGAGAGTTTCTCCAGATACCAAGAA 521
Qy      135 LeuCySgGlnGlyLySserThrLeu-----ValProThrCybSser 148
Db      522 TTCTGTTTAAACCAAGCGCTCGCAGCCATCCACCCCGGTTCCCGCCAGCCACA 581
Qy      149 GlnPro-----CybLeuProValAla-----AsnLleGlyPro 159
Db      582 GAGCCCTTGAGACTGAGCTGCTCTGTGGAGACCCCATACAGACAGAGAGAGTCT 641
Qy      160 ThrArgLleLeuProAsnLeuTyLeuGlyCySglnArgAspValLeuAsnLySgLeu 179
Db      642 GTGAGATCTCTTCCCTTCTACTCGGCAAGTGCCTACCATGCTGCCCGAGAGACATG 701
Qy      180 lLeGlnGlnAaenGlyTlLeGlyTrValLeuAsnAlaSerTyTrCybProLybProAsp 199
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Qy      200 PheLleProGlnSerHsiPheLeuArgValProValAaenAspSerPheCySgLybLySle 219
Db      759 TTGGAAGCACTATCATGATCAAGTGCATCCAGTGAAGATACACAGCCGACATTC 818
Qy      220 LeuProTrpLeuAspLySserValAspPheLleGlyLybAlaLySAsnGlyCyS 239
Db      819 AGCTCGTGTTCATGAGAGCATAGATCATGATGCCGTGAAGAGACTGCCGTGGCGC 878
Qy      240 ValLeuValHsiCySLeuAlaGlyLleSserArgSeraLtrLleAlaLleAlaLyLle 259
Db      879 GTGCTGTGCACTGCGCAGCGGCGCATCTCGGCTGCGCACCATCTGCTGCTTACTG 938
Qy      260 MetLySAspMetAspMetSerLeuAspGlnAlaTyArgPheValLySgLybLySArgPro 279
Db      939 ATGATGAAGAAACGGGTGAGGCTGAGAGAGCTTCGAGTTCGTTAAGACGCGCGCAGC 998
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Db      999 ATCATCTCGCCCAACTTCAAGCTTCATGAGGCGAGCTGTGCAAGTTCGAGTCCAGGTGCTG 1058
Qy      300 AaenGlnThrGlyValAserGlyProlySserLybLeuLeuHsiLeuGlnLySPro 319
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Qy      360 ValProSerValProSerValGlnProSserLeuLeuGlnAspSerProLeuValGlnAla 379
Db      1173 GTGCACTCGGCCCCCGACGAGCTGCTTACTTG-----CACAGCCCATCACCACCTCT 1226
Qy      380 LeuSer 381
Db      1227 CCCAGC 1232

RESULT 15
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; Sequence 803, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
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GenCore version 5.1.6
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Run on: February 14, 2005, 10:56:55 ; Search time 887.813 Seconds

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Perfect score: 3418

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MITLEN=0
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and is derived by analysis of the total score distribution.

SUMMARIES

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34	1302	38.1	2453	13	US-10-005-858-1
35	1262	36.9	2476	17	US-10-220-120-28
36	1075.5	31.5	2039	17	US-10-072-012-265
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41	707	20.7	425	18	US-10-357-930-10717
42	703	20.6	467	18	US-10-357-930-11969
43	703	20.6	467	18	US-10-357-930-40868
44	703	20.6	467	18	US-10-357-930-41017
45	698	20.4	427	18	US-10-357-930-10878

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USBS THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR APPLICATION NUMBER: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:

Pred. No.:	0	Length:	1998
Score:	3406.00	Matches:	663
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	0
Query Match:	99.65%	Indels:	0
DB:	9	Gaps:	0

US-10-029-345A-109 (1-665) x US-09-816-494-3 (1-1998)

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QY      21 SerGlyThrGlnValLeuLeuIleAspSerArgProPheValGlyTyrAsnThrSer 40
DB      61 AGTGGAAACGGAAAAAGGTGCTTAATGATAGCCGCTATTGTGAAATACATACATCC 120

QY      41 HisIleLeuGlnAlaIleAsnIleAsnGlySerLeuMetLysArgArgLeuGln 60
DB      121 CACATTTTGGAAACCATTAATCACTGCTCCAGCTTAATGAAAGGAGTTGCAACG 180

QY      61 AspLysValLeuIleThrGlnLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
DB      181 GACAAAGTGTATATACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTGACATTGAT 240

QY      81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB      241 TGGAGTCAGAAAGGTGTAGTTACGATCAAAAGCTCCCAAGATGTCCCTCTCTCTTCA 300

QY      101 AspCysPheLeuThrValIleLeuGlnLysLeuGlnLysSerPheAsnSerValHisLeu 120
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QY      121 LeuAlaGlyGlyPheAlaGlnPheSerArgCysPheProGlyLeuCysGlnGlyLysSer 140
DB      361 CTTCGAGGTGGGTTTCTGAGTTCTCTCGTGTGTTCCCTGGCTCTGTGAAAGGAAATCC 420

QY      141 ThrLeuValProThrCysAlleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB      421 ACTCTAGTCCCTACCTGCAATTCCTGAGCTTGTCTTACCTGTGCCAACTTGGCCMAC 480

QY      161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGlnLeuIle 180
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QY      221 ProTyrLeuAspLysSerValAspPheIleGlnLysAlaLysAsnGlyCysVal 240
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QY      241 LeuValHisCysLeuAlaGlyTyrLeuArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB      721 CTAGTGCACCTGTTTGTGGGATCTCCCGCTCCGACACCATCGCTATCGCTACATCATG 780

QY      261 LysArgMetAspMetSerLeuAsnArgValAlaTyrArgPheValLysGlnLysArgProThr 280
DB      781 AAGAGAGTAGACATGCTTATAGTAGAGCTTACAGATTTTGTAAAGAAAAAGACCTTCT 840

QY      281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlyLysLysIleLysAsn 300
DB      841 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGAGCTATGAGAAAGATTAAAGAAC 900

QY      301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlnLysArgProAsn 320

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DB      901 CAGACTGAGCATCAGGCGCCAAAGCAACTCAAGCTGCTGACCTGGAGAAAGCCAAT 960
QY      321 GluProValProAlaValSerGlnGlyGlyGlnLysSerGlnThrProLeuSerProPro 340
DB      961 GAACCTGTCCTCGCTGCTCTCAAGAGGTGGACAGAAAGGAGACCCCTCAGTCCACACC 1020

QY      341 CysAlaAspSerAlaThrSerGlnAlaIleGlyGlnArgProValHisProAlaSerVal 360
DB      1021 TGTGCCACTTGTACTTACCTCAGAGGACGAGCAAAAGCCCTGTGATCTCCGCAAGCTTG 1080

QY      361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380
DB      1081 CCAGAGTGTCCAGAGGTGAGCGTGGCTGTATAGAGACAGCCCGCTGGTACAGCGGCTC 1140

QY      381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnLysLeuLysArgSerPhe 400
DB      1141 AGTGGGCTGCACCTCTCCGACAGAGGCTGGAAAGACAAATTAAGCTCAAGCGTTCCTTC 1200

QY      401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaIleSerLeuHisGlyPhe 420
DB      1201 TCTTGATATCAATCAAGTTTCATATTCAGCCAGCATGAGCAATCCCTTACATGGCTTC 1260

QY      421 SerSerSerGlnAspAlaLeuGlnTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
DB      1261 TCCTCATCAGAAAGATGCTTGGAAATCTACAAACCTTCACATGCTGGATGGAGCCAAC 1320

QY      441 LysLeuCysGlnPheSerProValGlnGlnLysSerGlnGlnThrProGlnThrSerPro 460
DB      1321 AAGCTATCCAGATTCCTCCCTGTTTCAGAACTATTCGGAGCAGACTCCCGAAACCGACTCT 1380

QY      461 AspLysGlnGlnAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
DB      1381 GATTAAGAGGAAGCCAGCATCCCAAGAGCTGACACCGCCAGGCTTCAGACAGCCAG 1440

QY      481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
DB      1441 AGCAAGCATGATGATTCGCTGAGAAACAGACAGAGTGACACCGCCAGAGGTCCCTTTTA 1500

QY      501 SerProLeuHisArgSerGlySerValGlnAspAsnTyrThrSerPheLeuPheGly 520
DB      1501 TCTTCATGCAATCGAAGGTGAGGCGTGGAGACAAATTAACAACACAGCTTCCTTTTTCGGC 1560

QY      521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuGlyTyrHis 540
DB      1561 CTTTCCACACGACGACGACACTTCAGAAAGTCTGCTGGCTGGGCTTTAAGGCTGGCAC 1620

QY      541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheAla 560
DB      1621 TCGATATCTTGGCCCCCAAGACTCTACCCCTTCCTGACACAGCAGCTGGTATTTGGCC 1680

QY      561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
DB      1681 ACAAGTCTCTCAACTTACTGCTGCTCAGCCATCTACGAGGACAGGCCAGTTACTCT 1740

QY      581 AlaTyrSerCysSerGlnLeuProThrCysGlyLysPgnValTyrSerValArgArgArg 600
DB      1741 GCTTACAGCTCAGCCAGCAGCTCCCACTTGGGAAACCAAGCTATCTGTGCGAGGCGG 1800

QY      601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGlnGlnLysSerProPheGln 620
DB      1801 CAGAAAGCCAAAGTACAGAGCTGACTCGCGGGAGAGCTGAGTGAAGAGAGGCCCTTGAA 1860

QY      621 LysGlnPheLysArgArgSerCysGlnMetGlnPheGlyGlnSerIleMetSerGlnAsn 640
DB      1861 AAGCAGTTTAAACCCAGAAAGCTGCCAATGTGAATTTGAGAGCAATCATGTGAGAAAC 1920

QY      641 ArgSerArgGlnGlnLysGlyLysValGlySerGlnSerSerPheSerGlySerMetGln 660
DB      1921 AGCTCAACGGAAGAGCTGGGAAAGTGGCAGTCAAGTCACTTTTGGGACGATGGA 1980

QY      661 IleIleGlnValSer 665
DB      1981 ATCATTTGAGGTCTCC 1995

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RESULT 2
US-10-377-072-27
/ Sequence 27, Application US/10377072
/ Publication No. US20040009501A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals Inc.
/ APPLICANT: Curtis, Rory A.J.
/ APPLICANT: Logan, Thomas Joseph
/ APPLICANT: Glucksmann, Maria A.
/ APPLICANT: Meyers, Rachel E.
/ APPLICANT: Williamson, Mark J.
/ APPLICANT: Rudolph-Owen, Laura A.
/ APPLICANT: Chun, Myoung
/ APPLICANT: Teal, Peng-Ying
/ TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
/ TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
/ FILE REFERENCE: MFI03-0180NMIM
/ CURRENT APPLICATION NUMBER: US/10/377, 072
/ PRIOR FILING DATE: 2003-02-27
/ PRIOR APPLICATION NUMBER: US 09/895, 860
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215, 370
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: US 09/723, 806
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/187, 455
/ PRIOR FILING DATE: 2000-03-07
/ PRIOR APPLICATION NUMBER: US 09/843, 297
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: US 60/199, 801
/ PRIOR FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: US 09/861, 801
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: US 60/205, 508
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 09/816, 494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 09/815, 419
/ PRIOR FILING DATE: 2001-03-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 1998
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.: 0 Length: 1998
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
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DB 1 ATGGCCCATGAGATGATTGGAATCAATTTGATGAGAGGTGGTGGCTGCTGGAA 60
QY 21 SerGlyThrgIuLyEalLeuLeuIleAspSerArgProPhaValGluTyrtLenrSer 40
DB 61 AATGGAAACGAAAGTGTCTGCTAATTTGATGAGCCGCAATTTGTGAAATACATTCATCC 120
QY 41 HsIleLeuGluAlaIleAsnIleAsnCySerLyLeuMeLyArgRgLeugIn 60
DB 120 TCTTGATATCAATCAATGTTTCAATTCAGCCACATGCGATCTTATCATGGCTTC 1260
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DB 121 CACATTTGGAGACCATTAATATCAATGCTCCAACTTATGAGGAAAGTTGCAACAG 180
QY 61 AepLyValIleuIleThGluLeuIleGlnHIsSerAlaLeuHIsLyValAspIleAsp 80
DB 181 GACAAAGTTAATTAACAGAGCTCAACGACTTCAGCAAAACATDAAGTTGACATTGAT 240
QY 81 CySerGlnLyValValValTyAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 241 TGCAGTCAGAAAGTTGTAGTTTACATCAAACTCCCAAGATGTTGCCCTCTCTCTTCA 300
QY 101 AapCyEphLeuThValLeuLeuGlyLyLeuGluLySerPheAsnSerValHIsLeu 120
DB 301 GACTTTTCTCAGTACTTCTGGGTAACTGAGAAAGCTTCAACTCTTTCACCTG 360
QY 121 LeuAlaGlyLyPheAlaGluPheSerArgPheProGlyLeuCyGlnGlyLySer 140
DB 361 CTTCGAGGGGTTGCTAGTTCTCTCTTTCCTGCGCTCTGTAAAGAAATATCC 420
QY 141 ThrLeuValProThCyEilEserGlnProCyLeuProValAlaAsnIleGlyProThr 160
DB 421 ACTCTAGTCCCTACCTGCACTTCTCAGCTTCTTACCTGTTGCCAACTGGGCCAAC 480
QY 161 ArgIleLeuProAsnLeuTyLeuGlyCyGlnArgAspValLeuAsnLyGluLeuIle 180
DB 481 CGAATTTCTCCAACTTATCTTGGGTCGACGAGATGCTCTCAACAAGAGCTGATG 540
QY 181 GlnGlnAsnGlyIleGlyTyrtValLeuAsnAlaSerTyrtThCyEProLyProAspPhe 200
DB 541 CAGCAGAAATGGATGTGTTAATGTTAAATGACCAATACTGTCCAAAGCTGACTTT 600
QY 201 IleProGlySerHIsPheLeuArgValProValAsnAspSerPheCyGlnLyLyLeu 220
DB 601 ATCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ProTrPLeuAspLySerValAspPheIleGluLyValAlaLyAsnAsnGlyCyVal 240
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QY 241 LeuValHIsCyLeuValAglyIleSerArgSerAlaThrIleAlaIleAlaTyrtIleMc 260
DB 721 CTAGTGCACTGTTTGTAGCTGATCTCCGCTCCGCAACATGCTATGCTCCATCACT 780
QY 261 LyAspMetAspMetSerLeuAspGluAlaTyrtArgPheValIleGluLyLyArgProThr 280
DB 781 AAGAGATGAGATGCTTTAGATGAAGCTTCAAGTTTGTAAAGAAAGAAAGACTTACT 840
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrtGlyLyLeuValIleLyAsn 300
DB 841 AATCTCCAAATTCATTTCTGCGCAACTCTGACTATGAGAAAGATTAAGAAC 900
QY 301 GlnThrgIyAlaSerGlyProLySerLyLeuLyLeuLeuHIsLeuGlyLyProAsn 320
DB 901 CAGACTGGGATCGAGGCAAAAGCAAACTCAAGCTGCTCAGCTGAGAAAGCCAAAT 960
QY 321 GluProValProAlaValSerGlnGlyGlyGlyLyLySerGlyThThProLeuSerProPro 340
DB 961 GAACCTGTCCCTGCTGTCTCAGAGGTGACAGAAAGGAGAGGCGCTCAGTCCACCC 1020
QY 341 CyValAspSerValThrSerGlnAlaAlaGlyGlnArgProValHIsProAlaSerVal 360
DB 1021 TGTGCGAATCTGATACCTCAAGGCAAGGCAAGGACCAAGGCGGTGATCCCGCAGCG 1080
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
DB 1081 CCCACGCGCCAGGAGGTGACGCTGCTGTAGAGGACAGCCCGCTGTACAGGCGCTC 1140
QY 381 SerGlyLeuHIsLeuSerValAspArgLeuGluAspSerAsnLyLeuLyArgSerPhe 400
DB 1141 AGTGAGCTGCACTTCTCGACAGAGCTGAGAGGACAGATTAAGCTCAAGCTTCTTC 1200
QY 401 SerLeuAspIleLySerValSerTyrtSerAlaSerMetAlaAlaSerLeuHIsGlyPhe 420
DB 1201 TCTTGATATCAATCAATGTTTCAATTCAGCCACATGCGATCTTATCATGGCTTC 1260
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QY	421	SeSeSeSerGluSerAlaLeuGluTyrTyrTyrSerSerThrThrLeuAspGlyThrAsn	440
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QY	441	LySLeuCYGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro	460
Db	1321	AAGCTATGCGACAGTCTCCCTGTTACAGAACTATCGAGAGACACTCCGAAACCAAGTCT	1380
QY	461	AspLyGluGlnIleSerIleProLySLeuGlnThrAlaArgProSerAspSerGln	480
Db	1381	GATTAAGAGAAACCCAGCATCCCCCAAGACCTGCAGCCCGGACCTTACAGACGCCAG	1440
QY	481	SerLySArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu	500
Db	1441	AGCAAGCGATGTCATTGCTCGACAAACAGACAGAGTGGACCCCGCAGAGGTCCCTTTA	1500
QY	501	SerProLeuHisArgSerGlySerValGlnAspAsnThrHisThrSerPheLeuPheGly	520
Db	1501	TCTCCATGTCATGAAGTGGAGACGTGGAGAGACATTAACAACACAGACTTCTTTTGGC	1560
QY	521	LeuSerThrSerGlnGlnHisLeuThrLySSerAlaGlyLeuGlyLeuLySArgTyrHis	540
Db	1561	CTTTCACACGACGACAGACACTCAGAGAGTCTGTGGCTTGGGCTTAAGGGCTGGCAC	1620
QY	541	SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheAla	560
Db	1621	TGGAAATCTGGGCCCCCAGACCTTACCCCTTCCCTGACAGACAGCTGTATTTTGGC	1680
QY	561	ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer	580
Db	1681	ACAGAGTCTTCACACTTACTACTGCTGCTGACCATCTACAGGAGGAGTGCAGTTACTCT	1740
QY	581	AlaTyrSerCySerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg	600
Db	1741	GCTTACAGCTGACGCGACGCTGCCACTTGGGAGAGCAACATCTATCTTGGCCAGCGCG	1800
QY	601	GlnLyProSerAspArgAlaAspSerArgSerTyrHisGluGluSerProPheGln	620
Db	1801	CAGAAAGCCAAAGTACAGACCTGACTGCGCGGAGAGCTGGCATTAAGAGAGCCCTTTGAA	1860
QY	621	LySglnPheLyArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn	640
Db	1861	AAGCAGTTTAAACGCGAAAGCTGCCAAATGGATTGGAGAGGCAATCATGTCAAGAAAC	1920
QY	641	ArgSerArgGluGlnLeuGlyLySValGlySerGlnSerSerPheSerGlySerMetGln	660
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QY	661	IleIleGlnValSer	665
Db	1981	ATCATTTGAGGTCTCC	1995
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US-10-377-072-27			
Sequence 27, Application US/10377072			
Publication No. US20040157221A9			
GENERAL INFORMATION:			
APPLICANT: Millennium Pharmaceuticals Inc.			
APPLICANT: Curtis, Rory A.J.			
APPLICANT: Logan, Thomas Joseph			
APPLICANT: Glucksmann, Maria A.			
APPLICANT: Meyers, Rachel E.			
APPLICANT: Williamson, Mark J.			
APPLICANT: Rudolph-Owen, Laura A.			
APPLICANT: Chun, Miyoung			
APPLICANT: Tsai, Fong-Ying			
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,			
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES			
FILE REFERENCE: MP103-01802M1A			
CURRENT APPLICATION NUMBER: US/10/377, 072			
CURRENT FILING DATE: 2003-02-27			

	/	PRIOR APPLICATION NUMBER:	US 09/895,860	
	/	PRIOR FILING DATE:	2001-06-29	
	/	PRIOR APPLICATION NUMBER:	US 60/215,370	
	/	PRIOR FILING DATE:	2000-06-29	
	/	PRIOR APPLICATION NUMBER:	US 09/723,806	
	/	PRIOR FILING DATE:	2000-11-28	
	/	PRIOR APPLICATION NUMBER:	US 60/187,455	
	/	PRIOR FILING DATE:	2000-03-07	
	/	PRIOR APPLICATION NUMBER:	US 09/843,297	
	/	PRIOR FILING DATE:	2001-04-25	
	/	PRIOR APPLICATION NUMBER:	US 60/199,801	
	/	PRIOR FILING DATE:	2000-04-26	
	/	PRIOR APPLICATION NUMBER:	US 09/861,801	
	/	PRIOR FILING DATE:	2001-05-21	
	/	PRIOR APPLICATION NUMBER:	US 60/205,508	
	/	PRIOR FILING DATE:	2000-05-19	
	/	PRIOR APPLICATION NUMBER:	US 09/816,494	
	/	PRIOR FILING DATE:	2001-03-23	
	/	PRIOR APPLICATION NUMBER:	US 09/815,419	
	/	PRIOR FILING DATE:	2001-03-22	
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	/	ORGANISM:	Homo Sapiens	
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	/	NAME/KEY:	CDS	
	/	LOCATION:	(1)...(1998)	
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Oy		21 SerGIYThrGUlyeValleulenilleaspSerarGPoPheValglUrYAantHser 40		
Dd		61 AGTCGAACGAAAAATGCTGCTTAITTAGATGCCGCATTTTGGAATACAATACTCC 120		
Oy		41 HsiileleGlUnAlleasnilleanCysserilyseWettyBARgatgleUGln 60		
Dd		121 CAcatttTtgaaGccAtTaATCaAcTgcTCCAAGctTtaGaagCcagaGGttGcaacAg 180		
Oy		61 AspyLyVaIlleulleThngIUlenulllegIHtseserialysylsyVsVAapllEasp 80		
Dd		181 GAChAAgtGTATTAATTAACAGactCATccaGaatTCAGCAAACATAAGgtTGCAATGAT 240		
Oy		81 CySeSergnlHyevaIValValTYzaApGLnsereSergInsAPVALIsertLeusSer 100		
Dd		241 TGAAGTCAGAAggGTgaTtagTTAACATCAaaaGctCCaAGATgTtgCtCtcTCTTCA 300		
Oy		101 AspCYspHeleuthTyvalleuleugLIylysleugLUlysseRpleamSERValHlsleu 120		
Dd		301 GAcGTtTtTCTCACGTGActTCTGTGGTAACTGAGAAAGActTCACACTGTTCACTG 360		
Oy		121 LeuAlaglIGlYPhalaGlUpbeseryRGysphEPogILyeuCYSglULyLYSSer 140		
Dd		361 CTtGCAGGtGGgtTtGCTGAGATtCTCTGtTgTtTCCtTGcCtCTGTGAAGAAATTC 420		
Oy		141 ThrLeuValProthrCYslEseregLnProcysLeufRoVALlaaanillegyProthr 160		
Dd		421 ACCTGTAGTCCCACCgcatTTTCAGcctTtTACtGTGCAACATTTgGCCCCAAC 480		


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QY 161 ArgIleLeuProAsnLeuTyrLeuGIYCyGSIARgAPValLeuAsnLysGluLeu 180
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QY 181 GInGInAsnGlyIleGIYTyRValLeuAsnLaseTyrThrCyAProLysProAspPhe 200
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QY 201 ILeProGluSerHisPheLeuArgValProValAsnAspSerPheCyGluLysIleu 220
DB 601 ATCCCCGAGCTCATTTCTCGCTGCTGCTGCAATGACAGCCTTTGTGAGAAATTTTG 660
QY 221 ProTPrLeuAspLysSerValAspPheIleGIYValAlaLysLaseAsnGlyCySVal 240
DB 661 CCGTGCTGCACAAATCAGTAAATTCATTGAGAAAGCAAAAGCCTCCATGGATGTGT 720
QY 241 LeuValHisCyLeuValagIYIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 721 CTAGTGCATGTTTATGCTGGATCTCCGCTCCGCCACATGCTATGCTCATCATG 780
QY 261 LysArgMetAspMetSerLeuAspGluAlaIYArgPheValLysGluLysArgProThr 280
DB 781 AAGAGGATGACATGCTTATGATGAGCTTACAGATTGTGAGAAAGAAAGAAAGCCTACT 840
QY 281 ILeSerProAsnPheAsnPheLeuGIYGIYLeuLeuAspTyrGluLysValIleLysAsn 300
DB 841 ATATCTCCAAACTTCATATTTCTGGGCCAACTCTCGACTATGAGAAAGATTAAGAAC 900
QY 301 GlnThrGlyAlaSerGIYProLysSerLysLeuLysLeuLysIleuGIYLysProAsn 320
DB 901 CAGACTGGAGCATCAGGGGCCAAAGCAATCAAGCTCTGCACTGAGAGAACCAAT 960
QY 321 GluProValProAlaValSerGIYGIYGIYLysSerGIYThrProLysSerProPro 340
DB 961 GAACCTGTCTCCGTCTCTCAGAGGGGTGAGCAAGAAAGCAAGACGCCCTCAGTCCACCC 1020
QY 341 CySAIAspSerAlaThrSerGIYAlaIagIYGIYArgProValHisProLaseVal 360
DB 1021 TGTGGCAATCTGTACTTCAAGAGGAGCAAGCAAAAGCCCGTGTATCCCCCGACGG 1080
QY 361 ProSerValProSerValGlnProSerLeuLeuGIYAspSerProLeuValGlnAlaLeu 380
DB 1081 CCCACGCTGCCAGCGCTGACGCCGTGCTTGAAGAGACGCCCGCTGTTACAGCGCTTC 1140
QY 381 SerGIYLeuHisLeuSerAlaAspArgLeuGIYAspSerAsnLysLeuLysArgSerPhe 400
DB 1141 AGTGGGCTGCACCTGTCCGCAAGCAGGCTGAAAGACAGCAATTAAGCTCAAGGCTTCCTTC 1200
QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaLaseLeuHisGlyPhe 420
DB 1201 TCTCTGGAATATCAATCACTTTCATATTCAGCCAGATGGCAGCACTTTCATAGCTTTC 1260
QY 421 SerSerSerGIYAspAlaLeuGIYTyRValLysProSerThrThrLeuAspGlyThrAsn 440
DB 1261 TCCTCATCTGAAAGATGCTTGGAAATCTCAAACTTCCATCACTCTGATGGAGCAAC 1320
QY 441 LysLeuCyGlnPheSerProValGlnLysLeuSerGIYGIYThrProGluThrSerPro 460
DB 1321 AAGCTATGCGCAATTCCTCCCTGTTCAAGAACTATGAGACAGACTCCGAAACCACTCT 1380
QY 461 AspLysGluGluAlaSerIleProLysValLeuGlnThrAlaArgProSerAspSerGln 480
DB 1381 GATTAAGAGAGAACCAAGCATCCCAAGAGCTGCAACCCGCAAGGCTTTCAGACGCCAG 1440
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGIYThrAlaGlnArgSerLeuLeu 500
DB 1441 AACAAGCCGATTCATTCGCTCAGAACCAACAGAGGAGACCCGCCAGAGCTCCCTTTTA 1500
QY 501 SerProLeuHisArgSerGIYSerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
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QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
DB 1621 TCGGATATCTGGCCCCCAGACCTTACCCCTTCCGTACACGACAGCTGTATTTTGGC 1680
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerLaseTyrSer 580
DB 1681 ACAGAGTCTTCACACTTCTACTCTGCTCAGCATCTAGGAGGAGTCCAGTTACTCT 1740
QY 581 AlaTyrSerCySerGIYLeuProThrCySGIYAspGlnValTyrSerValArgArgArg 600
DB 1741 GCTTACGCTGCAGCCAGCTGCTCCACTTGGAGAGACCAAGTCTATTTCTGGCAGCG 1800
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluLysSerProPheGlu 620
DB 1801 CAGAGCCAAAGTACAGAGCTGACTCGCGCGAGCTGCAAGAGAGAGAGCCCTTTGAA 1860
QY 621 LysGlnPheLysArgArgSerGIYMetGluPheGlyLysSerIleMetSerGluAsn 640
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QY 641 ArgSerArgGluGluLeuGIYLysValGlySerGlnSerSerPheSerGIYSerMetGlu 660
DB 1921 AGCTACGGAGAGAGCTGGGGAAAGTGGGCACTGACTTTCGCGGACGATGAA 1980
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RESULT 4

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US-10-168-506-2
; Sequence 2, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:

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; APPLICANT: PLOMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: KANAMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10168, 506
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-168-506-2

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Alignment Scores:

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Pred. No.: 0 Length: 2732
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 17 Gaps: 0

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US-10-029-345A-109 (1-665) x US-10-168-506-2 (1-2732)

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QY 1 MetAlaHisGluMetIleGIYThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
DB 538 ATGGCCCATGTGATATTGGAATCTCAAAATTGTACTGAGAGGTTGTGTGCTGTGAA 597
QY 21 SerGIYThrGluValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:

Pred. No.:	0	Length:	3059
Score:	3406.00	Matches:	663
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.65%	Indels:	0
DB:	17	Gaps:	0

US-10-029-345a-109 (1-665) x US-10-257-026-1 (1-3059)

QY 1 MetAlaHLeuMeTLeuGlyThrgInuLeuValThrgInuArgLeuValAlaLeuLeuGlu 20
DB 127 ATGGCCCATGATGATGTAAGAACTCAAAATTGTTACTGAGAGGTGGTGGCTCTGCTGAA 186
QY 21 SerGlyThrgInuLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 187 AGTGAACGGAAGAAAGTGTCTGTAATGATGACCGGCAATTGTGGAATACAAATACATCC 246
QY 41 HisLeuLeuGluAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 247 CACATTTTGGAGCCCTTAATATCAATCTCTCAAGCTTAATAGAGGAGTTGCAACAG 306
QY 61 AspLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 307 GACAAAGTGTAAATACAGAGCTCATCCAGCAATTCAGCAAAATTAAGGTGACATGTAT 366
QY 81 CysSerGlnuLeuValValValValValValValValValValValValValValVal 100
DB 367 TGCAGTCAGAAAGTGTGTATTCAGATCAAGCTCCAGAAATGTGGCTCTCTCTCTCA 426
QY 101 AspCysPheLeuThrValLeuLeuLeuGlyLeuGluLeuSerPheAsnSerValHisLeu 120
DB 427 GACGTGTTTCTACGTATCTTCTGGGTAACCTGGAGAAAGCTTCAACTCTGTTCACTG 486
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlySer 140
DB 487 CTTCAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 546
QY 141 ThrLeuValProThrCysAlaSerGlnProCysLeuProValAlaAsnLeuGlyProThr 160
DB 547 ACTCTAGTCCCTACCTGCACTTCTCAGCTTCTTACCTGTGGCCAACTTGGGCCAAC 606
QY 161 ArgLeuLeuProAsnLeuLeuLeuGlyCysGlnArgAspValLeuAsnLeuGluLeu 180
DB 607 GCAATTTCTCCAACTCTTATCTTGGCTGCCAGCGAGATGCTCTCAACAGAGGCTGATG 666
QY 181 GlnGlnAsnGlyLeuGlyValValLeuAsnAlaSerValThrCysPheProAspPhe 200
DB 667 CAGCAGAAATGGGATGGTATGATGTTAAATGCGAGAAATACCTGTCAAAGGCTGACTT 726
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluValLeu 220
DB 727 ATCCCGAGTCTCATCTTCTGCTGGTGGCTGGAATGACAGCTTTGTGAGAAATTTTG 786
QY 221 ProTrpLeuAspLeuSerValAspPheLeuValValValValValValValValVal 240
DB 787 CCGTGGTGGAGCAATACATGATATTCATGAGAAAGCAAAAGCTTCCCAATGATGTGT 846
QY 241 LeuValHisCysLeuAlaGlyLeuSerArgSerAlaThrIleAlaIleAlaIleAla 260
DB 847 CTAAGTGCATGTTTGTAGCTGGATCTCCGCTCCGACACATGCTATGCTCAATCAATCA 906
QY 261 LysAlaGluMetAspMetSerLeuAspGluAlaValValValValValValValValVal 280
DB 907 AAGAGATGACATGCTTGTAGATGAGCTTACAGATTTGTGAAAGAAAGAAAGAAAGCT 966
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspValGluValValValValVal 300

DB 967 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTGAGCTATGAGAGAAATTAAGAAC 1026
QY 301 GlnThrgValAlaSerGlyProLeuSerLeuValLeuLeuHisLeuGluValProAsn 320
DB 1027 CAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTGCTGCTGCTGAGAGCCAAAT 1086
QY 321 GluProValProAlaValSerGluGluGlyGlnLeuSerGluThrProLeuSerPro 340
DB 1087 GAACTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
DB 1147 TGTGCGACTGCTACCTCAAGGAGAGAGCAAAAGCCGCTGATCCCGCAGCGCTG 1206
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
DB 1207 CCCAGCGTCCAGAGGTGAGCGCTGCTGTTAGAGACAGCCCGCTGCTGCTGCTGCTGCT 1266
QY 381 SerGlyLeuHisLeuSerValAspArgLeuGluAspSerAsnLeuValArgSerPhe 400
DB 1267 AGTGGGCTGACCTGTCTGAGACAGGCTGGAAGACAGCAATGACTCAAGGCTCTTC 1326
QY 401 SerLeuAspIleLeuSerValSerValSerValSerValSerValSerValSerVal 420
DB 1327 TCTCTGATATCAATCACTGTTCAATTCAGCCAGATGAGCACTTACATGCTTC 1386
QY 421 SerSerSerGluAspAlaLeuGluValValValValValValValValValValVal 440
DB 1387 TCTCATCAAGAAAGTGTGGATGTGAATACAACTTCCATCACTCTGATGGAGCAAC 1446
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
DB 1447 AAGCTATGCAATCTTCCCTGTTGAGAACTATGAGACAACTCCGAAACCACTCT 1506
QY 461 AspLeuGluGluAlaSerIleProValLeuGlnThrAlaArgProSerAspSerGln 480
DB 1507 GATTAAG 1566
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 1567 AGCAAGCAATTCATCTGGTGCAGAACCAAGAGCAATGGGACCGCCAGAGGTCCCTTTA 1626
QY 501 SerProLeuHisArgSerGlySerValGluAspArgValHisThrSerPheLeuPheGly 520
DB 1627 TCTTCACGTCATCGAAGTGGAGCGTGGAGCAATTAACCAACAGCTTCTTTTGGCC 1686
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTrpHis 540
DB 1687 CTTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1746
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpValPheAla 560
DB 1747 TCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGATTTTGGC 1806
QY 561 ThrGluSerSerHisPheValSerAlaSerAlaIleValGlyGlySerAlaSerValSer 580
DB 1807 ACAAGTCTCACTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866
QY 581 AlaTrpSerCysSerGlnLeuProThrCysGlyAspGlnValTrpSerValArgArg 600
DB 1867 GCTTACAGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1926
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPheGlu 620
DB 1927 CAGAGCCCAAGTGAAGAGCTGATCGCGCGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 1986
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluVal 640
DB 1987 AAGGATTTAAACGAGAGAGCTGCAAAATGGAATTTGAGAGAGATCATGTCAGAGAAC 2046
QY 641 ArgSerArgGluGluLeuGlyValValGlySerGlnSerSerPheSerGlySerMetGlu 660

Db 2047 AGGTCAAGGAGAGAGTGGGAGAAAGTGGAGCTAGTCTAGTCTTTGGGACAGATGAA 2106
Qy 661 |||||ValSer 665
Db 2107 ATCATTTAGGCTTC 2121

RESULT 6
US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucbe, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Alignment Scores:
Pred. No.: 0 Length: 3496
Score: 3406.00 Matches: 665
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
Gaps: 0

US-10-029-345A-109 (1-665) x US-09-964-277-1 (1-3496)

Qy 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 562 ATGGCCCAATGAGATGATGGAATCTCAAAATGTGTAATGAGAGGTGTGCTCTGCTGGAA 621

Qy 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 622 AGTGAACAGGAAAGAGTCTCTCTTAATTTAGTGGCCCAATTTGGAAATACATTCATCC 681

Qy 41 HisIleLeuGluAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 60
Db 682 CACATTTTGGAGCCATTAATATCAATCTCTCAAGCTTATGAGGAAAGTTGCAACAG 741

Qy 61 AspValValLeuIleThrGluLeuIleGlnIleSerAlaIleHisIleValAspIleAsp 80
Db 742 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTTGAT 801

Qy 81 CysSerGlnIleValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 802 TCCAGTCAGAAAGTGTAGTTTACATTCATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 861

Qy 101 AspCysPheLeuThrValLeuLeuGlyIleLeuGluIleValSerPheAsnSerValHisLeu 120
Db 862 GACTTTTCTCAGCTACTCTCTGGGTAAACTGAGAAAGAGCTTCAACTCTGTTCACTG 921

Qy 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyIleSer 140
Db 922 CTTGAGAGGTGGTGTGCTGAGTTCTCTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 981

Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 982 ACTCAAGTCCCTCACTGATTTCTCAAGCTTCTTACCTGTTGCCAATTTGGGCAAC 1041

Qy 161 ArgIleLeuProAsnLeuIleValGlyCysGlnArgAspValLeuAsnIleGlyLeuIle 180
Db 1042 CGAATTTCTTCCCAATCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101

Qy 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProIleProAspPhe 200

Db 1102 CAGCAGAAATGGGATTTGTTATGTGTTAATGCCAGCAATACCTGTCCAAAGCTGACTTT 1161
Qy 201 |||||ProGluSerHisPheLeuArgValProValAlaAspSerPheCysGluIleLeu 220
Db 1162 ATCCCGAGTCTCATTTCTCTGCTGTGCTGTGAAATGACAGCTTTTGTAGAGAAATTTTGG 1221

Qy 221 ProTrpLeuAspIleValAspPheIleGluIleValAlaIleValAlaIleValAlaIleVal 240
Db 1222 CCGTGTGTGACAAATCATGATTTCTATGAAAGCAAAAGCTTCCAAATGATGTGTT 1281

Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1282 CTAGTGCACTGTTTGTGATGATCTCCGCTCCGCAACATGCTGATGCTTACATCATG 1341

Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluIleArgProThr 280
Db 1342 AAGAGAAATGCAATGCTTTTGAATGAACTTAAGATTTGTGAAGAAAGAAAGCTTACT 1401

Qy 281 ILeSerProAsnPheAsnPheLeuGlyIleLeuLeuAspTyrGluIleValIleLysAsn 300
Db 1402 ATATCTCCAACTTCAATTTCTGGGCCCACTCTCGACATGAGAGAAATTTAGAAC 1461

Qy 301 GlnThrGlyAlaSerGlyProIleSerIleValLeuIleLeuHisIleLeuGluIleProAsn 320
Db 1462 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTGAGAGAAAGCAAT 1521

Qy 321 GluProValProAlaValSerGluGlyIleGlnIleSerGluIleProLeuSerProPro 340
Db 1522 GAACTGTCCCTGCTGTCTCAGAGGTGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1581

Qy 341 CysAlaAspSerAlaThrSerGluAlaAlaIleGlyGlnArgProValHisProAlaSerVal 360
Db 1582 TGTGCCGACTGTGCTACTCTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1641

Qy 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
Db 1642 CCCAGCGGCCAGCGTGCACCGCTCGTGTAAAGACACCGCTGTGATCAGAGCGCTC 1701

Qy 381 SerGlyLeuHisIleAspSerAlaAspArgLeuGluAspSerAsnIleValIleValIleVal 400
Db 1702 AGTGGCTGCACTGTCTCCGAG 1761

Qy 401 SerLeuAspIleIleValSerValSerTyrSerAlaSerMetAlaIleSerLeuHisIleGlyPhe 420
Db 1762 TCTCTGATATCAATCATGATTTCTATATTCAGCCAGCATGAGCATCTTATCATGAGCTTC 1821

Qy 421 SerSerSerGluAspAlaLeuGluTyrTyrIleProSerThrThrLeuAspGlyThrAsn 440
Db 1822 TCTCATCAAGAAAGTGTGGAATTAACAACCTTCCACTGATGAGATGGAGCAAC 1881

Qy 441 LysLeuCysGlnPheSerProValGlnIleLeuSerGluIleThrProGluIleThrSerPro 460
Db 1882 AAGCTATGCCAGTTCTCTCCCTGTTCAAGAACTATGAGAGAGACTCCCGAAACAGATCT 1941

Qy 461 AspIleGluGluAlaSerIleProIleValLeuGluIleThrAlaArgProSerAspSerGln 480
Db 1942 GATTAAGAGAGAAAGCAGACATCCCAAGAGCTGACAGCCGAGGCTTCAAGACAGCAG 2001

Qy 481 SerIleArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 2002 AGCAAGGATTTGATGTTGTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2061

Qy 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2062 TCTCATGCAATGCAATGGAGGTGAGAGCAATTTACACACAGACTTCTTTTGGCC 2121

Qy 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuIleGlyTyrPheHis 540
Db 2122 CTTTCCACAGCGAGCAGACATCAAGAAATGCTGCTGCTGCTGCTTAAAGGCTGGCAG 2181

Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerIleThrSerSerTyrPheAla 560
Db 2182 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGAGAGCTGTATTTTGGCC 2241

QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
DB 2242 ACAGAGTCTCTACACACTTCTACTCTGCTCTAGACCATTTACGAGAGCGAGTCCACTTCTCT 2301
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
DB 2302 GCTACAGCTGACGAGCTGAGCTGCCACTTCTGAGAGACCAAGTCTATTCTGCTGCGCAGCGG 2361
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTTrHisGlnGluLysProPheGln 620
DB 2362 CAGAAGCCCAAGTACGACGAGCTGCTGCGCGAGAGCTGCGATCAAGAGAGCCCTTTGAA 2421
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlnGluSerIleMetSerGluAsn 640
DB 2422 AAGCATTTAAACGACGAAAGCTGCCAAATGGAAATTTGGAGAGCATCTGTCAGAGAAC 2481
QY 641 ArgSerArgGlnGluLeuGlnLysValGlySerGlnSerSerPheSerGlySerMetGln 660
DB 2482 AGGTACCGGAAAGAGCTGGGAAAGTGGGCAATCACTTACGTTTTCGGGCAAGCATGAA 2541
QY 661 IleIleGlnValSer 665
DB 2542 ATCATTTGAGTCTCTCC 2556
RESULT 7
US-10-370-715B-261
Sequence 261, Application US/10370715B
GENERAL INFORMATION:
PatIn Docket Preview
APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY
APPLICANT: BRISDELL, HUNTE
APPLICANT: JACKMAN, JANET
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: MU THOMAS D.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370, 715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 261
LENGTH: 3521
TYPE: DNA
ORGANISM: Homo sapien
US-10-370-715B-261
Alignment Scores:
Pred. No.: 0 Length: 3521
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 18 Gaps: 0
US-10-029-345A-109 (1-665) x US-10-370-715B-261 (1-3521)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValIleThrGlnArgLeuValAlaLeuLeuGln 20
DB 564 ATGGCCCATGAGATGATGTAAGTCAATGTTACTGAGAGGATGGTGGCTGCTGCGAA 623
QY 21 SerGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGlnTyrAsnThrSer 40
DB 624 ATGGAGCGGAAAGAGTGTGCTTAATTGATGCGGCAATTTGTGAAATACAAATCATCC 683
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGlnGln 60
DB 684 CACATTTTGAAGCCATTATATCACTGCTCCAGCTTATGAGGAGGAGGTTGCAACAG 743

QY 61 AspLysValIleuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
DB 744 GACAAAGTTTAAATTAACAGGCTCAATCCAGCATTCAGCGCAACATTAAGTTGACATTGAT 803
QY 81 CysSerGlnLysValValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 804 TCCAGTCAGAAAGTTGTATGATTCAGATCAAACTCCCAAGATGTCCTCTCTCTTCA 863
QY 101 AspCysPheLeuThrValLeuLeuGlnLysLysGlnLysSerPheAsnSerValHisLeu 120
DB 864 GACTGTTTCTACCTGACTTCTGGGTAACTGGAGAAAGCTTCAACTCTGTCACCTG 923
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGlnGlyLysSer 140
DB 924 CTTCGACGTGGGTTTCTGAGTTCTCTGCTGTTTCCCTGCTCTGTAAGGAAATCC 983
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 984 ACTCTAGTCCCTACCTGCACTTCTCAGCTTCTTACCTTACCTGTCCAACATTTGGCCAAAC 1043
QY 161 ArgIleLeuProAsnLeuTyrLeuGlnCysGlnArgAspValLeuAsnLysGlnLeuIle 180
DB 1044 CGAATTTCTCCAAATCTTATCTTGGCTGCCAGCAAGTCTCTCAACAGAGCTGATG 1103
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
DB 1104 CAGCAAAATGGATTTGTTATGTTTAAATGCAAGAAATCCTGTCCAAGCTGACTT 1163
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlnLysIleLeu 220
DB 1164 ATCCCGAGTCTCATTTCTGCTGGCTGCTGCAATGACAGCTTTGTGAGAAATTTTG 1223
QY 221 ProTyrLeuAspLysSerValAspPheIleGlnLysValAlaLysSerAsnGlyCysVal 240
DB 1224 CCGTGGTGGCAAAATCAGTAAATTCATTGAGAAAGCAAAAGCTCCCAATGATGTGT 1283
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 1284 CTAGTGCACTGTTTACCTGGATCTCCGCTCCGACCATGCTTACCTCAATCATCAG 1343
QY 261 LysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValIleGlnLysArgProThr 280
DB 1344 AAGAGATGACATGCTTTAGATGAAAGCTTGTGAAAGAAAGAAAGAAAGAAAGAAAGCTTACT 1403
QY 281 IleSerProAsnPheAsnPheLeuGlnIleLeuLeuAspTyrGlnLysIleLysAsn 300
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QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlnLysProAsn 320
DB 1464 CAGACTGAGCATCAGGGCCCAAGAGCAACTCAAGCTGCTGACCTGAGAGAACCAAT 1523
QY 321 GluProValProAlaValSerGlnGlyGlnLysSerGlnThrProLeuSerProPro 340
DB 1524 GAACCTGTCCTGCTGCTGCTGCAAGAGGTGAGCAAGAAAGGAGAGCGCCCTCAGTCCACCC 1583
QY 341 CysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSerVal 360
DB 1584 TGTGCCACTGCTGCACTCAGAGGACAGGACAAAGGCCGTGATCCGCCAGCGG 1643
QY 361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380
DB 1644 CCCAGCTGACCCAGGCTGCAAGCTGCTGCTTAAAGAGACAGCCGCTGTACAGGCGCTC 1703
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnLysLysSerPhe 400
DB 1704 AGTGGCTGCACTGTCGCAAGACAGGCTGGAACAGCAAGAAATTAAGTCAAGGCTTCC 1763
QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
DB 1764 TCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCAATGGCAGCATCTTCAATGGCTTC 1823
QY 421 SerSerSerGluAspAlaLeuGlnTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440

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Db      1824  TCCTCATCAGAAAGCTTTGGAACTTACAAACCTTCCACTCTGAGTGGACCAAC 1883
Qy      441  LysleuCysGlnPheSerProValGlnGluLeuSerGlnGlnThrProGluThrSerPro 460
Db      1884  AACCTATGCGCAGTCTCCCTGTTCAAGAACTATCGAGACAGACTCCGAAACAGTCTT 1943
Qy      461  AspLysGlnGluAlaSerIleProLysLeuGlnThrAlaArgProSerAspSerGln 480
Db      1944  GATTAAGAGGAGCAGACATCCCAAGAACCTGACGCCCGGCTTTCAGACAGCCAG 2003
Qy      481  SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db      2004  AGCAGAGCATTTGCAATTCGTGACAGACAGCAGCAGTGGACCCGCCAGAGTCCCTTTA 2063
Qy      501  SerProLeuHisArgSerGlySerValGluAspAsnTrpHisThrSerPheLeuPheGly 520
Db      2064  TCTCCACTGCATGAAAGTGGAGCGTGGAGACAAATTACACACAGCTTCTTTTCGGC 2123
Qy      521  LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTrpHis 540
Db      2124  CTTTCCACCGACGACGACACTCAAGAGTCTGCTGGCTTAAAGGCTGGAC 2183
Qy      541  SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpTrpPheAla 560
Db      2184  TCGGATATCTTGGCCCCCGACAGCTCTACCCCTTCCCTGACGACAGCTGTATTGTC 2243
Qy      561  ThrGlnSerSerHisPheTrpSerAlaSerAlaIleTrpGlyGlySerAlaSerTrpSer 580
Db      2244  ACGAGATCTCTCAACATCTTCACTGCTCAGCCATCTACGAGAGCGAGTCCAGTTACTCT 2303
Qy      581  AlaTrpSerCysSerGlnLeuProThrCysGlyAspGlnValTrpSerValArgArgArg 600
Db      2304  GCTTACAGCTGCGACGACAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGGCCAGG 2363
Qy      601  GlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGlnGluSerProPheGln 620
Db      2364  CAGAACCCAAAGTACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGCCCTTTGAA 2423
Qy      621  LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGluAsn 640
Db      2424  AAGCAATTTAAACGAGAGCTGCCAAATGAATTTGAGAGCATCAATGTCAGAGAAC 2483
Qy      641  ArgSerArgGlnGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGln 660
Db      2484  AGGTCAAGGGAAGAGCTGGGGAAGTGGGCAATCACTTTCGCTTTCCGGCAGCATGGA 2543
Qy      661  IleIleGlnValSer 665
Db      2544  ATCATTGAGTCTCC 2558

RESULT 8
US-09-816-494-1
/ Sequence 1, Application US/09816494
/ Patent No. US20020034807A1
/ GENERAL INFORMATION:
/ APPLICANT: Meyers, Rachel A.
/ TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
/ TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
/ FILE REFERENCE: 10446-030002
/ CURRENT APPLICATION NUMBER: US/09/816,494
/ CURRENT FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 60/191,858
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 3544
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (589)...(2583)
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US-09-816-494-1
Alignment Scores:
Pred. No.: 0
Score: 3406.00
Percent Similarity: 99.85%
Best Local Similarity: 99.70%
Query Match: 99.65%
DB: 9
Gaps: 0

US-10-029-345A-109 (1-665) x US-09-816-494-1 (1-3544)
Qy      1  MetAlaHisGlnMetIleGlyThrGlnIleValThrGlyArgLeuValAlaLeuGln 20
Db      589  ATGGCCATGAGATGATGGAATGGAATGATGATGAGAGGTGGCTGCTGGAA 648
Qy      21  SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluTrpAsnThrSer 40
Db      649  AGTGGAGGGAAGAAAGTCTGCTGTAATGATGACCGGCATTTGTGAAATACATCATCC 708
Qy      41  HisIleLeuGlnAlaIleAsnIleAsnGlySerLysLeuMetLysArgArgLeuGln 60
Db      709  CACATTTTGGAAAGCCATTATATCAACTGCTCCAAAGTTATGAGACGGAAGTTGCAAG 768
Qy      61  AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
Db      769  GACAAAGTGTATATTAACAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 828
Qy      81  CysSerGlnLysValValValTrpAspGlnSerGlnAspValAlaSerLeuSerSer 100
Db      829  TGCAGTCAGAAAGTTGTGATTACATCAAGAGCTCCCAAGATGTTGCTCTCTCTTCA 888
Qy      101  AspCysPheLeuThrValLeuLeuGlyLysLeuGlnLysSerPheAsnSerValHisLeu 120
Db      889  GACTGTTTCTCAGTCACTTCTTGGGTAACTGGAGAAAGACCTTCACCTGTTCACTG 948
Qy      121  LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db      949  CTTCAGAGTGGGTTTGTGCAATTTCTCTGTTGTTCCCTGGCCCTCTGTGAAGGAAATCC 1008
Qy      141  ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db      1009  ACTTAGTCCCTTACCTGATTTCTCAGCTTGTCTTAACCTGTGCAACATGGGCAACC 1068
Qy      161  ArgIleLeuProAsnLeuTrpLeuGlyCysGlnArgAspValLeuAsnLysGlnLeuIle 180
Db      1069  GCAATTTTCCCAATCTTATCTTGGCTGCGCAGGAGATGTCCTCAACAAAGAGCTGATG 1128
Qy      181  GlnGlnAsnGlyIleGlyTrpValLeuAsnAlaSerTrpThrCysProLysProAspPhe 200
Db      1129  CAGCAGATGGGATTTGGTTATGCTTAATCCAGCAATACCTGTCCAAAGCTGACTTT 1188
Qy      201  IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
Db      1189  ATCCCGAGTCTCAATTCCTGCGCTGCTGTGAATACAGCTTTTGTGAAAAATTTTG 1248
Qy      221  ProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240
Db      1249  CGTGTTGGACAAATCATGATGATTTCAATTGAGAAACAAAGCTCCCAATGATGTGTT 1308
Qy      241  LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTrpIleMet 260
Db      1309  CTATGTGACATGTTTATAGTGGGATTCCTCCGCTCCGCCACATCGCTATCATCATG 1368
Qy      261  LysArgMetAspMetSerLeuAspGlnAlaTrpArgPheValLysGluLysArgProThr 280
Db      1369  AAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTTGAAAGAAAAAGACTTAAT 1428
Qy      281  IleSerProAsnPheAsnPheLeuGlyGlnLeuAsnAspTrpGlyLysLysIleLysAsn 300
Db      1429  ATATCTCCAAATCTCAATTTTCTGGGCAACTCTCTGACATGAGAAAGATTTAAAC 1488
Qy      301  GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlnLysProAsn 320
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Db      1489  CAGACTGAGACATCAGGCGCAAGACCAATCACTGCTGACCTGAGAGAACCAAT 1548
Qy      321  GUProValProAlaValSerGluGlyGlnLysSerGluThrProLysSerProPro 340
Db      1549  GAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1608
Qy      341  CysAlaAspSerLysThrSerGluAlaGlyGlnArgProValHisProAlaSerVal 360
Db      1609  TGTGCGGACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1668
Qy      361  ProSerValProSerValGlnProSerLeuLysGluAspSerProLeuValGlnAlaLeu 380
Db      1669  CCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGG 1728
Qy      381  SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerValLeuLysArgSerPhe 400
Db      1729  AGTGGGCTGACCTGTCTCCGACAGAGGCTGAAAGACAGCAATAGCTCAAGCGCTT 1788
Qy      401  SerLeuAspTleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db      1789  TCTCTGGAATACAAATCAGTTTCATATTCAGCCAGATGCGACATCTTACATGGCTTC 1848
Qy      421  SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrArg 440
Db      1849  TCTCTATCAGAAAGATCTTGGAAATCTACAAACCTTCCACTCTGATGGAGACCAAC 1908
Qy      441  LysLeuCysGlnPheSerProValGlnLysSerGluGlnThrProGluThrSerPro 460
Db      1909  AAGCTATGCGAGTTCTCCCTGTTTCAGAACTATCGAGACAGCTCCGAAACCACTCT 1968
Qy      461  AspLysGluGluAlaSerTleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db      1969  GATTAAGAGAAAGCGACATCCCAAGAAAGCTGACACCGCGCTTTCAGACACACAG 2028
Qy      481  SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db      2029  AGCAGAGCATTCGATTCGCTGCTGACAGACAGACAGAGGCGCCAGAGGCTCCCTTTA 2088
Qy      501  SerProLeuHisArgSerGlySerValGluAspAspTyrHisThrSerPheLeuPheGly 520
Db      2089  TCTCCACTGATCGAAGTGGAGCGTGGAGACAAATTAACAACCGACTTCTTTCGGCG 2148
Qy      521  LeuSerThrSerGlnGlnHisLysLeuThrLysSerHisGlyLeuLysGlyTyrPheHis 540
Db      2149  CTTTTCACAGCAGCAGACGACCTCAGAAAGTCTGCTGGCGCTTAAAGGCTGGCAC 2208
Qy      541  SerAspTleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db      2209  TCGGATATCTTGGCCCCCGACGACTTACCCCTTCCCTGACGACGCTGGTATTTTGGC 2268
Qy      561  ThrGluSerSerHisPheTyrSerAlaSerAlaLysTyrGlyLysSerAlaSerTyrSer 580
Db      2269  ACAGAGTCTCTCACACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2328
Qy      581  AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db      2329  GCGTACAGTGCAGCGCAGCTGCCACTTCCGAGACCAAGTCTATCTTGGCGCAGCGG 2388
Qy      601  GlnLysProSerAspArgAlaAspSerArgArgSerThrHisGlnGluLysSerProPheGln 620
Db      2389  CAGAACCCCAAGTACAGAGCTGACTGCGCGGAGGCTGGAGTGAAGAAAGCCCTTTGAA 2448
Qy      621  LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerLysMetSerGluAsn 640
Db      2449  AAGCAATTTAAACGAGAAAGCTGCCAAATGGAATTTGAGAGAGCATATGTCAGAGAAC 2508
Qy      641  ArgSerArgGluGlnLysLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db      2509  AGCTACCGGAAAGAGCTGGGGAAGTGGCGACAGTCACTTTCGCGGCGACGATGAA 2568
Qy      661  HisLeuGluValSer 665

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Db      2569  ATCATTTAGGCTCTCC 2583
RESULT 9
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Myoung
; APPLICANT: Tsai, Feng-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP103-0180NM1M
; CURRENT APPLICATION NUMBER: US/10/377, 072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895, 860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215, 370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723, 806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187, 455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843, 297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199, 801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861, 801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205, 508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816, 494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815, 419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2586)
US-10-377-072-25
Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 17 Gaps: 0
US-10-029-345A-109 (1-665) x US-10-377-072-25 (1-3544)
Qy      1  MetAlaHisGluMetTleGlyThrGlnLysValThrGluArgLeuValAlaLeuLeuGln 20
Db      589  ATGGCCCAATGAGATGATGAGATCAATTTGTTACTGAGAGGCTTGCTGCTGGA 648
Qy      21  SerGlyThrGlnLysValLeuLeuLysSerArgProPheValGlnTyrAsnThrSer 40
Db      649  AGTGAACGGAAGAAAGTGTCTGCTAATTTGATACCGGCCCATTTTGTGAATACATCATCC 708
Qy      41  HisLysLeuGluAlaLysHisLysHisLysHisLysHisLysHisLysHisLysHis 60

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Db 709 CACATTTGGAGGCAATTAATATCACTGCTCCAGGCTTATGAAGGCAAGTTGGCAACAG 768
Qy 61 AspIyValIleuIleThrGluLeuIleGlnHisSerAlaIySerIleAspIleAsp 80
Db 769 GACAAAGTGTAAATTACAGAGCTCATCAGCATTCACGAAACATAAGGTTGACATTGAT 828
Qy 81 CysSerGlnIyValIleValIyYrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCAGTACAGAAAGTTGAGTTTACGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 888
Qy 101 AspCysPheLeuThrValIleLeuGlyIyLeuGlyIyLysSerPheAsnSerValIleLeu 120
Db 889 GACGTTTCTCCTGACTTCTGAGTAACTGAGAAAGAGCTTCAACTCTGTTTCACTG 948
Qy 121 LeuAlaGlyIyGlyPheAlaGlyPheSerAspCysPheProGlyIyLeuGlyIyLysSer 140
Db 949 CTTCAGAGTGGGTTGCTGAGGTTCTCTGTTGTTTCCCTGCGCTGTGAAGAAATTC 1008
Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACCTGTTCCAAACATTTGGGCCAAC 1068
Qy 161 ArgIleLeuProAsnLeuIyIyLeuGlyIyCysGlnArgAspValIleuAsnIyGlyLeuIle 180
Db 1069 CGAATTCCTCCCAATCTTTATCTTGAGCTGCAGCGAGATGTCTCTCAACAAGAGAGCTGATG 1128
Qy 181 GlnGlnAsnGlyIleGlyIyValIleuAsnAlaSerIyThrCysPheProIyAspPhe 200
Db 1129 CACCAAAATGGAGTTGGTTATGTTTAAATGCCAGCAATTCCTGCCAAAGGCTGACTT 1188
Qy 201 IleProGlnSerHisPheLeuArgValIProValAsnAspSerPheCysGlnIySerIleLeu 220
Db 1189 ATCCCGAGAGCTCATTTCCGTGCGTGCCTGATGATGAGAGCTTTGTGAGAAATTTTG 1248
Qy 221 ProThrLeuAspIySerValIAspPheIleGlnIyValAlaIySerAsnGlyIyCysVal 240
Db 1249 CCGTGTGTGACAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCTCCCAATGATGTGTT 1308
Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIyIleMet 260
Db 1309 CTAGTGCACCTGTTTACCTGGAGATCTCCCGCTCCGCCAACATGCTTACCTTACATCATG 1368
Qy 261 LysArgMetAspMetSerLeuAspGlnAlaIyYrArgPheValIleGlnIyLysArgProThr 280
Db 1369 AAGAGAGATGACATGCTTATGTAAGCTTACAGATTGTGTAAGAAAGAAAGAAAGAAAGCTTACT 1428
Qy 281 IleSerProAsnPheAsnPheLeuGlyIyGlnLeuLeuAspTyrGlnIyLysIleIyAsn 300
Db 1429 ATATCTCCAAATTCATATTTCTGGGCCAACTCTGAGCTATGAGAAAGATTTAAGAAC 1488
Qy 301 GlnThrGlyAlaSerGlyProIySerIyLysLeuIyLeuLeuHisLeuGlnIyLysProAsn 320
Db 1489 CAGACTGGAGCATCAGGGCCAAAGAACAACTCAAGCTCTGCACTGAGAAAGCCAAAT 1548
Qy 321 GluProValIProAlaValSerGlyIyGlnIyLysSerGlnThrProLeuSerProPro 340
Db 1549 GAACCTGTCTCCGTCTGTCTCAGAGGGGTGACAGAAAGAGAGACCGCCCTCAGTCCACCC 1608
Qy 341 CysAlaAspSerAlaThrSerGlnAlaIleGlyIyGlnArgProValHisProAlaSerVal 360
Db 1609 TGTGCGACTCTGCTTACCTCAGAGGAGAGAGCAAAAGGCCCGGTGATCCGCCAGCGGTG 1668
Qy 361 ProSerValIProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380
Db 1669 CCCAGGTTGCCAGGCTGACGCGTGTGCTTGAAGAGACAGCCCGCTGTTAAGCCGCTC 1728
Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnIyLysIyLysArgSerPhe 400
Db 1729 AGTGGGCTGCACCTGTCCGACAGGCTGGAAGACAGCAATTAATCACTCAAGGTTCTTCC 1788
Qy 401 SerLeuAspIleLysSerValSerIySerAlaSerMetAlaIleSerLeuHisGlyIyPhe 420

Db 1789 TCTCTGATATCAATATCAGTTTCATATTTCAGCCAGATGGCAGCATCTTACATGGCTTC 1848
Qy 421 SerSerSerGlnAspAlaLeuGlnIyTyrIyLysProSerThrThrLeuAspGlyThrAsn 440
Db 1849 TCTCTATCAGAAAGATGCTTTGGATATACAAACCTTCCATCTGATGGAGCAAC 1908
Qy 441 LysLeuCysGlnPheSerProValGlnIyLeuSerGlnIyGlnThrProGlnIySerPro 460
Db 1909 AAGCTTATGCCAGTTCTCCCTGTCTGAGAACTATGAGACAGACTCCGAAACAGTCT 1968
Qy 461 AspIyGlyIyAlaSerIleProIyLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1969 GATTAAGAGAGAGAGCCAGCATCCCAAGAGCTGACAGCCGACGCTTACAGAGCCAG 2028
Qy 481 SerIyArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db 2029 AGCAAGCCATTCATTCGCTGAGAACCCAGCAGCAGATGGACCCGCCAAGGCTCTTTTA 2088
Qy 501 SerProLeuHisArgSerGlySerValGlnAspAsnIyHisThrSerPheLeuPheGly 520
Db 2089 TCTCAGCTGCATCGAAGTGGAGCTGAGAGCAATTAACACAGACTTCTTCTTCCGCG 2148
Qy 521 LeuSerThrSerGlnGlnHisLeuThrIySerSerAlaGlyLeuGlyIyLeuIyGlyIyTrpHis 540
Db 2149 CTTTCACACAGCAGCAGACACTCAAGAGTCTGCTGCGCTTGAAGGCTGGCAC 2208
Qy 541 SerAspIleuAlaIProGlnThrSerThrProSerLeuThrSerSerThrIyPheAla 560
Db 2209 TCGATATCTTGGCCCCCAGACCTTACCCCTCCCTGACAGCAGCTGTATTTTGGC 2268
Qy 561 ThrGlnSerSerHisPheTyrSerAlaSerAlaIleIyIyGlyIySerAlaSerTyrSer 580
Db 2269 ACAGAGTCTCACAATTTCTTACTGCTCCACAGCATCAGAGGAGGAGGCAAGTTACTCT 2328
Qy 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnIyIyIySerValArgArgArg 600
Db 2329 GCTTACAGCTCAGCAGCACTGCCCACTTGCAGAGCCAAAGCTTATCTGTCCGAGCGG 2388
Qy 601 GlnIyProSerAspArgAlaAspSerArgArgSerThrIleGlnIyLysProPheGln 620
Db 2389 CAGAGCCAAAGTACAGAGCTGACTCGCGGAGAGCTGGCATGAAAGAGGCCCTTTGAA 2448
Qy 621 LysGlnPheIyArgArgSerCysGlnMetGlnPheGlyIyGlnSerIleMetSerGlnAsn 640
Db 2449 AAGCAGTTTAAACGAGAGAGCTGCCAAATGGAATTTGGAGAGACATCATGTCAGAGAC 2508
Qy 641 ArgSerArgGlnIyLeuGlyIyValGlyIySerGlnSerPheSerGlySerMetGln 660
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Qy 661 IleIleGlnValSer 665
Db 2569 ATCATTTAGGTCTCC 2583
RESULT 10
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Myoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USRS THEREFOR
; FILE REFERENCE: MP103-01BOMNIM
; CURRENT APPLICATION NUMBER: US/10/377,072

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CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589) ... (2586)
US-10-377-072-25

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Score: 3406.00 Matches: 663
Percent Similarity: 99.854 Conservative: 1
Best Local Similarity: 99.704 Mismatches: 1
Query Match: 99.658 Indels: 0
DB: 18 Gaps: 0

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US-10-029-345A-109 (1-665) x US-10-377-072-25 (1-3544)

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QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 649 AGTGAACGAAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
QY 41 HisIleLeuGluAlaIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 709 CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAGGAAAGGTTGCAAC 768
QY 61 AspValValLeuIleThrGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 769 GACAAAGGTATTAACAGAGCTCAATCCAGCAATTCAGCGAAACATTAAGTTGAT 828
QY 81 CysSerGlnValValValValValValValValValValValValValValVal 100
DB 829 TGCAGTCAGAGGTTGATGATTAAGATCAAGATCCCAAGATGATGCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGluGlyValLeuGluValSerPheAsnSerValHisLeu 120
DB 889 GACTGTTTCTCAGCTACTTCTTGAGTAACAGAGAGAGCTTCAACTGTTCACTG 948
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DB 949 CTTCAGAGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160

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DB 1069 CGAATTCCTCCAACTTTATCTTGCTGCGCAGCGAGATGCTCTCAACAGAGCTGAAG 1128
QY 181 GlnGlnAsnGlyIleGlyThrValLeuAsnAlaSerThrCysPheProAspPhe 200
DB 1129 CAGCAGATGGATGGTGTATGTTATGTTAATGCGAGCAAACTGTCTCAAGCTGACTT 1188
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluValLeu 220
DB 1189 ATCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1248
QY 221 ProTrpLeuAspValSerValAsnPheIleGluValAlaValAsnAsnGlyCysVal 240
DB 1249 CCGGTGTGGCAAAATCAGTATGATTTCAATGGAAGAAAGCCCTCCATGATGTGTT 1308
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleMet 260
DB 1309 CTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCAACATGCTTACCTTACATCATG 1368
QY 261 LysArgMetAspMetSerLeuAspGluAlaValArgPheValIleGluValArgProThr 280
DB 1369 AAGAGGATGACATGCTTTAGATGAGCTTACAGATTTGTGAAAGAAAGAAAGCTTACT 1428
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DB 1549 GAACCTGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1608
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DB 1609 TGTGCCGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668
QY 361 ProSerValProSerValGlnProSerLeuGluValAspSerProValGlnAlaLeu 380
DB 1669 CCACGCTGCGCAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluValAspSerValLeuValArgSerPhe 400
DB 1729 AGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1788
QY 401 SerLeuAspIleLeuSerValSerTrpSerAlaSerMetAlaIleSerLeuHisGlyPhe 420
DB 1789 TCTCTGATATCAAAATCAGTTTCAATTCAGCAGCAATGCGAGCATCTTACATGCTTC 1848
QY 421 SerSerSerGluAspAlaLeuGluValTrpValProSerThrThrLeuAspIleThrAsn 440
DB 1849 TCTCATGAGAAAGATGCTTGGAAATATCAAAACCTTCCATCACTCTGATGAGCAAC 1908
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
DB 1909 AAGCTATGCGAATTTCTCCCTGTTTCAAGAACTATGAGAGCACTCCGAAACCACTCT 1968
QY 461 AspValGluGluAlaSerIleProValValLeuGlnThrAlaArgProSerAspSerGln 480
DB 1969 GATAAGGAGAAAGCAGAGATCCCAAGAAAGCTGAGAGCCGAGGCTTCAAGAGCCAG 2028
QY 481 SerLysArgLeuHisSerValArgHisSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 2029 AGCAAGCAGATTCATTCGATGAAACAGCAGCAATGAGCCGAGAGAGGCTCTTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnValHisThrSerPheLeuPheGly 520
DB 2089 TCTCAGCTGCAATGCAAGTGGAGCGTGAAGAGCAATTCACACAGCTTCTTTTGGGC 2148

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QY 521 LeuSerThrSerGlnGlnHisLeuThrIleSerAlaGlyIleuGlyLeuIleGlyTTPHis 540
Db 2149 CTTTCACCGACCGACGACCTCAGAGTCTGGCTGGACCTTAAGGGCTGGCAC 2208
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpYrPheAla 560
Db 2209 TCGGATATCTTGGCCCCCGACGACCTTACCCCTTCCCTGACGACGCTGGTATTGGCC 2268
QY 561 ThrGlnSerSerIlePheIleSerAlaSerAlaIleIleIleGlyGlySerAlaSerYrSer 580
Db 2269 ACGAGATCCCAACACTTCACTGCTCCTCAGCATCAACGAGCGAGTGCAGTTACTCT 2328
QY 581 AlaIleSerCysSerGlnLeuProThrCysGlyAspGlnValIleYrSerValaIleGlyGly 600
Db 2329 GCTTACAGCTGCGACCGACGCTGCCACTTGGCGAGACCAAGTCTATTCTGTGGCAGGCG 2388
QY 601 GlnIleProSerAspIleAlaAspSerArgArgSerTrpHisGlnGlnSerProPheGln 620
Db 2389 CAGAACCAAGTACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGCCCTTGA 2448
QY 621 IysGlnPheIleValArgArgSerCysGlnMetGlnPheGlyGlnSerIleMetSerGln 640
Db 2449 AAGCACTTAAAGCAGAACTGCGCAATGGATTGGAGAGAGCATGTCAGAGAAC 2508
QY 641 ArgSerArgGlnGlnIleuGlyIleValGlySerGlnSerSerPheSerGlySerMetGln 660
Db 2509 AGGTACGGGAGAGAGCTGGGGAAGTGGGACATGCTTACCTTTGGGCGAGCATGGA 2568
QY 661 IleIleGlnValSer 665
Db 2569 ATCATTTAGAGTCTCC 2583
RESULT 11
US-10-425-114-26234
/ Sequence 26234, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E.
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 26234
/ LENGTH: 3625
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234
Alignment Scores:
Pred. No.: 0 Length: 3625
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 17 Gaps: 0
US-10-029-345A-109 (1-665) X US-10-425-114-26234 (1-3625)
QY 1 MetAlaHisGlnMetIleGlyThrGlnIleValIleThrGlnArgLeuValAlaLeuIleuGln 20
Db 692 ATGGCCCATGAGATGATTGGAACCTCAAAATTGTTACTGAGAGAGTGTGGCTCTGCTGAA 751
QY 21 SerGlyThrGlnIleValLeuLeuIleAspSerArgProPheValGlnIleThrSer 40

Db 752 AGTGACCGAAGAAAGTCTGCTAATGATACCGGCACTTGTGAAATACATCATCC 811
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCysSerIleLeuMetIleArgArgLeuGlnGln 60
Db 812 CACATTTTGAAGCCATTAAATATCAAGTCTCAAGCTTATGAACGAAAGTTGCAAG 871
QY 61 AspIleValLeuIleThrGlnLeuIleGlnHisSerAlaIleHisIleValAspIleAsp 80
Db 872 GACAAAGTGTAAATACAGAGCTCATCAGCAATTCAGGAAACATTAAGTTGACATTGAT 931
QY 81 CysSerGlnIleValIleValIleYrAspGlnSerSerGlnAspValAlaSerIleuSerSer 100
Db 932 TCCAGTCCAGAGGTTGATGATTACATCAAAAGTCCCAAGATGTTGCTCTCTCTTCA 991
QY 101 AspCysPheLeuThrValLeuIleuGlyIleLeuGlnIleYrSerPheAsnSerValHisLeu 120
Db 992 GACTGTTTCTCAGTACTTCTGGGTAACTGGAGAAAGAGCTTCACTGTTCACCTG 1051
QY 121 LeuAlaGlyIlePheAlaGlnPheSerArgCysPheProGlyLeuCysGlnGlyIleYrSer 140
Db 1052 CTGGAGGTGGGTGGCTGAGTCTCTGTTGTTCCCTGGCCTCTGGAAGAAATCC 1111
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1112 ACTTAGTCCCTACTGATTTCTCAGCCTTGCTTACCTGTTGCCAATTTGGGCCAAC 1171
QY 161 ArgIleLeuProAsnLeuIleuGlyCysGlnArgAspValLeuAsnIleGlnLeuIle 180
Db 1172 CGAATCTTCCCAATCTTATCTTGGCTGCCAGCAATGTCCTCAACAAAGAGCTGATG 1231
QY 181 GlnGlnAsnGlyIleGlyIleValLeuAsnAlaSerYrTrpCysProIleProAspPhe 200
Db 1232 CAGCAATGGGATTTGGTTATGTTAATATCAGCAATACCTGTCCAAGCCTGACTT 1291
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnIleIleLeu 220
Db 1292 ATCCCGAGTCTCATTTCTCTGCTGGTGCCTGATGATGACACTTTTGAAGAAATTTG 1351
QY 221 ProTrpLeuAspIleSerValAspPheIleGlyIleValAlaSerAsnGlyCysVal 240
Db 1352 CCGGTGTGGAACAATCATGATTTTCAATGAAAGCAAAAGCCTCAATGGATGTGT 1411
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleMet 260
Db 1412 CTAGTGCACTTTTACCTGGGATCTCCGCTCCGCAACATGCTTATCGCTTACATCATG 1471
QY 261 LysArgMetAspMetSerLeuAspGlnAlaIleYrArgPheValIleGlyIleArgProThr 280
Db 1472 AAGAGATGAGCATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAGACACTACT 1531
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspYrGlyIleValAsn 300
Db 1532 ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACATGAGAAAGATTTAAAC 1591
QY 301 GlnThrGlnAlaSerGlyProIleSerIleLeuIleuHisLeuGlnIleYrProAsn 320
Db 1592 CAGACTGAGAGATAGGGCCAAAGAGCAAACTCAAGTCTGCACTGGAGAACCAAT 1651
QY 321 GlnProValProAlaValSerGlnGlyIleGlnIleYrSerGlnThrProLeuSerProPro 340
Db 1652 GAACCTTCTCCCTGCTGCTCAGAGGTGAGCAGAAAGCAGAGCGCCCTCAGTCCACCC 1711
QY 341 CysAlaAspSerAlaThrSerGlnAlaIleGlyGlnArgProValHisProAlaSerVal 360
Db 1712 TGTGCCACTCTGTTACTTCAAGAGCGCAGAGCAAAAGCCCGTGCATCCCGCAGGTTG 1771
QY 361 ProSerValProSerValGlnProSerLeuGlnIleuAspSerProLeuValGlnAlaLeu 380
Db 1772 CCGAGCGTGGCCAGCGGAGCGCTGCTGTTAGAGACAGCCCGCTGATACAGGCGCTC 1831
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAlaIleuIleuYrArgSerPhe 400

Db	1832	AGTGGGCTGCACCTGTCCGACAGAGGCTGGAAAGACAGCAATTAAGCTCAAGGTTCC	1891
Qy	401	SerLeuAapP1LeuVSerValSerTySerAlaSerMetC1aAlaSerLeuHiSglYphe	420
Db	1892	TCTCGAGATATCMAATCAAGTTTCATATTCAGCCACAGATGGGACATCTTACATGGCTTC	1951
Qy	421	SerSerSerGluAapAlaLeuGluYrTyTyLysPProSerThrThLeuAapGlyYThrAsn	440
Db	1952	TCCTATATCAGAGATGCTTGGAAATCTACAAACCTTCCACTACTCTTGATGGAGCAAC	2011
Qy	441	LysLeuCySgInPheSerProValGInGluLeuSerGluGInThProGluThSerPro	460
Db	2012	AAGCTATCCAGGTTCTCCCTGTTTCAAGGAATATCGAGACAGACTCCGAAACAGTCTCT	2071
Qy	461	AapYlSgIGluAlaSerT1LeProLysYlSleuGInThrAlaArgProSerAapSerGln	480
Db	2072	GATAAAGAGGAAGCCAGCATCCCAAGAAAGCTGCAGACCGCCAGGCTTTCAGACAGCCAG	2131
Qy	481	SerLysAArgLeuHiAseValArgThSerSerSerGlyThrAlaGlnArgSerLeuLeu	500
Db	2132	AGCAAGCCATTTGCATTGCGTCAAGAACCAAGCAGCAGAGTGGACCGCCCAAGAGTCCCTTTA	2191
Qy	501	SerProLeuHiAArgSerGlySerValGluAapAntYrHiSThSerPheLeuPheGly	520
Db	2192	TCTCCACTGCATCGAAGTGGAGCGCTGGAGACAAATTACACACAGCTTCTTTCCGGC	2251
Qy	521	LeuSerThSerGInGlnHiSleuThrLysSerAlaGlyLeuGlyLeuLysGlyYTrpHis	540
Db	2252	CTTTCACACACCCAGCAGCACCTCCAGAAAGTCTGCTGGCTTGGGCTTAAAGGCTGGCAC	2311
Qy	541	SerAapP1LeuAlaProGluThSerThrProSerLeuThrSerSerTTrpYrPheAla	560
Db	2312	TCGAGTATCTTGGCCCCCCAGACCTCTAACCCCTTCCCTGACACAGCAGCTGGATTTGGCC	2371
Qy	561	ThrGluSerSerHiApheTySerAlaSerAlaT1LeYrGlyGlySerAlaSerTySer	580
Db	2372	ACAGAGTCTCTACACTTACTTCTGCTCTCAAGCATCTACGAGGAGAGTCCAGTTACTCT	2431
Qy	581	AlaTySerCySseGInLeuProThrCySgLYAapGlnValTySerValArgAArg	600
Db	2432	GCCTACAGCTCAGCCAGCTGCGCCACTTGGCGGAAGCAAGTCTATCTGTGGGAGGGGG	2491
Qy	601	GlnLysPProSerAapArgAlaAapSerArgArgSerTTrpHisGluGluSerProPheGlu	620
Db	2492	CAGAAAGCCAAATGTCAGAGCTGACTCGCGCGGAGCTGCATGAAGAAAGCCCTTTGAA	2551
Qy	621	LysGInPheLYAArgArgSerCySgInMetGluPheGlyGlyUserT1LeMetSerGluAsn	640
Db	2552	AAGCATTTAAACCGAAGAGCTGCCAAATGGAAATTTGGAGAGAGCATATCTCAGAAAC	2611
Qy	641	ArgSerArgGluGluLeuGlyLYeValGlySerGInSerPheSerGlySerMetGlu	660
Db	2612	AGGTCAACCGGAAGAGCTGGGGAAAGTGGGAGTCACTTACTTTTCCGGCAGCATGGA	2671
Qy	661	IleIleGluValSer 665	
Db	2672	ATCATTTGAGTCTCC 2686	
RESULT 12			
US-10-343-357-17			
; Sequence 17, Application US/10343357			
; Publication No. US20040058341A1			
; GENERAL INFORMATION:			
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom			
; APPLICANT: ELLIOTT, VICKI S.; RAMKUMAR, Jayalakshmi			
; APPLICANT: YAO, Montique G.; BURFORD, Neil			
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.			
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.			
; APPLICANT: LEE, Eneestine A.; HAFALIA, April J.A.			
; APPLICANT: LU, Dyoung Alina M.; TRIBOUNAY, Catherine M.			
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.			
; APPLICANT: YUE, Henry; WARREN, Bridget A.			
; APPLICANT: NGUYEN, Daniel B.; CHAWLA, Nandinder K.			

	APPLICANT KEARNEY, Liam	
/	TITLE OR INVENTION: PROTEIN PHOSPHATASES	
/	FILE REFERENCE: PI-0173 PCT	
/	CURRENT APPLICATION NUMBER: US/10/343,357	
/	CURRENT FILING DATE: 2003-01-28	
/	PRIOR APPLICATION NUMBER: PCT/US01/23716	
/	PRIOR FILING DATE: 2001-07-26	
/	PRIOR APPLICATION NUMBER: US 60/221,679	
/	PRIOR FILING DATE: 2000-07-28	
/	PRIOR APPLICATION NUMBER: US 60/223,272	
/	PRIOR FILING DATE: 2000-08-03	
/	PRIOR APPLICATION NUMBER: US 60/224,309	
/	PRIOR FILING DATE: 2000-08-10	
/	PRIOR APPLICATION NUMBER: US 60/226,728	
/	PRIOR FILING DATE: 2000-08-18	
/	PRIOR APPLICATION NUMBER: US 60/229,254	
/	PRIOR FILING DATE: 2000-08-30	
/	PRIOR APPLICATION NUMBER: US 60/231,366	
/	PRIOR FILING DATE: 2000-09-08	
/	NUMBER OF SEQ ID NOS: 20	
/	SOFTWARE: PERL Program	
/	SEQ ID NO 17	
/	LENGTH: 3766	
/	TYPE: DNA	
/	ORGANISM: Homo sapiens	
/	FEATURE:	
/	NAME/KEY: misc_feature	
/	OTHER INFORMATION: Incycle ID No. US20040058341A1 7480570CB1	
US-10-343-357-17		
Alignment Scores:		
Pred. No.:	0	Length: 3766
Score:	3406.00	Matches: 663
Percent Similarity:	99.85%	Conservative: 1
Best Local Similarity:	99.70%	Mismatches: 1
Query Match:	99.65%	Indels: 0
DB:	17	Gaps: 0
US-10-029-345A-109 (1-665) x US-10-343-357-17 (1-3766)		
OY	1 MetAlHAGlWetClEGLYThrgInlleValThrgIuarGleauVaAlaleuLeugln 20	
Dd		
	538 ATGGCCCATGGAATGATTGAACTCAAAATTGTACTGAGAAGTGGTGCGCTTCGTGGAA 597	
OY	21 SerGIyThrgInlyuVallleuLeulleAsPserArGrProPhenValGluyrASnthSer 40	
Dd		
	598 AGTGGAAAGAAAAGAGCTGCTTAATTGATAGCCGCCATTGTGGAAATACATCACACC 657	
OY	41 HislleluenglualalleamilleasnCysserLyseulewettyBarGARgleungln 60	
Dd		
	658 CACATTTTGGAGCCTAATAATATCAACTGCCTCCAAGCTTATGAAGCCGAAGGTTCACAAG 717	
OY	61 AspIysrValleunilleThrgInlleuIlleglhIsSerAlayshlsylsValAspDilesp 80	
Dd		
	718 GACAAAGTGTAAATTACAGAGCTCATCAGATTACAGAAACATAAGGTGACATTGAT 777	
OY	81 CysserGlnlysuValvalValtyrAspGlnSerSerGlnAspValAlaserLeusSer 100	
Dd		
	778 TGCAGTCAGAAAGTGTtngttTAGCAACAAAGCTCCCAGAtgttgcttcctccttcca 837	
OY	101 AsPCysPheleuthrValleuLeuglyLyalyeuglnulysserPheanSerValHisleu 120	
Dd		
	838 GACTGTTTTCTCACTGACTTCTGGGTAAATCGAGAAAGAGCTTCAACTCTGTCACTGG 897	
OY	121 LeuaAlactylgPheaIagluPheserArgCypherProglyleuCYsgluglylysSer 140	
Dd		
	898 CTTCAGAGTGGGTGTGTGAAGTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGAAAAATCC 957	
OY	141 ThrIeuValProThrCysIlesSerGlnProCysleuProValalaenanileglyProThr 160	
Dd		
	958 ACTCTAGTCCCTACCTGCATTTCTCAGACCTTGCTTACTCTGTGGCAAATGGGCCAAC 1017	
OY	161 ArgIIleudProAnleutyryLeuglyCyseglnarGapValleuanlyvguluLeulle 180	

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Db      1018 CGAATCTTCCCAATCTTATCTTGGCTGCAGAGATCTCTCAACAGAGCGTGAAG 1077
Qy      181 GInGlnAenGly11eglyTyValLeuAenA1SerTyThrCySerProlypProAephe 200
Db      1078 CACAGAAATGGGATGGTATGTTATGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 1137
Qy      201 ILAProGluSerHisPheLeuAArgValProValAsnApsSerPheCySerGlyuS1leu 220
Db      1138 ATCCCGAGTCTCAATTTCTGCGTGCGTGAATGACAGCTTTGTGAAATTTTG 1197
Qy      221 ProTrpLeuAps1SerSerValAapPhe11eglyuS1alysA1aserAenGlyCyVal 240
Db      1198 CCGTGGTGGACAATCAGTAGATTTCATTGAGAAAGCAAAACCTCCCAATGATGTGTT 1257
Qy      241 LeuValHisCyA1eulAagly11eserAArgSerValThr11eal1ealA1y11emet 260
Db      1258 CTAGTCACTGTTTAACTGGGATCTCCGCTCCGCAACCTATCGCTACATCATG 1317
Qy      261 LysArgMetAepMetSerLeuAapGlyuA1A1yArgPheVal1yGlyuSArgProThr 280
Db      1318 AAGAGATGACATGCTCTTATGATGAAGCTTACAGATTGTGAAGAAAGAAAGACCTACT 1377
Qy      281 ILeserProAenPheAenPheLeuGlyGlnLeuLeuApsTyrglyuS1yS11eysAen 300
Db      1378 ATATCTCCAAACTTCAATTTTCTGGGCAACTCTGAGCTATGAGAAAGAAATTAAGAC 1437
Qy      301 GlnThrGlyA1aserGlyProlypSerTyS1eulysLeuLeuHis1leuGlyuSProAen 320
Db      1438 CAGACTGGAGCATCAGGGCCAAAGCAAACTCAACCTCTGCACTGAGAGAAAGCCAAAT 1497
Qy      321 GluProValProA1AvalSerGluGlyGlnLysSerGlyuThrProLeuSerProPro 340
Db      1498 GAACCTGTCTCTCTCTCTCTCAGAGGTTGAGACAGAAAGGAGAGCGCCCTCACTCCACC 1557
Qy      341 CyA1AasPserA1aThrSerGlyuA1aA1aglyGlnArgProValHisProA1aserVal 360
Db      1558 TGGCCGACTGCTGCTACTCAAGAGGAGAGCAAGCAAAAGCCGCTGATCCCGCAGCGTG 1617
Qy      361 ProSerValProSerValGlnProSerLeuLeuGlyuAapSerProLeuValGlnA1eul 380
Db      1618 CCCAGGGTCCCGAGCGGTGAGCGGTGTGTAAGAGAACCGCCGTGTGTACAGGGCGTC 1677
Qy      381 SerGlyLeuHis1leuSerA1AaPArgLeuGlyuAapSerA1a1yS1eulysArgSerPhe 400
Db      1678 AGTGGCTGCACTGTCTCCGAGACAGAGCTGGAAGACAGAA1AAGTCAAGGCTTCTTC 1737
Qy      401 SerLeuAps11e1ySerSerValSerTySerA1aserMetA1a1aserLeuHis1eglyPhe 420
Db      1738 TCTCTGATATCAATCAGTTTCATATTCAGCCAGCATGGAGCATCTTACATGGCTTC 1797
Qy      421 SerSerSerGlyuApsA1eulGlyuTyTyTyTyProSerThrThrLeuApsGlyuThrAen 440
Db      1798 TCTCTATCAAGAAAGTCTTGAATACTCAAACTTCCACTGTGATGGAGCAAC 1857
Qy      441 LysLeuCySglNpHeserProValGlnGlyuLeuSerGlnGlnThrProGluThrSerPro 460
Db      1858 AAGCTATGCACTTCTCCCTGTTCAGAACTATCGAGACAACTCCGAAACCACTCTCT 1917
Qy      461 AapLyGluGlyuA1aser11eProlypLyS1eulGlnThrA1aArgProSerApsSerGln 480
Db      1918 GATTAAGAGAGAAAGCAAGCATCCCAAGAGCTGAGACCGCAGGCTTCAAGAGCCAG 1977
Qy      481 SerLyAArgLeuHisSerValArgThrSerSerSerGlyuThrA1GlnArgSerLeuLeu 500
Db      1978 ACAAAGCCAGTTCATTCGCTGAGAAACAGACAGACAGTGGCCGCAAGAGTCCCTTTTA 2037
Qy      501 SerProLeuHisArgSerGlySerValGlyuApsAenTyHisThrSerPheLeuPheGly 520
Db      2038 TCTTCACATGCACTGAGAGTGGAGCGGTGAGAGCAATTAACAACAGCTCTCTTTCCGGC 2097
Qy      521 LeuSerThrSerGlnHis1leuThrLyS1eulA1aglyLeuGlyLeuLyS1yTrpHis 540

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Db      2098 CTTTCACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2157
Qy      541 SerAps11eulA1ProGlnThrSerThrProSerLeuThrSerSerTyTrpPheA1a 560
Db      2158 TCGGATATCTTGGCCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2217
Qy      561 ThrGluSerSerHisPheTySerSerA1aserA1a1eTyrglyGlySerA1aserTySer 580
Db      2218 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2277
Qy      581 A1aTySerCySerGlnLeuProThrCySglAapGlnValTySerValAArgArg 600
Db      2278 GCTTACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2337
Qy      601 GlnLyPProSerApsA1AaPserAArgSerTyTrpHisGluGlyuSerProPheGly 620
Db      2338 CAGAAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2397
Qy      621 LysGlnPheLyAArgSerCySglNpMetGluPheGlyuSer11emetSerGlyuAen 640
Db      2398 AAGCATTTTAAAGCAGAAAGCTGCCAATGGAATTTGAGAGAGAGATATGTCAGAGAC 2457
Qy      641 ArgSerArgGlyuGlyuLeuGlyLyS1eulGlySerGlnSerSerPheSerGlySerMetGly 660
Db      2458 AGGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2517
Qy      661 IL1e1eGlyuA1Ser 665
Db      2518 ATCATTTGAGGTCTCC 2532

RESULT 13
US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648, 593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Alignment Scores:
Pred. No.: 0 Length: 4790
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
Gaps: 0
DB: 18

US-10-029-345A-109 (1-665) x US-10-648-593-115 (1-4790)

Qy      1 MetA1HisGluMet11eglyTyGln11eValThrGluArgLeuValA1a1eulGlyu 20
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Qy      21 SerGlyThrGlyuSValLeuLeu11eApsSerArgProPheValGlyTyAenThrSer 40
Db      244 AGTGAAGAGAAAGAGCTGCTATGATGATGAGCCGAGCATTTGTGGAAATCAATACATCC 303
Qy      41 His1leuGlyuA1a1eAen11eAenCySerLyS1eulMetTyAArgArgLeuGln 60
Db      304 CACATTTTGGAGGACCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAGTTGCAACAG 363

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QY 61 AapLyVaIlleuIleThrgIleuIleGIInHISerAlaYBHisLyVaIlaPleap 80
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 QY 81 CysSerGIInLyVaIValIyYraPgiInSerSerGIInaPvaIaIaSerLeuSer 100
 DB 424 TGCAGTCAGAAAGTTAGTTAGATCAAGCTCCCAAGATGTCCTCTCTCTCA 483
 QY 101 AapCyPheLeuThrValleuLeuGIyLyBleuGIuLySerPheAnsSerValHISleu 120
 DB 484 GACTGTTTCTCACTGACTCTGGGGTAACTGGAGAAAGAGCTTCAACTCTGTTCACTGG 543
 QY 121 LeuAlaGIyGIyPheAlaGIuPheSerArgCyPheProGIyLeuCySgiuGIyLySer 140
 DB 544 CTTCGAGGTGGGTTTCTGAGTTCTCTGTTGTTTCTGAGCTCTGTTGAAGAAATCC 603
 QY 141 ThrLeuValProThrCySIIeserGIInProCyBleuProValaIaAnsIleGIyProthr 160
 DB 604 ACTCTAGTCCCTACCTGCATTTCTAGCCTTGTCTACCTGGCCAACTTGGGCCAAC 663
 QY 161 ArgIleuProAnsLeuIyrieuGIyCySgiInArgAspValleuAnsIySgiuLeuIle 180
 DB 664 CCAATTCCTCCCAATCTTATCTTGGCTCCAGCCAGATGCTCTCAACAGAGAGCTGAG 723
 QY 181 GIInGIInaPngIyIleGIyTrValleuAnsIaSerTy-ThrCyBProLySProaPhe 200
 DB 724 CAGCGAAATGGAGTTGGTATGATGTAATGCCAGAAATCCGTCTCAAGAGCTGACTT 783
 QY 201 IleProGIuSerHisPheLeuArgValProValAnsAspSerPheCySgiuLyIleu 220
 DB 784 ATCCCGAGTCTCATTTCTGGGTGGCCGTGAATGACAGCTTTGTGAGAAATTTTG 843
 QY 221 ProTrPLeuAspLySerValaPheIleGIuLyValaLyAlaSerAnsGIyCyVal 240
 DB 844 CGGTGGTTGCAAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCCTCAATGATGTGT 903
 QY 241 LeuValHISCyLeuAlaGIyIleSerArgSerAlaThrIleAlaIleAlaIyIleMet 260
 DB 904 CTAGTGACATGTTTACGTGGAACTCCCGCTCCGCCACCATGCTATCCCTACATCATG 963
 QY 261 LyBArgMetAspMetSerLeuAspGIuAlaIyArgPheValIleSgiuLyArgProthr 280
 DB 964 AAGAGATGACATGCTTATAGATGAAGCTTACAGTTTGTGAAGAAAAAGACTACT 1023
 QY 281 IleSerProAnsPheAnsPheLeuGIyGIInLeuLeuAspTyTGIuLyLyIleLyBaa 300
 DB 1024 ATATCTCCAACTTCAATTTCTGGGCCAACTCTGAGCTATGAGAAAGATTAAAGAC 1083
 QY 301 GIInThrgIyAlaSerGIyProLySerLyBleuLyBleuHISleuGIuLySProaAn 320
 DB 1084 CAGACTGGAGCATCAGGGCCAAAGCAAACTCAAGCTCTGACTGAGAAAGCCCAAT 1143
 QY 321 GIuProValProAlaValSerGIuGIyGIInLySerGIuThrProLeuSerProPro 340
 DB 1144 GAACCTGTCTCTGTCTCTCAGAGGTGACAGAAAGGAGAACGCCCTCTCACTCAACC 1203
 QY 341 CyBAlaAspSerAlaThrserGIuAlaAlaGIyGIInArgProValHISProAlaSerVal 360
 DB 1204 TGTGCGCACTGTCTGCTCCTCAGAGGAGAGCAAAAGCCCGTGATCCGCCAGCGTG 1263
 QY 361 ProSerValProSerValGIInProSerLeuLeuGIuAspSerProLeuValGIInAlaLeu 380
 DB 1264 CCCAGGGTCCAGAGCTGAGCGCTGCTGTAGAGAGAGCCCGCTGTATACAGGGGCTC 1323
 QY 381 SerGIyLeuHISLeuSerAlaAspArgLeuGIuAspSerAnsLyBleuLyArgSerPhe 400
 DB 1324 ACTGGGCTGCACTGTCCGACAGAGCTGGAAGACAGAAATAGTCAAGCTTCTTC 1383
 QY 401 SerLeuAspIleuLySerValSerTySerAlaSerMetAlaAlaSerLeuHISGIyPhe 420
 DB 1384 TCTCTGATATCAAAATCAGTTTCAATTCAGCCAGCATGAGCATCTTACATGAGCTTC 1443

QY 421 SerSerSerGIuAspAlaLeuGIuIyTyTyLySProSerThrThrLeuAspGIyThraAn 440
 DB 1444 TCTCTATCAGAAAGATCTTTGGAAATATCTCAAACTTCCACTACTGTGATGGAGCAAC 1503
 QY 441 LyBLeuCySgiInPheSerProValGIInGIuLeuSerGIuGIInThrProGIuThrsSerPro 460
 DB 1504 AAGCTATGCCAGTTCTCCCTGTTCCAGAAATATCGAGACAGACCTCCGAAACCACTCT 1563
 QY 461 AapLyBGIuGIuAlaSerIleProLyBleuGIInThrAlaArgProSerAspSerGIIn 480
 DB 1564 GATTAAGAGAGAAAGCCAGCATCCCAAGAGCTGACAGCCAGGCTTTCAGACACCCAG 1623
 QY 481 SerLyArgLeuHISerValArgThrsSerSerSerGIyThrAlaGIInArgSerLeuLeu 500
 DB 1624 AGCAAGCATTTGATTCGGTTCAGAACAGACAGAGCTGGACCCGACAGGCTTCTTTA 1683
 QY 501 SerProLeuHISArgSerGIySerValGIuAspAnsTyThISerPheLeuPheGIy 520
 DB 1684 TCTCCACTGATCGAAGTGGAGCGTGGAGAGCAATTAACACAGCTTCCCTTTCCGGC 1743
 QY 521 LeuSerThrserGIInGIInHISleuThrLySserAlaGIyLeuGIyLeuLySgiIyTrPHis 540
 DB 1744 CTTCACACAGCCAGACAGCACTCAAGAGTGTGCTGGCTGGCTTAAAGGCTGGCAC 1803
 QY 541 SerAspIleLeuAlaProGIInThrsSerThrProSerLeuThrsSerTrpTyTrPheAla 560
 DB 1804 TCGATATCTTGGCCGCCACAGCTTACCTTCCCTTCCAGACAGCTGATTTTGGC 1863
 QY 561 ThrGIuSerSerHisPheTySserAlaSerAlaIleTyGIyGIySerAlaSerTySser 580
 DB 1864 ACAGAGTCTTCACACTTACTCTGCTCAGCACTACAGAGGAGCTGCCAGTTACTCT 1923
 QY 581 AlaTySserCySserGIInleuProThrCySgiIyAspGIInValTySserValArgAGArg 600
 DB 1924 GCTTACAGCTGAGCCAGCTGCCCTTGGGAGACCAAGTATTTCTGTGGCAGGCCG 1983
 QY 601 GIuLySProSerArgArgAlaAspSerArgAspSerTrpHISGIuGIuSerProPheGIu 620
 DB 1984 CAGAAAGCCAGTACAGACTTACTGCGCGGAGCTGCAAGAAAGAGCCCTTTGAA 2043
 QY 621 LySgiInPheLyArgArgSerCySgiInMetGIuPheGIyGIuSerIleMetSerGIuAn 640
 DB 2044 AAGCATTTAAACGAGAAAGCTGCCAAATGAAATTTGGAGAGACATCATGCAAGAAC 2103
 QY 641 ArgSerArgGIuGIuLeuGIyLyValGIySergIInSerPheSerGIySergIyMetGIu 660
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 QY 661 IleIleGIuValSer 665
 DB 2164 ATCATTTAGGTCTCC 2178
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 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; PRIOR FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454

; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20824
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-357-930-20824

Alignment Scores:

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Best Local Similarity:	99.70%	Mismatches:	0
Query Match:	99.65%	Indels:	0
DB:	18	Gaps:	0

US-10-029-345A-109 (1-665) x US-10-357-930-20824 (1-5145)

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DB	589	ATGGCCCATGATGATGATGAACTCAATTTGTTACTGAGAGGTGTGCTCTGCTGGAA	648
QY	21	SerGlyThrGlnIleValLeuLeuIleAspSerArgProPheValGlnIleThrSer	40
DB	649	AGTGAACGAAAGAAAGTGTCTGCTAAATGATAGCCGCCATTTGTGAATACATCATCC	708
QY	41	HisIleLeuGluAlaIleAsnIleAsnIleAsnIleSerIleLeuMetIleArgLeuGln	60
DB	709	CACATTTTGGAAGCCATTAAATCACTCTCCAGCTTATAGCGAAGTTGCAACG	768
QY	61	AspIleValLeuIleThrGlnLeuIleGlnIleSerIleAlaIleHisIleValAspIleAsp	80
DB	769	GACAAAGTGTATATACAGAGCTCATCCAGATTGCGAAGCATATAGGTTGACATTGAT	828
QY	81	CysSerGlnIleValIleValIleValIleValIleValIleValIleValIleValIleVal	100
DB	829	TTCAGTCAGAGGTGTGTATGATTCATGATCAAGTCCCAAGATGTTGCCCTCTCTCTCA	888
QY	101	AspCysPheLeuThrValIleLeuGlnIleGlnIleSerIleAlaIleHisIleValIleLeu	120
DB	889	GACTGTTTCTCACTGTACTTCTGGGTAACTGGAGAAAGCTTCACTCTGTCACTTG	948
QY	121	LeuAlaGlyIlePheAlaGlnPheSerArgCysPheProGlyLeuCysGlnIleIleSer	140
DB	949	CTTGAGAGGT	1008
QY	141	ThrIleValIleProThrCysIleSerGlnProCysIleProValAlaAsnIleGlyProThr	160
DB	1009	ACTCTAGTCCCTCACTGCT	1068
QY	161	ArgIleLeuProAsnIleIleValIleValIleValIleValIleValIleValIleValIle	180
DB	1069	CGAATTTCTTCCAACTTTATTTTGTGGCTGCCAGCAAGATGCTCTCAACAAGAGCTGATG	1128
QY	181	GlnGlnIleValIleGlyIleValIleValIleValIleValIleValIleValIleValIle	200
DB	1129	CAGCAATGAGGATTTGTTATGTTAAATGCGCAAAATACCTGCTCAAAAGCTGACTTT	1188
QY	201	IleProGlnIleHisPheLeuArgValProValAsnAspSerPheCysGlnIleIleLeu	220
DB	1189	ATCCCCAGATCTCATTTCTGCTGCTGTGCTGTGATGACAGCTTTTGTGAGAAATTTTG	1248

QY	221	ProTrpLeuAspIleSerValAspPheIleGlnIleValIleValIleValIleValIleValIle	240
DB	1249	CCGTGTTGAGCAAAATCAGTGAATTTCAATGAAAGCAAAAGCTCCAAAGAGATGTT	1308
QY	241	IleValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleIleMet	260
DB	1309	CTAGTGCATGTTTATGCTGGATCTCCGCTCCGCAACATCGCATATGCGCTACATCATG	1368
QY	261	LeuArgMetAspMetSerLeuAspGlnIleValIleValIleValIleValIleValIleVal	280
DB	1369	AAGAGATGACATCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	1428
QY	281	IleSerProAsnPheAsnPheLeuGlnIleLeuIleValIleValIleValIleValIleVal	300
DB	1429	ATATCTCCAACTTCAATTTTCTGGGCCCACTCTGGACTTTGAGAAAGATTTAAGAAC	1488
QY	301	GlnThrGlnIleAspGlyProIleSerIleValIleValIleValIleValIleValIleVal	320
DB	1489	CAGACTGAGCATCAGGCGCAAGCAAGCAAACTCAAGCTGTGCACTCGAAGAGCCAAAT	1548
QY	321	GluProValProAlaValIleSerGlnIleGlnIleSerGlnIleProLeuSerProPro	340
DB	1549	GAACTGTCTCTGTCTCTCAAGGCTGAGACAGAAAGCAAGAGCCCTCAGTCCACCC	1608
QY	341	CysAlaAspSerAlaThrSerGlnIleAlaIleGlnIleValIleValIleValIleValIle	360
DB	1609	TGTGCCGCTCTGCTTACTCTCAAGAGCAGACAGACAAAGCCCGTGCATCCGCGAGCGTG	1668
QY	361	ProSerValProSerValGlnProSerLeuLeuIleAspSerProLeuValGlnAlaLeu	380
DB	1669	CCAGCGTCCAGAGGTGCACCGTCTGTGAGAGCAGCCGCTGTGATCAGGCGCTC	1728
QY	381	SerGlyLeuHisIleSerAlaAspArgLeuGlnAspSerAlaIleValIleValIleValIle	400
DB	1729	AGTGGCTGACCTGTCTGAGACAGAGCTGAGAAACAGCAATAGCTTCAACGTTCTTC	1788
QY	401	SerLeuAspIleValSerValIleSerIleSerIleSerIleSerIleSerIleSerIleSer	420
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DB	1849	TCTCATCAGAAAGATGCTTGTGAATATCAAACTTCCACTCACTGAGAGGAGCAAC	1908
QY	441	LeuLeuCysGlnIlePheSerProValGlnIleLeuSerGlnIleProIleThrSerPro	460
DB	1909	AAGCTATCCAGTCTCTCCCTGTTCAAGAACTATTCGAGAGCACTCCGAAACCAAGTCT	1968
QY	461	AspIleGlnIleValIleSerIlePheProIleValIleValIleValIleValIleValIle	480
DB	1969	GATTAAGAGAGAGCAGCATCTCCCAAGAGCTGAGACCGCAGGCTTCAAGACGCCG	2028
QY	481	SerIleValLeuHisIleSerValIleValIleValIleValIleValIleValIleValIle	500
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QY	501	SerProLeuHisAspSerGlnIleValIleValIleValIleValIleValIleValIleVal	520
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QY	521	LeuSerThrSerGlnIleHisIleThrIleSerAlaIleGlnIleValIleValIleValIle	540
DB	2149	CTTTCCACAGCCAGCAGCATCTCAAGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	2208
QY	541	SerAspIleLeuAlaProGlnIleThrSerThrProSerLeuThrSerSerIleIleValIle	560
DB	2209	TGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCACTGTATTTTGGCC	2268
QY	561	ThrGlnIleSerHisPheIleValIleValIleValIleValIleValIleValIleValIle	580
DB	2269	ACAGATCTCCACCTTCTACTGCTTCCAGCAATTCAGAGGACATGCGCATGATCTCT	2328
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QY 401 SerLeuAsp1LeuSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db 1789 TCCTCGAATAATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGCTTC 1848
QY 421 SerSerSerGluAspAlaLeuGluTyrTyrTyrLeuProSerThrThrLeuAspGlyThrAsn 440
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QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGlnGlnThrProGluThrSerPro 460
Db 1909 AAGCTATGCCAGTTCTCCCTGTTTCAGAACTATCGAGAGCAGCTCCGAAACCACTCCT 1968
QY 461 AspLysGlnGluAlaSer1LeuProLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1969 GATTAAGAGAGAACCCGACATCCCAAGAAAGCTGCAGACCGCCAGGCTTCAGACAGCCAG 2028
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 2029 AGCAACGCAATTGATTGGTTCAGAACCAAGCAGCAGCTGGCACCGCCAGAGGTCCTTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2089 TCTCCACTGCATGAAAGTGGAGCGTGAAGAGCAATTAACCAACACAGCTTCCTTTTCGGC 2148
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db 2149 CTTTCCACCAAGCAGCAGCAGCACTTCAGAAAGTCTGCTGGCTGGCTTAAGGGCTGGCAC 2208
QY 541 SerAsp1LeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheAla 560
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QY 601 GlnLysProSerAspArgAlaAspSerArgSerTyrHisGluGluSerProPheGlu 620
Db 2389 CAGAGCCAGTGAAGAGACTGACTGCGCGGAGCTGGCATGAAGAGGCCCTTTGAA 2448
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QY 661 Ile1LeuValSer 665
Db 2569 ATCATTTGAGGCTCTCC 2583

Search completed: February 14, 2005, 14:04:12
Job time : 940.813 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 9, 2005, 12:00:17 ; Search time 19.363 Seconds
(without alignments)
1164.285 Million cell updates/sec

Title: US-10-029-345A-109_COPY_1_302
Perfect score: 1564
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1552	99.2	665	4	US-09-816-494-2
2	989	63.2	661	4	US-09-949-016-9121
3	654.5	41.8	170	4	US-09-544-716-14
4	654.5	41.8	170	4	US-09-557-921-15
5	654.5	41.8	170	4	US-09-564-357-17
6	654.5	41.8	170	4	US-09-619-380-16
7	619	39.6	155	4	US-09-955-732A-6
8	469	30.0	482	4	US-09-557-921-2
9	466.5	29.8	491	4	US-09-949-016-8486
10	425	27.2	314	4	US-09-371-671B-11
11	425	27.2	367	2	US-08-990-379-6
12	425	27.2	394	2	US-08-530-230-23
13	425	27.2	394	4	US-09-702-705-805
14	425	27.2	394	4	US-09-702-705-805
15	425	27.2	394	4	US-09-736-457-805
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17	425	27.2	394	4	US-09-736-457-805
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24	425	27.2	394	4	US-09-658-824-805
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27	415	26.5	367	2	US-08-530-230-24

28	415	26.5	367	4	US-09-919-497-60	Sequence 60, Appl
29	415	26.5	449	4	US-09-949-016-10840	Sequence 10840, A
30	409.5	26.2	313	2	US-08-990-379-7	Sequence 7, Appl
31	409	26.2	314	3	US-09-164-193-22	Sequence 22, Appl
32	409	26.2	314	4	US-09-221-448A-22	Sequence 22, Appl
33	408	26.1	421	4	US-09-949-016-10488	Sequence 10488, A
34	377.5	24.1	393	2	US-08-990-379-4	Sequence 4, Appl
35	357	22.8	302	4	US-09-702-705-806	Sequence 806, App
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37	357	22.8	302	4	US-09-614-124B-806	Sequence 806, App
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40	357	22.8	302	4	US-09-658-824-806	Sequence 806, App
41	351	22.4	384	4	US-09-949-016-6494	Sequence 6494, Ap
42	349.5	22.3	397	2	US-08-990-379-8	Sequence 8, Appl
43	346.5	22.2	168	4	US-09-544-716-13	Sequence 13, Appl
44	346.5	22.2	168	4	US-09-557-921-13	Sequence 13, Appl
45	346.5	22.2	168	4	US-09-564-357-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1									
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; Sequence 2, Application US/09816494									
; Patent No. 6664089									
; GENERAL INFORMATION:									
; APPLICANT: Meyers, Rachel A.									
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY									
; FILE REFERENCE: 10448-030002									
; CURRENT APPLICATION NUMBER: US/09/816,494									
; PRIOR FILING DATE: 2001-03-23									
; PRIOR APPLICATION NUMBER: US 60/191,858									
; NUMBER OF SEQ ID NOS: 10									
; SOFTWARE: FASTSEQ for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 665									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-816-494-2									
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Best Local Similarity 99.3%; Pred. No. 3.9e-161;									
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DB	61	DKVLITELIHSANRKYDIDCSQKVVVYDQSSQDVASISDCPLTVLLGKLEKSFNSVHL	120						
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DB	121	LAGEFAERSRCPGLGCKSTLVPTCTISQPLCPVANGPTTILNLYIGCORVLANKEIL	180						
QY	181	QONGIGVLANASYCPRPDFIPESHFLRVPNVNSDFCEKILPMLKSVDFIEKAVASNGCV	240						
DB	181	QONGIGVLANASYCPRPDFIPESHFLRVPNVNSDFCEKILPMLKSVDFIEKAVASNGCV	240						
QY	241	LVNHLAGISSATTAIYAIYIMKRMDSIDBAVRFYKERTTISPNNFLGQLLDYEKKIKN	300						
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RESULT 2
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; Sequence 9121, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9121
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9121

Query Match          63.2%; Score 989; DB 4; Length 661;
Best Local Similarity 63.1%; Pred. No. 2,1e-99;
Matches 190; Conservative 55; Mismatches 54; Indels 2; Gaps 2;

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DB 37 MAGDRLPRKVMADAKLIALRGPGGLVIDSRSEYEVNHWLVSNNVICSKLVTGRRLQ 96
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QY 60 QDKVLTETLICHSAHKYVIDSCQKVVVYDSSQVVALSSPCELTVLIGLKEKSFNVH 119
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QY 120 LLAGFAEBSRCFPGLEGK-STLVPTCISQCLPVANIGPTRILPNLYLGGQRDVLANKE 178
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 157 ILTGFAFPFSSCFPLGCEKRAALPMSISQPCLVPSVGLTRILPHLYLGSQDVANKD 216
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 179 LIQNGIGVYLNASTYCPKDFIPBSHPLRVVNDSCFEKILPWLDSKVDPIEKXASNG 238
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 217 LMTQNGISYVLNASSNCPKDFICESRFRVPIINDNYCEKILPWLDSKIEFIDKAKLSSC 276
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 239 CVLVHCLAGISRSATIALAYIMKRMDSLDEAYRFVKEKRPPTISPNFNLGQLLDYEKKI 298
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 277 QVIVHCLAGISRSATIALAYIMKTMGMSDDAYRFVVDKRRPISPNFNLGQLLEYERTL 336
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 299 K 299
   |
DB 337 K 337

RESULT 3
US-09-544-716-14
; Sequence 14, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: LucHE, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-14
```

```
Query Match          41.8%; Score 654.5; DB 4; Length 170;
Best Local Similarity 72.5%; Pred. No. 1,4e-63;
Matches 121; Conservative 27; Mismatches 18; Indels 1; Gaps 1;

QY 134 GLCEGK-STLVPTCISQCLPVANIGPTRILPNLYLGGQRDVLANKEILIQNGIGVYLNAS 192
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 1 GLCEGKPAALLPMSLSQPCLVPSVGLTRILPHLYLGSQDVANKDLMTQNGISYVLNASS 60
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 193 YTCCKPPIPSHPLRVVNDSCFEKILPWLDSKVDPIEKXASNGCVLVHCLAGISRSA 252
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 61 NSCKPPIPSHPLRVVNDSCFEKILPWLDSKVDPIEKXASNGCVLVHCLAGISRSA 120
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 253 TIALAYIMKRMDSLDEAYRFVKEKRPPTISPNFNLGQLLDYEKKIK 299
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 121 TIALAYIMKTMGMSDDAYRFVVDKRRPISPNFNLGQLLEYERTIK 167
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||

RESULT 4
US-09-557-921-15
; Sequence 15, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: LucHE, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-15

Query Match          41.8%; Score 654.5; DB 4; Length 170;
Best Local Similarity 72.5%; Pred. No. 1,4e-63;
Matches 121; Conservative 27; Mismatches 18; Indels 1; Gaps 1;

QY 134 GLCEGK-STLVPTCISQCLPVANIGPTRILPNLYLGGQRDVLANKEILIQNGIGVYLNAS 192
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 1 GLCEGKPAALLPMSLSQPCLVPSVGLTRILPHLYLGSQDVANKDLMTQNGISYVLNASS 60
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 193 YTCCKPPIPSHPLRVVNDSCFEKILPWLDSKVDPIEKXASNGCVLVHCLAGISRSA 252
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 61 NSCKPPIPSHPLRVVNDSCFEKILPWLDSKVDPIEKXASNGCVLVHCLAGISRSA 120
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
QY 253 TIALAYIMKRMDSLDEAYRFVKEKRPPTISPNFNLGQLLDYEKKIK 299
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 121 TIALAYIMKTMGMSDDAYRFVVDKRRPISPNFNLGQLLEYERTIK 167
   ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||

RESULT 5
US-09-564-357-17
; Sequence 17, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: LucHE, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-17

Query Match          41.8%; Score 654.5; DB 4; Length 170;
```


Beat Local Similarity 72.5%; Pred. No. 1.4e-63;
Matches 121; Conservative 27; Mismatches 18; Indels 1; Gaps 1

```

0y      134 GLCEBK-STVPTCSIQPCLEVANISETRIENLYEGCQBDVLTNKEILQNGIGVYNAS 192
        ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
db      1  GLCEBKPAALLPMSLSQPCLEVPSPVGLTRILPHLYLGSQKDVLTNKEILQNGISVYNAS 60

```

```
0y      193 YTCPPDFFIESHPCLVPMVDSFCCKLLPMDLKSVPFTEKAKASNGCTLVHCLAGISSA 252
          :||||| | |:|::||::||::||::||::||::||::||::||::||::||::||
Db      61 NSCPDPFLCESRFMKVPINDNYCEKLLPMDLKSIEIFDKAYLSSCQYIVHCLAGISSA 120
```

```

QY      253  TIAIAIMRRMDSSLDEAIRKFKVKKRPITISPNFNFLQLLDYERKIK 299
          ||| :|||::|:|||||:|:|:|
Db      121  TIAIAIMKTGMSSDDAIRFVKDRRPSISPNFNFLQLLLEYERTLK 167

```

RESULT 6
US-09-619-380-16
Sequence 16 Amplification US/06c1a3a0

/ FACILE NO. 8645591
 ; GENERAL INFORMATION:
 ; APPLICANT: Lucche, Ralf M.
 ; APPLICANT: Wei, Bo

```

; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 170

```

US-09-619-380-16

Best Local Similarity 72.5%; Pred. No. 1.4e-63; Matches 121; Conservative 27; Mismatches 18; Indels 1; Gaps 1.

```
Db      121 TIAIYIMKTGMSDDAYRFVQDRRPSISPNFNLGQLLEYERTLK 167
```

US-09-955-732A-6
; Sequence 6, Application US/09955732A
; Patent No. 6825021

APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE

Matches 113; Conservative 25; Mismatches 15; Indels 0; Gaps 0;

Db 1 LSGPCLPVBSVGLTRILPHLYLGSKDVLKDKMLQNGISIVLMASSNCPRKDFICSRF 60

61 MRVPINDNCEKLLPMLDKSIEFIDPKAKSSQGVIVHCLAGISRSATIALAIYIMKTGMGS 120

```

207  |DDDAIAE VAAAE IAEENNE DDGDDDLDAIAA 208
      |:|||||:|:|||||:|:|||||:|:|
Db   121 SDDAYRFVCDRPSISPNFNFLGQLLEYERTLK 153

```

RESULT 8
US-09-557-921-2
; Sequence 2, Application US/09557921
Default Value: 00000000

```

; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OR INVENTION:  DSP-10 MINI-SPECTROSCOPY PROCESSOR

```

```

FILE REFERENCE: 200125.418
CURRENT APPLICATION NUMBER: US/09/557,921
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 20

```

```

; SEQ ID NO 2
;
; LENGTH: 482
;
; TYPE: PRT
;

```

Query Match	Score	DB 4	length
US-09-557-921-2	469	4	482

Matches 107; Conservative 65; Mismatches 96; Indels 30; Gaps 7

D0	173	VIIDCRPEWYNKSHI0GAVHINCADKISRRL00GKITVLDLISCREGKUSFKRIJFSKE	2322
0Y	85	VVVYD0SSQDVASLSSDCFLTVLLGKLEKSFNSVHLLAGGAEFBRCPFGLCEG-----	139

Dd 233 IIVYDENTNEPSRVMPQPLHIVLSLKREGEKEPLVLKGGISFKQNHENLCDNSIQIQE 292

Oy 140 -----STIVPTCTISQPCLP-VANIGPTRILPNLVLGQQRDVNLKELIQNGIGY 187

RESULT 9

```

; Sequence 8486, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for windows Version 4.0
;; SEQ ID NO 8486
;; LENGTH: 491
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-8486

Query Match 29.8%; Score 466.5; DB 4; Length 491;
Best Local Similarity 34.1%; Pred. No. 2.7e-42;
Matches 110; Conservative 63; Mismatches 105; Indels 45; Gaps 7;

QY 19 LESGTEKVLIDSRPFVEYNTSHILEAININCSKLMKRLQODKVLITELIOHSA-KHKV 77
DB 137 LELGNERLLIMCRFOELYESHIESAIWVALPGIMRLQKGNLPVRLFTRGEDRDRF 196
QY 78 DIDC-SQKVVVYDQSSOD-VASISDCEFLTVLLGKLEKSFNSVHLLAGGFAEFSRCFPG 135
DB 197 TRCGTDVTVLDESSSDMNENTGGESVGLLKKLKDEGCAFLLEGFSKFOAEFSIH 256
QY 136 CEGKSTLVPTC-ISQPCLFVANIG----- 158
DB 257 CE--TNLDGSCSSSPFLVGLIGLIRISDSSSDIESDLDSDPNSATDSDGSPLSNQP 314
QY 159 --PTHLPLVLYGCCQDVLNKLQONGIGVYLNASVTCPRK-DPIPSHFLRPVNSF 215
DB 315 SPFVELLPVLYGCADSTNLDVLEFGLKTYLNTVPLNPLPENAGSEFKYQIPISHW 374
QY 216 CEKILPWLDSKVDPIFEKAKANGCVLVHCLAGISSRSATIAIYIMKMDMSLDEAYRFVK 275
DB 375 SQNLQOFPEALSFIDEARGKNGCVLVHCLAGISSRSVTVVAYLNGKNTLSNDAVDIVK 434
QY 276 EKRPITSPRNFGLQGLDYEKKI 298
DB 435 MKKSNISPFNFMGLDLFERLT 457

RESULT 10
US-09-371-671B-11
;; Sequence 11, Application US/09371671B
;; Patent No. 6548743
;; GENERAL INFORMATION:
;; APPLICANT: Sheen, Jen
;; APPLICANT: Chiu, Man-ling
;; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
;; TITLE OF INVENTION: DUAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
;; FILE REFERENCE: 00786/370002
;; CURRENT APPLICATION NUMBER: US/09/371,671B
;; CURRENT FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: 60/155,934
;; PRIOR FILING DATE: 1999-01-14
;; PRIOR APPLICATION NUMBER: 60/095,938
;; PRIOR FILING DATE: 1998-08-10
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-371-671B-11

Query Match 27.2%; Score 425; DB 4; Length 314;
Best Local Similarity 34.3%; Pred. No. 5e-36;
Matches 104; Conservative 48; Mismatches 129; Indels 22; Gaps 5;

QY 15 LVALLSEGTETKVLIDSRPFVEYNTSHILEAININCSKLMKRLQODKVLITELIOHSAK 74
DB 13 LRALLRREGAQCULLDCRSFFAFNAGHTAGSVNVRFSFIVRRRAKAGMLEHIYPNAELR 72
QY 75 HKVDIDCSQKVVVYDQSSQDVASLSSDCFLTLLGKL--EKSFNSVHLLAGGFAEFSRCF 132

DB 73 GRLLAGYHAVVLLDEBSASLDGAKRQDTLALAGALCREARSTQVFFLQGGYAFSASC 132
QY 133 PGLCEGKSTLVPTCISQP-----CLPVANI-----GPTRLPLNLYLCCQGDVL 175
DB 133 PELCSKOST--PTGLSLPLSTSVDPDSAESGSSCSTPLYDQGVLEILSFYLSAYHAS 190
QY 176 NKEILQONGIGVYLNASVTCRPPDPIPSHFLRPVNSDFCEKILPWLDSKVDPIFEKAKA 235
DB 191 RKMULDALGITALLINVSANCN-HFEGHYQYKSLPVEDNKHADISSWFNEAIDFTDISIKD 249
QY 236 SNGCVLVHCLAGISSRSATIAIYIMKMDMSLDEAYRFVEKRPITSPNPNFLQGLDYE 295
DB 250 AGRVFVHCOAGISRSATICTIAYIMRTNRVYLDEAFEFVQRRSIISPNFSFWGQLQFE 309
QY 296 KKI 298
DB 310 SQV 312

RESULT 11
US-08-990-379-6
;; Sequence 6, Application US/08990379
;; Patent No. 5998188
;; GENERAL INFORMATION:
;; APPLICANT: Stork, Philip J
;; APPLICANT: Miska-Press, Anita
;; TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
;; TITLE OF INVENTION: Their Biologically Active Expression Products
;; FILE REFERENCE: 4104-0003220SA
;; CURRENT APPLICATION NUMBER: US/08/990,379
;; CURRENT FILING DATE: 1997-12-15
;; EARLIER APPLICATION NUMBER: PCT/US96/10402
;; EARLIER FILING DATE: 1996-06-14
;; EARLIER APPLICATION NUMBER: 60/000,263
;; EARLIER FILING DATE: 1995-06-16
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 367
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-08-990-379-6

Query Match 27.2%; Score 425; DB 2; Length 367;
Best Local Similarity 34.3%; Pred. No. 6.3e-38;
Matches 104; Conservative 48; Mismatches 129; Indels 22; Gaps 5;

QY 15 LVALLSEGTETKVLIDSRPFVEYNTSHILEAININCSKLMKRLQODKVLITELIOHSAK 74
DB 13 LRALLRREGAQCULLDCRSFFAFNAGHTAGSVNVRFSFIVRRRAKAGMLEHIYPNAELR 72
QY 75 HKVDIDCSQKVVVYDQSSQDVASLSSDCFLTLLGKL--EKSFNSVHLLAGGFAEFSRCF 132
DB 73 GRLLAGYHAVVLLDEBSASLDGAKRQDTLALAGALCREARSTQVFFLQGGYAFSASC 132
QY 133 PGLCEGKSTLVPTCISQP-----CLPVANI-----GPTRLPLNLYLCCQGDVL 175
DB 133 PELCSKOST--PTGLSLPLSTSVDPDSAESGSSCSTPLYDQGVLEILSFYLSAYHAS 190
QY 176 NKEILQONGIGVYLNASVTCRPPDPIPSHFLRPVNSDFCEKILPWLDSKVDPIFEKAKA 235
DB 191 RKMULDALGITALLINVSANCN-HFEGHYQYKSLPVEDNKHADISSWFNEAIDFTDISIKD 249
QY 236 SNGCVLVHCLAGISSRSATIAIYIMKMDMSLDEAYRFVEKRPITSPNPNFLQGLDYE 295
DB 250 AGRVFVHCOAGISRSATICTIAYIMRTNRVYLDEAFEFVQRRSIISPNFSFWGQLQFE 309
QY 296 KKI 298
DB 310 SQV 312

RESULT 12
US-08-530-290-23
; Sequence 23, Application US/08530290
; Patent No. 5958721
; GENERAL INFORMATION:
; APPLICANT: Marshall, Christopher John
; APPLICANT: Ashworth, Alan
; APPLICANT: Hughes, David Anthony
; TITLE OF INVENTION: Method for Screening of Substances for
; TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,290
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB94/00694
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9402573.1
; FILING DATE: 10-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9307250.2
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Basilian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 084611-000000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-530-290-23

Query Match 27.2%; Score 425; DB 2; Length 394;
Best Local Similarity 33.1%; Pred. No. 7e-38;
Matches 99; Conservative 62; Mismatches 116; Indels 22; Gaps 8;

QY 19 LESGTEKVLIDSRPVEYNTSHILEAININCSKLMKRLQODKVLITELI--QHSAGHK 76
DB LPSSG-GKCLLDRCRPLHSAAGYILGSVNVRCNTIVRR-AGSGVSLQILPAEEVVAR 96
QY 77 VDIDSGQKVVVYDSSQDVASLSDCFVLTLGKLEKSF--NSVHLAGFAEFSRCPG 134
DB LRSGLYSAVIYDERSPRAESLRDSTVSLVQALRRNAERTDCLLKGYSERSESEYE 156
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPMLYLGGORDVANKEL 179
DB FCSKTKALAAIPPPVPSPATEPLDLDCSSCGTPLHDGSPVEILPFLYLSAYHAAARDM 216
QY 157 FCSKTKALAAIPPPVPSPATEPLDLDCSSCGTPLHDGSPVEILPFLYLSAYHAAARDM 216
DB 97 LRSGLYSAVIYDERSPRAESLRDSTVSLVQALRRNAERTDCLLKGYSERSESEYE 156
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPMLYLGGORDVANKEL 179
DB 157 FCSKTKALAAIPPPVPSPATEPLDLDCSSCGTPLHDGSPVEILPFLYLSAYHAAARDM 216
QY 180 IQONGIGVVLNASYTCPEKDFIPESHFLRVPNDSFCEKILPMLDKSVDFTEKAKASNGC 239
DB 217 LDALGITLALNVSSDCPN-HFEGHYQYKCIPEVDNHRKADISWMEALEYIDAVYDCRGR 275
QY 240 VLVHCLAGISRSATIAIAYIMKRMDSIDEAYRFVKEKRPITSPNPNLQGLLDYEKKI 298

DB 276 VLVHCLAGISRSATIAIAYIMKRMDSIDEAYRFVKEKRPITSPNPNLQGLLDYEKKI 334
RESULT 13
US-09-702-705-805
; Sequence 805, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-702-705-805

Query Match 27.2%; Score 425; DB 4; Length 394;
Best Local Similarity 33.1%; Pred. No. 7e-38;
Matches 99; Conservative 62; Mismatches 116; Indels 22; Gaps 8;

QY 19 LESGTEKVLIDSRPVEYNTSHILEAININCSKLMKRLQODKVLITELI--QHSAGHK 76
DB LPSSG-GKCLLDRCRPLHSAAGYILGSVNVRCNTIVRR-AGSGVSLQILPAEEVVAR 96
QY 77 VDIDSGQKVVVYDSSQDVASLSDCFVLTLGKLEKSF--NSVHLAGFAEFSRCPG 134
DB LRSGLYSAVIYDERSPRAESLRDSTVSLVQALRRNAERTDCLLKGYSERSESEYE 156
QY 97 LRSGLYSAVIYDERSPRAESLRDSTVSLVQALRRNAERTDCLLKGYSERSESEYE 156
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPMLYLGGORDVANKEL 179
DB FCSKTKALAAIPPPVPSPATEPLDLDCSSCGTPLHDGSPVEILPFLYLSAYHAAARDM 216
QY 157 FCSKTKALAAIPPPVPSPATEPLDLDCSSCGTPLHDGSPVEILPFLYLSAYHAAARDM 216
DB 97 LRSGLYSAVIYDERSPRAESLRDSTVSLVQALRRNAERTDCLLKGYSERSESEYE 156
QY 180 IQONGIGVVLNASYTCPEKDFIPESHFLRVPNDSFCEKILPMLDKSVDFTEKAKASNGC 239
DB 217 LDALGITLALNVSSDCPN-HFEGHYQYKCIPEVDNHRKADISWMEALEYIDAVYDCRGR 275
QY 240 VLVHCLAGISRSATIAIAYIMKRMDSIDEAYRFVKEKRPITSPNPNLQGLLDYEKKI 298
DB 276 VLVHCLAGISRSATIAIAYIMKRMDSIDEAYRFVKEKRPITSPNPNLQGLLDYEKKI 334

RESULT 14
US-09-702-705-827
; Sequence 827, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14

```

; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 827
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-827
```

```

Query Match          27.2%; Score 425; DB 4; Length 394;
Best Local Similarity 33.4%; Pred. No. 7e-36;
Matches 100; Conservative 64; Mismatches 113; Indels 22; Gaps 9;
```

```

QY 19 LESGTEKVLIDSRPEVEYNTSHLEAININCSKLMKRLQODKYLITELI--QHSAGHK 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 LPSSG-GKCLLDRCRFLAHSAAYILGSAVVRNTYVRRR-AGSVSLQDILPAEEVVAR 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 VDIDCSQKVVYDQSSQDVASLSSDCFTVLIGKLEKSF--NSVHLLAGFAEFSRCFPG 134
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
DB 97 LRSGLYSAVIYVDERSPRAESLRDSTVSLVQALRRNAERTDICLKGGERFSSEYPE 156
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 135 LCEGKSTL-----VPTCISQP-----C-LPVANI-CPTILPNLYIGCORVDLANKEL 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 FCSKTKALAAIPPPVPPSPATEPPLDGCSSCGTPLHDGGPVAILPFLYLSAAYHAARDM 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 IQONGIGVYLNASYTCPKPDFIPESHFLRPVNDSEFCSEKILPWLDKSVDFIEKAKASNGC 239
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DB 217 LDALGITLALNVSSDCPN-HFEGHYQYKCIPIVEDNHKADISSWFEALIEYIDAVDCRGR 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 240 VLVHCLAGISRSATITAIYIMKRMDSLDEAYRFPYKERRPTISPNFNLGQLLDYEKKI 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 276 VLVHCQAGISRSATITCLAYIMMKRRVRLAEAFVKKRRSITSPNFSFGQLQFESQV 334
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RESULT 15
US-09-736-457-805
; Sequence 805, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
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; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-805
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Query Match          27.2%; Score 425; DB 4; Length 394;
Best Local Similarity 33.1%; Pred. No. 7e-36;
Matches 99; Conservative 62; Mismatches 116; Indels 22; Gaps 8;
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DB 39 LPSSG-GKCLLDRCRFLAHSAAYILGSAVVRNTYVRRR-AGSVSLQDILPAEEVVAR 96
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QY 77 VDIDCSQKVVYDQSSQDVASLSSDCFTVLIGKLEKSF--NSVHLLAGFAEFSRCFPG 134
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DB 97 LRSGLYSAVIYVDERSPRAESLRDSTVSLVQALRRNAERTDICLKGGERFSSEYPE 156
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QY 135 LCEGKSTL-----VPTCISQP-----C-LPVANI-CPTILPNLYIGCORVDLANKEL 179
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DB 157 FCSKTKALAAIPPPVPPSPATEPPLDGCSSCGTPLHDGGPVAILPFLYLSAAYHAARDM 216
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QY 240 VLVHCLAGISRSATITAIYIMKRMDSLDEAYRFPYKERRPTISPNFNLGQLLDYEKKI 298
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Search completed: February 9, 2005, 12:13:09
Job time : 20.363 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 12:09:54 ; Search time 57.152 Seconds
(without alignments)
1721.062 Million cell updates/sec

Title: US-10-029-345a-109_COPY_1_302
Perfect score: 1564
Sequence: 1 MAHEMIGQIVTERLVALL.....PNNFLGQLDYKKIKKQT 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	99.2	662	15	US-10-072-012-258
2	1552	99.2	665	9	US-09-816-494-2
3	1552	99.2	665	9	US-09-964-277-2
4	1552	99.2	665	15	US-10-377-072-26
5	1552	99.2	665	15	US-10-072-012-660
6	1552	99.2	665	15	US-10-168-506-14
7	1552	99.2	665	15	US-10-343-357-7
8	1552	99.2	665	15	US-10-257-026-2
9	1552	99.2	665	16	US-10-648-593-240
10	1552	99.2	665	16	US-10-648-593-247
11	1552	99.2	665	16	US-10-377-072-26
12	1552	99.2	690	15	US-10-072-012-679
13	1552	99.2	690	15	US-10-072-012-703

14	1552	99.2	690	15	US-10-425-114-54204	Sequence 54204, A
15	1545	98.8	665	15	US-10-094-749-2312	Sequence 2312, Ap
16	1545	98.8	665	15	US-10-072-012-681	Sequence 681, App
17	1544	98.7	672	15	US-10-295-115-1259	Sequence 1259, Ap
18	1517	97.0	660	15	US-10-072-012-682	Sequence 682, App
19	1514	96.8	677	15	US-10-072-012-683	Sequence 683, App
20	1504.5	96.2	680	15	US-10-072-012-256	Sequence 256, App
21	988	63.2	625	15	US-10-072-012-699	Sequence 699, App
22	985	63.0	663	15	US-10-072-012-700	Sequence 700, App
23	837	53.5	616	15	US-10-072-012-266	Sequence 266, App
24	807	51.6	155	9	US-09-964-277-7	Sequence 7, Appl
25	654.5	41.8	169	14	US-10-346-356-15	Sequence 15, Appl
26	654.5	41.8	170	9	US-09-775-925-26	Sequence 26, Appl
27	654.5	41.8	170	9	US-09-847-519A-11	Sequence 11, Appl
28	654.5	41.8	170	14	US-10-314-058-14	Sequence 14, Appl
29	654.5	41.8	170	14	US-10-405-808-16	Sequence 16, Appl
30	654.5	41.8	170	15	US-10-655-073-16	Sequence 16, Appl
31	646	41.3	517	9	US-09-964-277-21	Sequence 21, Appl
32	631.5	40.4	461	15	US-10-072-012-701	Sequence 701, App
33	620	39.6	501	15	US-10-072-012-702	Sequence 702, App
34	619	39.6	155	9	US-09-964-277-6	Sequence 6, Appl
35	619	39.6	155	9	US-09-955-732-6	Sequence 6, Appl
36	566	36.2	140	17	US-10-803-738-12	Sequence 12, Appl
37	469	30.0	444	9	US-09-964-899-47	Sequence 47, Appl
38	469	30.0	482	14	US-10-346-356-2	Sequence 2, Appl
39	469	30.0	482	15	US-10-058-270A-130	Sequence 130, App
40	469	30.0	482	16	US-10-648-593-164	Sequence 164, App
41	462.5	29.6	381	14	US-10-184-832-2	Sequence 2, Appl
42	440.5	28.2	419	16	US-10-472-380-2	Sequence 25, Appl
43	426	27.2	394	14	US-10-060-065-25	Sequence 46, Appl
44	426	27.2	394	14	US-10-059-585-46	Sequence 805, App
45	425	27.2	394	9	US-09-736-457-805	

ALIGNMENTS

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RESULT 1
US-10-072-012-258
; Sequence 258, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tehernev, Vellizar
; APPLICANT: Spyrek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patnirajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Baha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alasbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
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/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 258
/ LENGTH: 662
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-258
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Best Local Similarity 99.3%; Pred. No. 2,1e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MAHEMIGTQIVTERLVALLSSTGTEKVLIDSRPFVEYNTSHILEAININCSKLMKRLQ 60
QY 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSODVASLSDCFLTVLLGKLEKSFNSVHL 120
DB 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSODVASLSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGFAFSPRCFPGLCGKSTLVPTCISOPCLPVANIGPTRIIPNLVYGQORDVANKELI 180
DB 121 LAGFAFSPRCFPGLCGKSTLVPTCISOPCLPVANIGPTRIIPNLVYGQORDVANKELI 180
QY 181 QONGIGYVLNASYTCPEKDFIPESHFLRVPNVDSFCEKILPWLKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLNASYTCPEKDFIPESHFLRVPNVDSFCEKILPWLKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAYIMKMDMSLDEAYRFVKEKPTISPNNFLGQLLDYEKKIKN 300
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RESULT 2
US-09-816-494-2
/ Sequence 2, Application US/09816494
/ Patent No. US20020034807A1
/ GENERAL INFORMATION:
/ APPLICANT: Meyers, Rachel A.
/ TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
/ FILE REFERENCE: 10448-030002
/ CURRENT APPLICATION NUMBER: US/09/816,494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 60/191,858
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 665
/ TYPE: PRT
/ ORGANISM: Homo sapiens
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US-09-816-494-2

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Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSODVASLSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGFAFSPRCFPGLCGKSTLVPTCISOPCLPVANIGPTRIIPNLVYGQORDVANKELI 180
DB 121 LAGFAFSPRCFPGLCGKSTLVPTCISOPCLPVANIGPTRIIPNLVYGQORDVANKELI 180
QY 181 QONGIGYVLNASYTCPEKDFIPESHFLRVPNVDSFCEKILPWLKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLNASYTCPEKDFIPESHFLRVPNVDSFCEKILPWLKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAYIMKMDMSLDEAYRFVKEKPTISPNNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAYIMKMDMSLDEAYRFVKEKPTISPNNFLGQLLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302
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RESULT 3
US-09-964-277-2

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/ Sequence 2, Application US/09964277
/ Patent No. US20020137170A1
/ GENERAL INFORMATION:
/ APPLICANT: Luche, Ralf M.
/ TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
/ FILE REFERENCE: 200125,434
/ CURRENT APPLICATION NUMBER: US/09/964,277
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 665
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-964-277-2
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Query Match          99.2%; Score 1552; DB 9; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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RESULT 4

US-10-377-072-26
Sequence 26, Application US/10377072
Publication No. US2004009501A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Tsai, Peng-Ying
APPLICANT: Chun, Mlyoung
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
FILE REFERENCE: MP103-0180NMIM
CURRENT APPLICATION NUMBER: US/10/377, 072
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 665
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-377-072-26

Query Match 99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2,2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMGTOTVTERVALVLESGETEKLILDSRFEVFNTHSHLEAININCSKLMKRRLQ 60
Db 1 MAHEMGTOTVTERVALVLESGETEKLILDSRFEVFNTHSHLEAININCSKLMKRRLQ 60
QY 61 DKVLITELIQHSAKHKVDIDSCQKVVVYDQSSQDVASISSDCFLTVLLGKLEKSFNSVHL 120
Db 61 DKVLITELIQHSAKHKVDIDSCQKVVVYDQSSQDVASISSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGGFABRRCFPGLECGKSTVPTCTISQPCLPVANIIGFRLIPNLYLGGQDVANKELI 180
Db 121 LAGGFABRRCFPGLECGKSTVPTCTISQPCLPVANIIGFRLIPNLYLGGQDVANKELI 180
QY 181 QONGIGVYVNASATCPKDPFIPESHFLRVVNDSPCEKILPMLDKSVDFIEKAKASNGCV 240
Db 181 QONGIGVYVNASATCPKDPFIPESHFLRVVNDSPCEKILPMLDKSVDFIEKAKASNGCV 240

Db 181 QONGIGVYVNASATCPKDPFIPESHFLRVVNDSPCEKILPMLDKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATIAIAYMKRMDSLDEAYRFVKEKRPITSPNPFGLQLLDYEKIKN 300
Db 241 LVHCLAGISRSATIAIAYMKRMDSLDEAYRFVKEKRPITSPNPFGLQLLDYEKIKN 300
QY 301 QT 302
Db 301 QT 302

RESULT 5

US-10-072-012-680
Sequence 680, Application US/10072012
Publication No. US2004003493A1
GENERAL INFORMATION:
APPLICANT: Tchernyev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zehnusen, Bryan
APPLICANT: Patnursajan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esba
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Molenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Groesse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: Patencin Ver. 2.1
SEQ ID NO 680
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-680

Query Match 99.2%; Score 1552; DB 15; Length 665;

Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPFVEYNTSHILEAININCSKMKRRLOO 60
DB 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPFVEYNTSHILEAININCSKMKRRLOO 60
QY 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDCFITVLIGLKEKSPNSVHL 120
DB 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDCFITVLIGLKEKSPNSVHL 120
QY 121 LAGGFAFSRCFPGLCGKSTIVPTCISQPCLPVANIGPTRILPNLYLGGQDVINKELI 180
DB 121 LAGGFAFSRCFPGLCGKSTIVPTCISQPCLPVANIGPTRILPNLYLGGQDVINKELI 180
QY 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLDKSVDFTEKAKANGCV 240
DB 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLDKSVDFTEKAKANGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPPTISPENFPLGQLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPPTISPENFPLGQLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302
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RESULT 6

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US-10-168-506-14
; Sequence 14, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANNAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168,506
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-506-14
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Query Match 99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPFVEYNTSHILEAININCSKMKRRLOO 60
DB 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPFVEYNTSHILEAININCSKMKRRLOO 60
QY 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDCFITVLIGLKEKSPNSVHL 120
DB 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDCFITVLIGLKEKSPNSVHL 120
QY 121 LAGGFAFSRCFPGLCGKSTIVPTCISQPCLPVANIGPTRILPNLYLGGQDVINKELI 180
DB 121 LAGGFAFSRCFPGLCGKSTIVPTCISQPCLPVANIGPTRILPNLYLGGQDVINKELI 180
QY 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLDKSVDFTEKAKANGCV 240
DB 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLDKSVDFTEKAKANGCV 240
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QY 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPPTISPENFPLGQLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPPTISPENFPLGQLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302
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RESULT 7

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US-10-343-357-7
; Sequence 7, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: ELIOTT, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HARALIA, April J.A.
; APPLICANT: LU, Dying Aina M.; TRIBOUTY, Catherine M.
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Daniel B.; CHAWLA, Nandinder K.
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: US/10/343,357
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CD1
US-10-343-357-7
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Query Match 99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPFVEYNTSHILEAININCSKMKRRLOO 60
DB 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPFVEYNTSHILEAININCSKMKRRLOO 60
QY 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDCFITVLIGLKEKSPNSVHL 120
DB 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDCFITVLIGLKEKSPNSVHL 120
QY 121 LAGGFAFSRCFPGLCGKSTIVPTCISQPCLPVANIGPTRILPNLYLGGQDVINKELI 180
DB 121 LAGGFAFSRCFPGLCGKSTIVPTCISQPCLPVANIGPTRILPNLYLGGQDVINKELI 180
QY 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLDKSVDFTEKAKANGCV 240
DB 181 QONGIGVYLNASTYCPKDPFIPESHFLRPVNDSPCEKILPWLDKSVDFTEKAKANGCV 240
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Db 181 QONGIGYVLMASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
Qy 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFLGQLLDYEKKIN 300
Db 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFLGQLLDYEKKIN 300
Qy 301 QT 302
Db 301 QT 302

RESULT 8

US-10-257-026-2
; Sequence 2, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KXMS
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-026-2

Query Match 99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAHEMIGTQIVTERLVALLSEGTKEVLLIDSRPFVEYNTSHLEAININCSKLMKRRLQ 60
Db 1 MAHEMIGTQIVTERLVALLSEGTKEVLLIDSRPFVEYNTSHLEAININCSKLMKRRLQ 60
Qy 61 DKVLTTELIOHSAKHKVIDCSQKVVYDOSQDVASLSDCFITVLLGKLEKSFNSVHL 120
Db 61 DKVLTTELIOHSAKHKVIDCSQKVVYDOSQDVASLSDCFITVLLGKLEKSFNSVHL 120
Qy 121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
Db 121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
Qy 181 QONGIGYVLMASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
Db 181 QONGIGYVLMASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
Qy 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFLGQLLDYEKKIN 300
Db 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFLGQLLDYEKKIN 300
Qy 301 QT 302
Db 301 QT 302

RESULT 9

US-10-648-593-240
; Sequence 240, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557

; SOFTWARE: Patentin version 3.2
; SEQ ID NO 240
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-240

Query Match 99.2%; Score 1552; DB 16; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAHEMIGTQIVTERLVALLSEGTKEVLLIDSRPFVEYNTSHLEAININCSKLMKRRLQ 60
Db 1 MAHEMIGTQIVTERLVALLSEGTKEVLLIDSRPFVEYNTSHLEAININCSKLMKRRLQ 60
Qy 61 DKVLTTELIOHSAKHKVIDCSQKVVYDOSQDVASLSDCFITVLLGKLEKSFNSVHL 120
Db 61 DKVLTTELIOHSAKHKVIDCSQKVVYDOSQDVASLSDCFITVLLGKLEKSFNSVHL 120
Qy 121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
Db 121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
Qy 181 QONGIGYVLMASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
Db 181 QONGIGYVLMASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
Qy 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFLGQLLDYEKKIN 300
Db 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFLGQLLDYEKKIN 300
Qy 301 QT 302
Db 301 QT 302

RESULT 10

US-10-648-593-247
; Sequence 247, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 247
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-247

Query Match 99.2%; Score 1552; DB 16; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAHEMIGTQIVTERLVALLSEGTKEVLLIDSRPFVEYNTSHLEAININCSKLMKRRLQ 60
Db 1 MAHEMIGTQIVTERLVALLSEGTKEVLLIDSRPFVEYNTSHLEAININCSKLMKRRLQ 60
Qy 61 DKVLTTELIOHSAKHKVIDCSQKVVYDOSQDVASLSDCFITVLLGKLEKSFNSVHL 120
Db 61 DKVLTTELIOHSAKHKVIDCSQKVVYDOSQDVASLSDCFITVLLGKLEKSFNSVHL 120
Qy 121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
Db 121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180

61 DKVLTELIQHSAKHKVDIDCSQKVVYDDOSSQDVASLSSDCFLTVLGKLEKSFNSVHL 120

Remaining Prior Application data removed - See File Wrapper or PALM.
PRIOR FILING DATE: 2001-02-06

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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 679
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-679

Query Match      99.2% Score 1552; DB 15; Length 690;
Best Local Similarity 99.3%; Pred. No. 2.3e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRLQO 60
DB 26 MAHEMIGTQIVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRLQO 85
QY 61 DKVLTTELIOHSAKAKVIDCSQKVVYVDOSSQDVASLSSDCLFYLLGKLEKSPSVHL 120
DB 86 DKVLTTELIOHSAKAKVIDCSQKVVYVDOSSQDVASLSSDCLFYLLGKLEKSPSVHL 145
QY 121 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPMLYLGQORDVANKELI 180
DB 146 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPMLYLGQORDVANKELI 205
QY 181 QONGIGYVLMASNTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKSNGCV 240
DB 206 QONGIGYVLMASNTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKSNGCV 265
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITSPNFFLGQLLDYEKKIK 300
DB 266 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITSPNFFLGQLLDYEKKIK 325
QY 301 QT 302
DB 326 QT 327

RESULT 13
US-10-072-012-703
; Sequence 703, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernyev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Patuturajan, Weera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Beha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Raastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupler Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsdbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072, 012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265, 514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265, 517

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; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265, 412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265, 395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266, 406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266, 767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267, 057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266, 975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267, 459
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 703
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-703

Query Match      99.2% Score 1552; DB 15; Length 690;
Best Local Similarity 99.3%; Pred. No. 2.3e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRLQO 60
DB 26 MAHEMIGTQIVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRLQO 85
QY 61 DKVLTTELIOHSAKAKVIDCSQKVVYVDOSSQDVASLSSDCLFYLLGKLEKSPSVHL 120
DB 86 DKVLTTELIOHSAKAKVIDCSQKVVYVDOSSQDVASLSSDCLFYLLGKLEKSPSVHL 145
QY 121 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPMLYLGQORDVANKELI 180
DB 146 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPMLYLGQORDVANKELI 205
QY 181 QONGIGYVLMASNTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKSNGCV 240
DB 206 QONGIGYVLMASNTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKSNGCV 265
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITSPNFFLGQLLDYEKKIK 300
DB 266 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITSPNFFLGQLLDYEKKIK 325
QY 301 QT 302
DB 326 QT 327

RESULT 14
US-10-425-114-54204
; Sequence 54204, Application US/10425114
; Publication No. US20040034688A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54204
; LENGTH: 690
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: clone ID: LTB4119-028-H6_FLI pep
US-10-425-114-54204

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Query Match	99.2%	Score 1552;	DB 15;	Length 690;
Best Local Similarity	99.3%	Pred. No. 2.3e-143;		
Matches 300; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	MAHEMIGTOIVTERLVAALLESGETEKVILIDSRPFVEVNTSHILEAININCSKMKRRLQ	60
Dh	MAHEMIGTOIVTERLVAALLESGETEKVILIDSRPFVEVNTSHILEAININCSKMKRRLQ	85
Qy	DKVLITIELLOHSAKXKXVDIDCSQKVVVYDQSSQDVAISSDPCITVLTLGKLEKSPNSVHL	120
Dh	DKVLITIELLOHSAKXKXVDIDCSQKVVVYDQSSQDVAISSDPCITVLTLGKLEKSPNSVHL	145
Qy	LAGGPAFBSRCPFGLECEKSTLVPTICISQPCLPVANIIPTRILPMLYGCORVDYANKELI	180
Dh	LAGGPAFBSRCPFGLECEKSTLVPTICISQPCLPVANIIPTRILPMLYGCORVDYANKELI	205
Qy	QONGIGVYLNASTTCRKPDPPIBESHFLRPVNDSECEKILPMLDKSDVLEKAAVNSGCV	240
Dh	QONGIGVYLNASTTCRKPDPPIBESHFLRPVNDSECEKILPMLDKSDVLEKAAVNSGCV	265
Qy	LVHCLAGISRSATIAIAYIMKMDMSLDIAAYFVFEKASPTISPNPNFAGOLLDEVKIKIN	300
Dh	LVHCLAGISRSATIAIAYIMKMDMSLDIAAYFVFEKASPTISPNPNFAGOLLDEVKIKIN	325
Qy	QT 302	
Dh	QT 327	

Query Match	98.8%	Score 1545;	DB 15;	Length 665;
Best Local Similarity	99.0%	Pred. No. 1e-142;		
Matches 299; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0

Qy	1	MAHEMIGTOIYVERLIVALLESTGEKVLLIDSRPFVENVSHILKAINNOSKJMKRRLQ	60
Db	1	MAHEMIGTOIYVERLIVALLESTGEKVLLIDSRPFVENVSHILKAINNOSKJMKRRLQ	60
Qy	61	DKYLITELLQHSKAKHVDIDCSQKVVVDOSSODVASLSDCFLTVLLGKLEKFSNSVHL	120
Db	61	DKYLITELLQHSKAKHVDIDCSQKVVVDOSSQDVASLSDCFLTVLLGKLEKFSNSVHL	120
Qy	121	LAGEFAEFSRCEPGLCEGKSTLVPTCISQPLPVANIGPTRILPNLYLGCQRDVLANKEI	180
Db	121	LAGEFAEFSRCEPGLCEGKSTLVPTCISQPLPVANIGPTRILPNLYLGCQRDVLANKEI	180
Qy	181	QONGIGYVLNASYTCPKPDIPESHFLFVPVNDSECEKILFMDLKSVDPIEKAVASNGCV	240
Db	181	QONGIGYVLNASYTCPKPDIPESHFLFVPVNDSECEKILFMDLKSVDPIEKAVASNGCV	240
Qy	241	LVHCLAGISRSATIAIYIMKMDSLDEAIVFYKEKRPITISPNFNLGQLLDYEKKIKN	300
Db	241	LVHCLAGISRSATIAIYIMKMDSLDEAIVFYKEKRPITISPNFNLGQLLDYEKKIKN	300
Qy	301	QT 302	
Db	301	QT 302	

Search completed: February 9, 2005, 12:28:42
Job time : 58.152 secs

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RESULT 15
US-10-094-749-2312
Sequence 2312, Application US/10094749
GENERAL INFORMATION:
  APPLICANT: ISOGAI, TAKAO
  APPLICANT: SUGIYAMA, TOMOYASU
  APPLICANT: OTSUKI, TETSUJI
  APPLICANT: MAKAMATSU, AI
  APPLICANT: SATO, HIROYUKI
  APPLICANT: ISHII, SHIZUO
  APPLICANT: YAMAMOTO, JUN-ICHI
  APPLICANT: ISONO, YUUKO
  APPLICANT: HIO, YURI
  APPLICANT: OTSUKA, KAORU
  APPLICANT: NAGAI, KEIICHI
  APPLICANT: IRIE, RYOTARO
  APPLICANT: TAMECHIKA, ICHIRO
  APPLICANT: SEKI, NAOHICO
  APPLICANT: YOSHIKAWA, TSUTOMU
  APPLICANT: OTSUKA, MOTOKI
  APPLICANT: NAGAHARI, KENJI
  APPLICANT: MASUHO, YASUHIKO
  TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
  FILE REFERENCE: 08435/0160
  CURRENT APPLICATION NUMBER: US/10/094,749
  CURRENT FILING DATE: 2002-03-12
  PRIOR APPLICATION NUMBER: 60/350,435
  PRIOR FILING DATE: 2002-01-24
  PRIOR APPLICATION NUMBER: JP 2001-328381
  PRIOR FILING DATE: 2001-09-14
  NUMBER OF SEQ ID NOS: 3381
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 2312
  LENGTH: 665
  TYPE: PRT
  ORGANISM: Homo sapiens
  OS=10-094-749-2312

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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 14, 2005, 09:42:14 ; Search time 133.355 Seconds
(without alignments)
3705.573 Million cell updates/sec

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Perfect score: 1564
Sequence: 1 MAHEMIGQIVTERLVALL.....PNNFNLGQLDYKKIKKQ 302

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	99.2	1998	4	US-09-816-494-3
2	1552	99.2	3544	4	US-09-816-494-1
3	989	63.2	2351	4	US-09-949-016-3250
4	988	63.2	2377	4	US-09-920-668-3
5	475	30.4	333	4	US-09-513-999C-2877
6	469	30.0	1830	4	US-09-557-921-1
7	467.5	29.9	2109	4	US-09-016-434-1135
8	467.5	29.9	2109	4	US-09-023-655-946
9	466.5	29.8	2475	4	US-09-949-016-2615
10	464.5	29.7	13782	4	US-09-949-016-14992
11	426	27.2	2240	4	US-09-016-434-1100
12	425	27.2	944	4	US-09-371-671B-10

13	425	27.2	1238	2	US-08-530-230-11	Sequence 11, Appl
14	425	27.2	1238	4	US-09-702-705-803	Sequence 803, App
15	425	27.2	1238	4	US-09-736-457-803	Sequence 803, App
16	425	27.2	1238	4	US-09-614-124B-803	Sequence 803, App
17	425	27.2	1238	4	US-09-671-325-803	Sequence 803, App
18	425	27.2	1238	4	US-09-589-184-803	Sequence 803, App
19	425	27.2	1238	4	US-09-658-824-803	Sequence 803, App
20	425	27.2	1238	4	US-09-702-705-825	Sequence 825, App
21	425	27.2	1238	4	US-09-736-457-825	Sequence 825, App
22	425	27.2	1238	4	US-09-614-124B-825	Sequence 825, App
23	425	27.2	1238	4	US-09-671-325-825	Sequence 825, App
24	425	27.2	1238	4	US-09-589-184-825	Sequence 825, App
25	425	27.2	1238	4	US-09-658-824-825	Sequence 825, App
26	425	27.2	1238	4	US-09-702-705-826	Sequence 826, App
27	425	27.2	1238	4	US-09-736-457-826	Sequence 826, App
28	425	27.2	1238	4	US-09-614-124B-826	Sequence 826, App
29	425	27.2	1238	4	US-09-671-325-826	Sequence 826, App
30	425	27.2	1238	4	US-09-589-184-826	Sequence 826, App
31	425	27.2	1238	4	US-09-658-824-826	Sequence 826, App
32	425	27.2	1238	4	US-09-702-705-826	Sequence 826, App
33	423.5	27.1	1993	2	US-08-990-379-2	Sequence 2, Appl
34	415	26.5	2000	4	US-09-016-434-1291	Sequence 1291, Ap
35	415	26.5	2000	4	US-09-918-497-10	Sequence 10, Appl
36	415	26.5	2015	4	US-09-949-016-4969	Sequence 4969, Ap
37	408	26.1	2283	4	US-09-949-016-4617	Sequence 4617, Ap
38	408	26.1	2303	4	US-09-922-146-3	Sequence 3, Appl
39	382	24.4	1987	2	US-08-990-379-1	Sequence 1, Appl
40	380	24.3	279	4	US-09-016-434-91	Sequence 91, Appl
41	357	22.8	1619	4	US-09-702-705-801	Sequence 801, App
42	357	22.8	1619	4	US-09-736-457-801	Sequence 801, App
43	357	22.8	1619	4	US-09-614-124B-801	Sequence 801, App
44	357	22.8	1619	4	US-09-671-325-801	Sequence 801, App
45	357	22.8	1619	4	US-09-589-184-801	Sequence 801, App

ALIGNMENTS

RESULT 1
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816, 494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3
Alignment Scores:
Pred. No.: 2.74e-200
Score: 1552.00
Length: 1998
Matches: 300
Percent Similarity: 99.67%
Best Local Similarity: 99.34%
Mismatch: 1
Query Match: 99.23%
Indels: 0
Gaps: 0
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QY 1 MetLAHAGTUMETIEGLYThGInleValThrgluArgLeuValAlaLeuLeu 20
DB 1 ATGCCCATGAGATTCGAACTCAATTCCTAGAGAGCTGCTCTCGGAA 60
QY 21 SerGlyThrgluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40

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Db      61 AGTGAACGGAAGAAAGTGTGTAATTGATGCGCGCATTTGTGAATATCAATATATCC 120
Qy      41 HsilleuGlua1a1leaenlleaenCyserleuMeu1eYargleuGln 60
Db      121 CACATTTTGGAAAGCCATTAATATCAACTGCTCCAACTTATGAAGGAGTTGGCAACAG 180
Qy      61 AspLyValleu1leThrgleu1leGlnHsSerAlaYshlsYValAsp1leAaP 80
Db      181 GACAAAGTGTAAATTCAGAGCTCATCCAGCATTCAGCAAAACATAGATTGACATTGAT 240
Qy      81 CySerGlnuYValValValYraSpGlnSerSerGlnAspValAlaSerLeuSer 100
Db      241 TGCAGTCAGAAAGTTGATTAGATCAATCAAGCTCCCAAGATGTTGCTCTCTCTCA 300
Qy      101 AspCyPheLeuThrValleu1leuGlyYValleuGlnuYSerPheAsnSerValHsleu 120
Db      301 GACTGTTTCTCAGCTGACTTCTGGGTAAACTGGAGAAAGCTTCAACTCTGTCACCTG 360
Qy      121 LeuAlaGlyGlyPheAlaGluPheSerArgCyPheProGlyLeuCyGlnGlyYSer 140
Db      361 CTTCGACGTGGGTTGCTGATGTTCTCTGTTGTTCCCTGCTCTGTAAAGAAATCC 420
Qy      141 ThrLeuValProThrCysIleSerGlnProCySleuProValAlaAsn1leGlyProThr 160
Db      421 ACTCTAGTCCCTACCTGACATTTCTCAGCCTTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy      161 Arg1leuProAsnLeuThrleuGlyCySglnArgAspValleuAsn1leGlyleu 180
Db      481 CGAATTTCTCCCAATCTTATCTGTGGCTCCAGCCAGATGCTCTCAACAAAGAGCTGAG 540
Qy      181 GlnGlnAsnGly1leGlyYrValleuAsnAlaSerYrThrCyProLySerProAspPhe 200
Db      541 CAGCAAGATGGAGTTGATTATGTTAATGCCAGCAATCCTGCTCCAAAGCTGACTTT 600
Qy      201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnuYSer 220
Db      601 ATCCCCGAGTCCATTTCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy      221 ProTrpLeuAspLySerValAspPhe1leGlnuYValAlaValAlaSerPheGlyYSer 240
Db      661 CCGGTGTGGACAAATCAGTAATTCATATGAGAAAGCAAAAGCCCTCCAAATGAGATGTT 720
Qy      241 LeuValHsCySleuAlaGlyIleSerArgSerAlaThr1leAla1leAlaYr1leMet 260
Db      721 CTAGGCACTGTTTGGTGGATCTCCGCTCCGCAACCATGCTATGCTCATCATC 780
Qy      261 LysArgMetAspMetSerLeuAspGlnAlaYrArgPheValYsGlnuYSerProThr 280
Db      781 AAGAGATGACATGCTTTAGATGAGCTTACAGATTTGTGAAAGAAAGAAAGAAAGCTT 840
Qy      281 IleSerProAsnPheAsnPheLeuGlyGlnleuAspYrGlnuYSer1leYsAsn 300
Db      841 AATATCTCCAAACTCAATTTCTGGGCCAACTCTCGACTATGAGAAAGATTAAGAAC 900
Qy      301 GlnThr 302
Db      901 CAGACT 906

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RESULT 2

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US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Alignment Scores:
Pred. No.: 7.39e-200 Length: 3544
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0

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Qy      1 MetAlaHsGlnMet1leGlyThrGln1leValThrgluArgLeuValAlaLeuGln 20
Db      589 ATGGCCCAATGAGATGATTGGAATCAATATGTTACTGAGAGTTGGTGGCTCTGCTGAA 648
Qy      21 SerGlyThrgluYsValleu1leu1eAspSerArgPropheValGluYrAsnThrSer 40
Db      649 AGTGAACGGAAGAAAGTCTCTAATGATAGTCCGCGCATTTGTGAAATCAATATCATCC 708
Qy      41 HsilleuGlua1a1leaenlleaenCyserleuMeu1eYargleuGln 60
Db      709 CACATTTTGGAAAGCCATTAATATCAACTGCTCCAAAGCTTATGAAAGCAAGGTTGCCAAC 768
Qy      61 AspLyValleu1leThrgleu1leGlnHsSerAlaYshlsYValAsp1leAaP 80
Db      769 GACAAAGTGTAAATTCAGAGCTCATCCAGCATTCAGCAAAACATAGATTGACATTGAT 828
Qy      81 CySerGlnuYsValValValYraSpGlnSerSerGlnAspValAlaSerLeuSer 100
Db      829 TGCAGTCAGAAAGTTGATTAGTTAATGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 888
Qy      101 AspCyPheLeuThrValleu1leuGlyYValleuGlnuYSerPheAsnSerValHsleu 120
Db      889 GACTGTTTCTCAGCTGATCTTCTGGGTAAACTGGAGAAAGAGCTTCAACTGTTCACTG 948
Qy      121 LeuAlaGlyGlyPheAlaGluPheSerArgCyPheProGlyLeuCyGlnGlyYSer 140
Db      949 CTTCGACGTGGGTTGCTGAGTTCTCTGTTGTTCCCTGCTCTGTGAGAAAGAAATCC 1008
Qy      141 ThrLeuValProThrCysIleSerGlnProCySleuProValAlaAsn1leGlyProThr 160
Db      1009 ACTCTAGTCCCTACCTGACATTTCTCAGCCTTGCTTACTGTGTCACATTTGGGCCAAC 1068
Qy      161 Arg1leuProAsnLeuThrleuGlyCySglnArgAspValleuAsn1leGlyleu 180
Db      1069 CGAATTTCTCCCAATCTTATCTTGGCTGCGCAGGAAATGCTTCCCAAGAGAGCTGATG 1128
Qy      181 GlnGlnAsnGly1leGlyYrValleuAsnAlaSerYrThrCyProLySerProAspPhe 200
Db      1129 CAGCAAGATGGAGTTGATTATGTTAATGCCAGCAATCCTGCTCCAAAGCTGACTTT 1188
Qy      201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnuYSer 220
Db      1189 ATCCCCGAGTCTATTTCTGCGGTGCTGCTGATGATGACGCTTTGTGAAAGAAATTTTG 1248
Qy      221 ProTrpLeuAspLySerValAspPhe1leGlnuYValAlaYsAlaSerAsnGlyCyVal 240
Db      1249 CCGGTGTGGACAAATCAGTAATTCATTCATGAGAAAGCAAAAGCTCCCAATGATGTTG 1308
Qy      241 LeuValHsCySleuAlaGlyIleSerArgSerAlaThr1leAla1leAlaYr1leMet 260
Db      1309 CTAGTGACTGTTTGGTGGAGATCTCCGCTCCGCAACATGCTATGCTTCAATCATATG 1368
Qy      261 LysArgMetAspMetSerLeuAspGlnAlaYrArgPheValYsGlnuYSerProThr 280

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DB 1369 AAGAGATGAGCATGCTTAAATGATGAGCTTACAGATTGTGAAAGAAAAGAGCTACT 1428
QY 281 ILESERPROASPhAaBnPhelenglylneuleuAaPpTyrglulysyllellysAn 300
DB 1429 ATATCTCCAAACTTCAATTTCTGGGCCAACTCTGGACTATAGAGAAAGATTAAAGAC 1488
QY 301 GlnThr 302
DB 1489 CAGACT 1494

RESULT 3
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250

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Pred. No.: 1.59e-123 Length: 2351
Score: 989.00 Matches: 190
Percent Similarity: 81.40% Conservative: 55
Best Local Similarity: 63.12% Mismatches: 54
Query Match: 63.24% Indels: 2
DB: 4 Gaps: 2

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QY 1 MetAlaHsGluMetIleGlyThrGlnIleVal---ThrgluAArgLeuValAlaLeuLeu 19
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QY 20 GluSerGlyThrGlnLysValLeuLeuIleAaPpSerAArgProPheValGlnIlyrAnThr 39
DB 169 CGGGGCGGGCGCTGGGGGCGCGCTGGTCAATCGACACCCGCTCTTGCTGAGATCAACAGC 228
QY 40 SerHisIleLeuGluAlaIleAenIleAaNCysSerIlyLeuMetIlyAArgIleGln 59
DB 229 TGGCATGTGCTACGCTCCGTCAACATCTGCTCTCCAAAGCTGTGTAAAGCGGGCTGGAG 288
QY 60 GlnAaPpLysValLeuIleThrgluLeuIleGlnIleSerAlaIlyAaIlyValAaPpIle 79
DB 289 CAGGCAAGAGTGACATTCGCGAGCTCATCCAGCGGCTGACGACGACGAGGTGAGGCT 348
QY 80 AaPpCysSerGlnLysValValIlyrAaPpGlnSerSerGlnAaPpValAlaSerLeuSer 99
DB 349 ACGGAGCCACAGAGAGTGCTGTATGACAGACAGCGCGGAGCCAGCTGTCTGGCC 408
QY 100 SerAaPpCysPheLeuThrValLeuLeuGlyLysLeuGlnLysSerPheAaSerValHis 119
DB 409 GCAAGCAGCTTCTCTCTCATCTGCTGACAAAGCTGAGAGCGTCTTGACACGCTGGCC 468
QY 120 LeuLeuAlaGlyIlyPheAlaGlnPheSerAArgCysPheProGlyLeuCysGlnIlyr 139
DB 469 ATCTCACTAGGGGGCTTGGCCACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 528
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QY 140 ---SerThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAaenIleGly 158
DB 529 CCGTGTGCGCTGCTCAATCCCATAGAGCTCTCCAGCCCTGCTGCTCTGCGCCAGCGTGGC 588
QY 159 ProThrArgIleLeuProAaenLysIlyrGlyCysGlnAArgAaPpValLeuAaenLysGln 178
DB 589 CTGACCCGCAATCTGCTCACTTACCTGAGGCTGCGAGAAAGAGCTCTTAAGAAGAT 648
QY 179 LeuIleGlnGlnAaenGlyIlyrIlyrValLeuAaenAlaSerIlyrThrCysProIlyrPro 198
DB 649 CTGATGAGCAAAATGAAATAGCTACGCTCCAGAGCCAGCAAGCTCTGCCCCAAGCT 708
QY 199 AaPpHeileProGluSerHisPheLeuAArgValProValAaenAaPpSerPheCysGlnLys 218
DB 709 GACTTCACTGCGAGAGCCGCTTCACTGGCGGCTCCCATCAACAGACACTACTGTAAAAA 768
QY 219 ILeuProTrpLeuAaPpLysSerValAaPpHeileGlnLysValAlaLysAaenGly 238
DB 769 CTGCTGCCCTGGCTGACAAAGTCAATGATGATTAAGCCAGCTCTCCAGCTGC 828
QY 239 CysValLeuValHisCysLeuAlaGlyIlySerAArgSerAlaThrIleAlaIleAArg 258
DB 829 CAAGTCATCGTCCACTGTCTGCTGGCATCTCCGCTCTGCCACCATCGCCATTCGCTAC 888
QY 259 IleMetLysAArgMetAaPpMetSerLeuAaPpIlyrAArgPheValLysGlnLysAArg 278
DB 889 ATCATGAAGACCAATGGCATGTCTCCAGCAAGCGCTTCAAGTTGTGAAGACAGCGCC 948
QY 279 ProThrIleSerProAaenPhaBnPhelenglylneuleuAaPpTyrglulysylle 298
DB 949 CGGTCACTCGGCCCACTTCACTTCTGGGCCAGCTGCTGAGATAGAGCGAGCGCTG 1008
QY 299 Lys 299
DB 1009 AAG 1011

RESULT 4
US-09-920-668-3
; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Coweart
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: R1S-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (135)...(2012)
US-09-920-668-3

Alignment Scores:
Pred. No.: 2.21e-123 Length: 2377
Score: 988.00 Matches: 190
Percent Similarity: 81.40% Conservative: 55
Best Local Similarity: 63.12% Mismatches: 54
Query Match: 63.17% Indels: 2
DB: 4 Gaps: 2

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DB 135 ATGGCTGGGAGACCGGCTCCCGAGGAAGTGATGATGCCAAGAGCTGGCCAGCTGCTG 194
QY 20 GluSerGlyThrGlnLysValLeuLeuIleAaPpSerAArgProPheValGlnIlyrAnThr 39
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Dd 195 CGGGGCGGGCCCTGGGGGGGCCGCTGCATTCAGACGCCCTCTTCCGTGGAGTCAACACG 254

Gy 40 SerHisIleLeuGlulAlaIleasnIIeaNcYseSerIylaeUeUlySargAgleuGln 59
Dd 255 TGGCAGTGCTCAGCTCCGTCACAACATCTGCTCTCCAGCTGGTAGAGCGCGCTGCAG 314

Gy 60 GlnAepIylValIeuIleThrgIuleuIIegIHIsSerIlalysHslalySVaLapIle 79
Dd 315 CAGGGCAAGSTGACCATTGGAGACTATCCAGCCCGGCTGCACGACCGCAGAGTGGAGCT 374

Gy 80 AapCySeSerGlnYlvalValIalYrAapGInSerSerGlnAapValAlaserIeUser 99
Dd 375 ACCGAGCCACAGAGACCTGGTGGTCTATGACACAGACGCGGGGACCGCGTGGCC 434

Gy 100 SerAapCyPheIeuThrValIeuIleuGlyIylSeuGlnUlysSerPheIeasnsrVAlHls 119
Dd 435 GCAGAGAGCTTCCTCTCCAATCCGCTGAGACAGACTGAAGCGCTGTTCCACACCGTGGCC 494

Gy 120 IeuIleuAlagIylGlyPheaIaguPheSerArgCySPheProGlyIyeuCySGluGlyIlys 139
Dd 495 ATCTCATCTGGGGGGCTTGGCCACCTTCTCTCTGCTTCCC GGCGCTCTGCGAGGGCAA 554

Gy 140 ---SerThrIeuValProThrcYsIleserGlnProcYleuProValAlaasnIlegly 158
Dd 555 CCTGCTGCCCTGCTCCCAAGAAGCCCTCCAGCCCTGCTGCTGCTGCCAGCGTGGCC 614

Gy 159 ProThrArgIleIeuProasnIeuTryleuGlyCySGlnArgAspValIeuasnlySGlu 178
Dd 615 CTGACCCCGATCTGCTCACTTAACCTGGGCTGCGAACAGACOTCTTAACAAAGAT 674

Gy 179 LeuIleglnGlnasnGlyIleglyTrValIeuasnAlaserTyThrCysProIylPro 198
Dd 675 CTGAAGAAGCAAAATGATAATAGCTACGCTCCACAGCGACAACTCCGGCCCAAGCT 734

Gy 199 AspPheIleProGlnSerIshPheIeuArgValProValasnAspSerPheCySGluYs 218
Dd 735 GACTTCATCTGCGAAGCGCGCTTCAAGCGGGTCCCATTAAGACAATACGTGTAAGAAA 794

Gy 219 IleIeuProTrpIeuAspIylSerValaspPheIlegUlalalyAlalyalaSerasnGly 238
Dd 795 CTGCTGCCCTGGCTGACAAATGCTCATCGAGTTCAATGATTAAGCCAGCTCTCCAGCTC 854

Gy 239 CysValIeuValHIscYleuAlaIagIylIeserArgSerAlathrlIeAlalealatyR 258
Dd 855 CAAGTCATCTGTCACCTGTGCTGCGATCTCCGCTCTGCACCATGCCCATGCCCTAC 914

Gy 259 IleMetIylsArgMetAspMetSerIeuAspGlnalYrArPheValIylsGluYsArg 278
Dd 915 ATCATGAAGACCATGCGGATGTCCTCCGACACGCGCTACAGTTCTGTAAAGACAGGCC 974

Gy 279 ProThrIleSerProasnPheasnPheIeuGlyGlnIleuAspTryGlnUlyIylsile 298
Dd 975 CGGTCATCTGCGCCCACTTCAACTTCTGGGCGAGCTGTGAGTACGAGCGCACGCTG 1034

Gy 299 Lys 299
Dd 1035 AAG 1037

RESULT 5
US-09-513-999C-2877
; Sequence 2877, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIORITY FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487

```

/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 2877
/ LENGTH: 333
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 127..333
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 17
/ OTHER INFORMATION: h=a or c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: y=c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 19
/ OTHER INFORMATION: k=g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 36
/ OTHER INFORMATION: n=a, g, c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 58
/ OTHER INFORMATION: r=a or g
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 237
/ OTHER INFORMATION: w=a or t
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 37
/ OTHER INFORMATION: Xaa=His or Gln
/ US-09-513-999C-2877

Alignment Scores:
Pred. No.:      5e-55      length:      333
Score:          475.00     Matches:      106
Percent Similarity: 93.81%   Conservative: 10
Best Local Similarity: 93.81%   Mismatches: 5
Query Match:      30..37%     Indels:      3
DB:               Gaps:      0

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-513-999C-2877 (1-333)
QY      12  ThGluArgLeuValAlaLeuLeuGluSerGlyThr-GluLysValLeuLeuIleAspSe 31
Db      1  ACTGAGAGGTTGGTGGTHYK--CTGGAAGGTGGAAACGNAAAAAGCGCTGAATTGATAR 58
QY      31  rATGpTropheValGluTyr-AsnThrSerHisIleLeuGluAlaIleAsnIleAsnCysS 51
Db      59  CGCGCATTTGTGSAATACCAATACATCCCATTTTGAAGCCATTATATTCACATGCT 118
QY      51  erLysLeuMetLysARGATgLeuGInGInAspLysValLeuIleThrGluLeuIleGln 71
Db      119  CCAAGCTTATGAAGCGAAGGTTGCAACAGAAAGTGTATATTACAGAGCTCATCCAGC 178
QY      71  iSerLAlaLysHisLysValAlaIleAspCysSerGlnLysValValValTyrAspGlns 91
Db      179  ATTCAACGAAACCTAAGGTTGACATTGATTCAGTCAGAAAGTTGTGTATTCAGATCAMA 238
QY      91  erSerGlnAspValAlaSerLeuSerSerAspCysPheLeuThrValLeuLeuGlyLysL 111
Db      239  GCTCCCAAGATGTGCTCTCTCTCTTTCAGACTGTTTTTCTCACTGTACTTCTGGGTAAAC 258
QY      111  euGluLysSerPheAsnSerValHisLeuLeuAla 122
Db      299  TGGAGAAGAGCTTCAACTCTGTTCACTGCTTGGC 333

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RESULT 6
US-09-557-921-1
; Sequence 1, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557, 921
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-921-1

Alignment Scores:
Pred. No.: 6,296-53 Length: 1830
Score: 469.00 Matches: 107
Percent Similarity: 57.72% Conservative: 65
Best Local Similarity: 35.91% Mismatches: 96
Query Match: 29.99% Indels: 30
DB: 4 Gaps: 7

US-10-029-345a-109_COPY_1_302 (1-302) x US-09-557-921-1 (1-1830)
Qy 27 LeuLeuIleAspSerArgProPheValGluTyrAsnThrSerHisIleLeuGluAlaIle 46
Db 603 GTCAATCATGATGAGAGCCCTTCATGAGTACAAAGACAGTCAAGAGAGCTGC 662
Qy 47 AsnIleAsnCySer--LysIleuNerIySarGArgLeuGlnGlnAspIyValIle 65
Db 663 CACATTAACTGCGCCGATGATGACGCGCGAGAGCTGCAGCAGGCAAGTCACTGC 722
Qy 66 ThrGluIleGln--HisSerAlaIyHisIyValAspIleAspCySerGlnIy 84
Db 723 CTAGACTGATTCTCTGAGGAGCAAGGACTCTTTCAGAGAGATCTTTCAGAGAA 782
Qy 85 ValValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSerAspCySerHeu 104
Db 783 ATTATAGTTATGATGAGAAATTCATATGACCAAGCCAGTATCCCTCCAGCACTT 842
Qy 105 ThrValIleuGlyIyLeuGluIyLysSerPheAsnSerValHisIleuAlaGlyIy 124
Db 843 CACATAGTCTCTGAGTCCCTGAGAGAGAGAAAGCAAAAGCTGTGTGAAAGTGA 902
Qy 125 PheAlaGluPheSerArgCyPheProGlyLeuCyGluGlyIyLys----- 139
Db 903 CTTAGTACTTTTAAACAGAAACCATGAAACCTCTGTGACACTCCCTCAGCTCCAG 962
Qy 140 -----SerThrIleValProThrCySerIleSer 148
Db 963 TGCCTGGAGGTGGGGGGGCGGCATCCGGGCGCTGAGAGCTTGTACCTCAGCCATC 1019
Qy 149 GlnProCyLeuPro--ValAlaAsnIleGlyProThrArgIleLeuProAsnLeuTyr 167
Db 1020 ---CCCACACCCCTGAGATGAGAAAGGTGAGTCAACCCCATCTTCCCTCTGTTTC 1076
Qy 168 LeuGlyCyGlnArgAspValIleuAsnIyGluIleGlnGlnAsnGlyIleGlyTyr 187
Db 1077 CTGGCAATGAGCAGATGCTCAGAGACTGACACATGACAGCGGCTGAAACATCGCTAC 1136
Qy 188 ValIleAsnAlaSer-----TyrThrCyProIyProAspPheIlePro 202
Db 1137 GTCAATCAACGTACCACTCATCTTCCCTCTACCACTATGAGAAAGGCTGTTCC----- 1190
Qy 203 GluSerHisPheLeuArgValProValAsnAspSerPheCyGluIyIleLeuProTyr 222
Db 1191 -----AACTACAAAGCGGCTGCCAGCACTGACACAGCAACAGCAAACTGCGGCAGTAC 1244

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Qy 223 LeuAspIySerValAspPheIleGluIyAlaIyAlaSerAsnGlyCySerValIleuVal 242
Db 1245 TTGAGAGGCTTTTGAATTCATTGAGAGACTACCAAGTGTGGAGGGCTTCTCATC 1304
Qy 243 HisCyIleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMetIyArg 262
Db 1305 CACTGCCAGCGCTGGGGGTCTCCCGCTCCGCCACATCTGCATCGCTTACTGATGAAGCAC 1364
Qy 263 MetAspMetSerLeuAspGluAlaTyrArgPheValIyGluIyArgProThrIleSer 282
Db 1365 ACTCGAGTACCATCTGATGATGCTTATTAATTTGCAAGGCAAGCAACATTAATCTCC 1424
Qy 283 ProAsnPheAsnPheLeuGlyIleuLeuAspTyrGluIyIyIleIyAsn 300
Db 1425 CCAATCTTAATCTTATGAGGCGAGTGTCTAGAGTTCAGAGAACTTAACAC 1478

RESULT 7
US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1418933
; US-09-016-434-1135

Alignment Scores:
Pred. No.: 1,296-52 Length: 2109
Score: 467.50 Matches: 110
Percent Similarity: 53.56% Conservative: 63
Best Local Similarity: 34.06% Mismatches: 105
Query Match: 29.89% Indels: 45
DB: 4 Gaps: 7

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Db      670 GAGAAATACGGGCGCGAGCTGTTGCTCGGCTGCTCTCAAGAACTCAAGACGAGGAGC 729
      116 AenserValHisLeuValIaGlyPheAlaGluPheSerArgCysPheProGlyLeu 135
Db      730 TCGCCGGCGCTTCACTCGAAGGTGGCTTCAGTAAGTTCACAGCGAGTTCCTCCGCAAT 789
      136 CysGluGlyLysSerThrLeuValProThrCys---IleSerGlnProCysLeuProVal 154
      790 TCGAG-----ACCAATCTAGACGGCTGCTGTAAGACAGACGCTCGCCGCTTCCAGT 843
      155 AlaAenIleGly----- 158
Db      844 CTGGGCTCGGGGCGCTGGCGATCAGCTCTGACTTCTCCGACATGAGTGTGACTT 903
      158 ----- 158
Db      904 GACCGAGACCCCAATAGTCAACAGACTCGAGTGTAGTCCGCTGCCAACAGCCGCT 963
      159 -----ProThrArgIleLeuProAlaLeuValCysGlnArgSerValLeuAla 176
      964 TCCCTCCAGTGAAGATCTTGCCTTCTCTACTTGGCTGCTGCCAAAGCTCCACCAAC 1023
      177 LysGluLeuIleGlnIleAsnGlyIleGlyTyrrValLeuAlaSerTyrrThrCysPro 196
      1024 TTGACAGCTGTGGAGAAATTCGGCATCAAGTACATCTTGAAAGCCCAATTTGCCG 1083
      197 LysPro---AspPheIleProGluSerHisPheLeuArgValProValAlaAspSerPhe 215
      1084 AATCTCTTTGAGAACGACGAGAGTTTAATACAAACATCCCATTCGATCACTG 1143
      216 CysGluValIleLeuProThrLeuAlaLysSerValAspPheIleGluValAlaVal 235
      1144 AGCCAAACCTGCTCCAGTTTCCCTGAGGCCATTCTTCTTACATAGTAAGCCCGG 1203
      236 SerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAla 255
      1204 AAGAACTGTGTCTTGTGATCTTGTCTGCTGCGATAGCCGCTCAGACTGTGACT 1263
      256 IleAlaTyrrIleMetLysArgMetLysPheSerLeuAlaGlyAlaTyrrArgPheVal 275
      1264 GTGGCTTACTTATGCAAGCTCAATCTGTGATGACATGATGCCATATGATTCGAA 1323
      276 GluLysArgProThrIleSerProAlaPheAlaPheAlaGlyGluLeuAlaAspTyrr 295
      1324 ATGAAAAATCCAAATATCCCTTACTTCACTTCAATGATGATGCTGAGCTTCGAG 1383
      296 LysLysIle 298
      1384 AGGAGCGCTG 1392

```

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; ORGANISM: Human
US-09-949-016-2615

Alignment Scores:
Pred. No.: 2,336-52
Score: 466.50
Percent Similarity: 53.56%
Best Local Similarity: 34.06%
Query Match: 29.83%
DB: 4 Gaps: 7

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-949-016-2615 (1-2475)

      19 LeuGluSerGlyThrGluValLeuLeuIleAlaAspSerArgProPheValGluTyrraen 38
      519 CTGAGCTGGGACAGAGGCGCTGCTGTAAGTACGCTCCGCGACATGATGCTGGCGGCTG 578
      39 ThrSerHisIleLeuGluAlaIleAlaAlaLeuAlaCysSerLysLeuMetLysArgIleu 58
      579 TCGTCGACATCGAGTGGCGCATCAACGCGCATCCGCGCATCATGCTGGCGGCTG 638
      59 GlnGluAlaPheValLeuIleThrGluLeuIleGlnHisSerAla---LysHisVal 77
      639 CAGAAAGGTAACTCGCGGTGCGCGCTTTCACGCGCGGAGAGACCGGAGCGCTTC 698
      78 AspIleAspCys---SerGlnLysValValValTyrrAspGlnSerSerGlnAsp---Val 95
      699 ACCCGCGCTGTGGACCAACGACAGTGTGCTTCTTCAGACAGACAGCAGCACTGGAAC 758
      96 AlaSerLeuSerSerAspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPhe 115
      759 GAGAAATACGGGCGGAGAGTGGCTCGCGGCTGCTGCTCAAGAGCTCAAGACGAGCGAG 818
      116 AenserValHisLeuValIaGlyPheAlaGluPheSerArgCysPheProGlyLeu 135
      819 TCCCGGCGCTTCTTACTGGAAGGTGGCTTCAAGTTCAGACCGAGTTCTCCCTGCAT 878
      136 CysGluGlyLysSerThrLeuValProThrCys---IleSerGlnProCysLeuProVal 154
      879 TCGAG-----ACCAATCTAGACGGCTGCTGTAAGACAGCTCGCCGCTTCCAGT 932
      155 AlaAenIleGly----- 158
      933 CTGGGCTCGGGGCGCTCGGATCAGCTCTGCTTCTCGGACATGAGTGTGACTT 992
      158 ----- 158
      993 GACCGAGACCCCAATAGTCAACAGACTCGATGTAGTCCGCTGTCCAAACAGCCGCT 1052
      159 -----ProThrArgIleLeuProAlaLeuValCysGlnArgSerValLeuAla 176
      1053 TCCCTCCAGTGAAGATCTTGCCTTCTCTTACTTGGCTGTGCCAAAGCTCCACCAAC 1112
      177 LysGluLeuIleGlnIleAsnGlyIleGlyTyrrValLeuAlaSerTyrrThrCysPro 196
      1113 TTGACAGCTGTGGAGAAATTCGGCATCAAGTACATCTTGAAAGCTCAACCCCAATTTGCCG 1172
      197 LysPro---AspPheIleProGluSerHisPheLeuArgValProValAlaAspSerPhe 215
      1173 AATCTCTTTGAGAACGACGAGAGTTTAATACAAACATCCCATCTCGGATCACTGG 1232
      216 CysGluValIleLeuProThrLeuAlaLysSerValAspPheIleGluValAlaVal 235
      1233 AGCCAAACCTGCTCCAGTTTCCCTGAGGCCATTCTTCTTATAGATGAAAGCCCGGCG 1292
      236 SerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAla 255
      1293 AAGAACTGTGTCTTGTGATCTTGTCTGCTGCGATAGCCGCTCAGTCACTGTGACT 1352
      256 IleAlaTyrrIleMetLysArgMetLysPheSerLeuAlaGlyAlaTyrrArgPheVal 275
      1353 GTGGCTTACTTATGCAAGACTCAATCTGTGATGAGACGATGACCTATGATCAATTTGCAA 1412

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Qy	276	GluyIyArgrrothrlIeSeRrPronapheanPheuIuGhIuIeIuemaSpYrXtU	295
Db	1413	ATGAAAAAACCAACATATCCCTTACTTCATTCAGCTGCTGAGCTGCAG	1472
Qy	296	LyelYsIle	298
Db	1473	AGGACGCTG	1481

RESULT 10
US-09-949-016-14992
; Sequence 14992, Application US/09949016

```

? PATENT NO. 6812339
? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? RILE REFERENCE: C1001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 14992
? LENGTH: 13782
? TYPE: DNA
? ORGANISM: Human
? US-09-949-016-14992

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Alignment Scores:	
Pred. No.:	8,56e-51
Score:	464.50
Percent Similarity:	29.69%
Best Local Similarity:	24.50%
Query Match:	29.70%
DB:	4
Gaps:	4
Length:	1378
Matches:	130
Conservative:	22
Mismatches:	25
Indels:	347
Gaps:	4

US-10-029-345A-109_COPY 1_302 (1-302) X US-09-949-016-14992 (1-13782)

Oy		12	GlyGlyPheAlaGluPheserArgCysPheProGluLeuCysGluGlyLys---SerThr	141
Db		8879	GGGGGCTTGCCACACTTCTCTCCCTGCCTCCCCCGGCTCTGCAGAGGCAAGCCTGCTGCC	8933
Oy		142	LeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThrArg	161
Db		8939	GTGCTACCATAGAGCTCTCCACAGGCTGCTGCCTGTGGCCAGCGAGGACTGAACCCG	8999
Oy		162	IleLeuProAsnLeuTyrIleuGlyCysGlnIhrAspValIleuAsnIlyGlu-----	178
Db		8999	ATTCGTGCTCACTCTTACTCTGGGCTCGCAGAAGAGACGTCTTAACAAGGT- GTGTGTGCA	9055
Oy		178	-----	178
Db		9058	GTGAGATTCCGGGGGGGTGTCATGTGGAAAGGGGCGAGAGCTCCAGAAGCAGCTTGGACG	9111
Oy		178	-----	178
Db		9118	GGAGCGGGGAGATGATGAGGAGAAAAGAGCTGAAGCAGTAGATGAGCTGGGTGGGAGAA	9177
Oy		178	-----	178
Db		9178	GCATGGGTGGGGGCCCAAGAGAGACCCAGAGCTCCCACCCATGCCCCCTGGAGAGACACA	9237
Oy		178	-----	178
Db		9238	GGAAGGCTTTGCCGGAGGGGCCGGCAGAGGCTTCGGGGGAGAGACGGGAGAGCTGGCATGCCAA	9297
Oy		178	-----	178

[illegible]


```
Db      282 GCTAAGGGCTCCGCTGAGAGCATCTGCGCCGCGGAGAGAGGTACGCCCGCCG 341
Qy      77 ValAapIleAapCySerGlnlyValValTYAapGlnSerSerGlnAapValA 96
Db      342 TTGCGCTCCGGCTTACTCTCGCGGCTCATGTTCTACGAGACGCGACCGCCGCCG 401
Qy      97 SerLeuSerSerAapCyAapPheLeuThrValLeuLeuGlyLyLeuGlnlySerPhe--- 115
Db      402 AGCCTCCGGAGACAGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 461
Qy      116 ---AanSerValHISLeuLeuValaglyTyValLeuAalAserTYrThrCyA 134
Db      462 CGCACCGCATCTGCTGCTGCTCAAGCGGCTATGAGAGGTTTCTCCGACGACCA 521
Qy      135 LeuCyGlnGlyLySerThrLeu-----ValProThrCyAIlleSer 148
Db      522 TTCTGTTCTAAACCAAGGCTTGGACAGCATCCACCCCGGTTCCCGACGCGCA 581
Qy      149 GlnPro-----CysLeuProValAala-----AanIleGlyPro 159
Db      582 GAGCCCTTGAGACTGAGCTGAGCTCTGTGGAGACCCACTACAGACAGAGAGGTCT 641
Qy      160 ThrArgIleLeuProAanLeuTYrLeuGlyCyGlnArgAapValLeuAanly 179
Db      642 GTGAGATCTCTCCCTTCTACTACCTCGGACAGTGCCTACATGCTGCCGAGAGAC 701
Qy      180 IleglnGlnAanGlyIleGlyTYrValLeuAanAalAserTYrThrCyAPro 199
Db      702 CTGACGCGCTGGGACATACCGGCTGTGTAATGTTCTCTCGACTGCCCAAC--- 758
Qy      200 PheIleProGlnUserHisPheLeuArgValProValAanAapSerPheCysGln 219
Db      759 TTTGAAGACACTACATGACAGAGTCATCCAGATGGAAGATACACAGGCCACATC 818
Qy      220 LeuProTYrLeuAapLySerValAapPheIleGlyLyValAalAserAanGly 239
Db      819 AGCTCTGATTCTATGAGAACCATAGATACATGATGCCGTGACAGACTGCCGTGG 878
Qy      240 ValLeuValHISCyLeuAalaglyIleSerArgSerAalThrIleAalAalTy 259
Db      879 GTGCTGTGACATGTCAGCGCGGCTATCTCGCGTGGCCACCATCTGCTGCCCT 938
Qy      260 MetLyAapMetAapMetSerLeuAapGlnAalTYrArgPheVallyGlnlyAap 279
Db      939 ATGATGAAGAAACGGGTGAGCTGAGAGGCTTCTGAGTTGTTAAGAGGCGC 998
Qy      280 ThrIleSerProAanPheAanPheLeuGlyGlnLeuAapTYrGlnlyAap 298
Db      999 ATCATCTGCGCCAACTTCAGCTTCATGGGGGACGCTGCTGAGATCCCAAG 1055

RESULT 14
US-09-702-705-803
; Sequence 803, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; NUMBER OF SEQ ID NOS: 2000-10-30
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 803
```

```
/ LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-803

Alignment Scores:
Pred. No.: 3,12e-47 Length: 1238
Score: 425.00 Matches: 99
Percent Similarity: 53.85% Conservative: 62
Best Local Similarity: 33.11% Mismatches: 116
Query Match: 27.17% Indels: 22
DB: 4 Gaps: 8

US-10-029-345a-109_copy_1_302 (1-302) x US-09-702-705-803 (1-1238)

Qy      19 LeuGlnSerGlyThrGlnlyValLeuLeuIleAapSerArgProPheValGlnTy 38
Db      168 CTGCGAGCGGC---GGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 224
Qy      39 ThrSerHisIleLeuGlnAalAalAanIleAanCySerTyLeuMetLyAapArg 58
Db      225 GCGGCTACATCTTCTAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 281
Qy      59 GlnGlnAapLyValLeuIleThrGlnlyLeuIle-----GlnHisSerAlaLy 76
Db      282 GCTAAGGGCTCGTGAAGCTGAGAGCATCTGCCCGCGAGAGAGAGTACGCGCCG 341
Qy      77 ValAapIleAapCySerGlnlyValValTYAapGlnSerSerGlnAapValA 96
Db      342 TTGCGCTCCGCTTACTCTCGCGGCTCATGCTTCTACGACGAGCGGACCGCG 401
Qy      97 SerLeuSerSerAapCyAapPheLeuThrValLeuLeuGlyLyLeuGlnlySer 115
Db      402 AGCCTCCGAGACAGACACCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 461
Qy      116 ---AanSerValHISLeuLeuValaglyTyValLeuAalAserTYrThrCyA 134
Db      462 CGCACCGCATCTGCTGCTGCTCAAGCGGCTATGAGAGGTTTCTCCGACGACCA 521
Qy      135 LeuCyGlnGlyLySerThrLeu-----ValProThrCyAIlleSer 148
Db      522 TTCTGTTCTAAACCAAGGCTTGGACAGCATCCACCCCGGTTCCCGACGCGCA 581
Qy      149 GlnPro-----CysLeuProValAala-----AanIleGlyPro 159
Db      582 GAGCCCTTGAGACTGAGCTGAGCTCTGTGGAGACCCACTACAGACAGAGAGGTCT 641
Qy      160 ThrArgIleLeuProAanLeuTYrLeuGlyCyGlnArgAapValLeuAanly 179
Db      642 GTGAGATCTCTCCCTTCTACTCTCGGACAGTGCCTACATGCTGCCGAGAGACAT 701
Qy      879 GTGCTGTGACATGTCAGCGCGGCTATCTCGCGTGGCCACCATCTGCTGCCCT 938
Qy      180 IleglnGlnAanGlyIleGlyTYrValLeuAanAalAserTYrThrCyAPro 199
Db      702 CTGACGCGCTGGGACATACCGGCTGTGTAATGTTCTCTCGACTGCCCAAC--- 758
Qy      200 PheIleProGlnUserHisPheLeuArgValProValAanAapSerPheCysGln 219
Db      759 TTTGAAGACACTACATGACAGTCATCCAGTGAAGATACACACAGGCCGACATC 818
Qy      220 LeuProTYrLeuAapLySerValAapPheIleGlyLyValAalAserAanGly 239
Db      819 AGCTCTGATTCTATGAGAACCATAGATACATGATGCCGTGACAGACTGCCGTGG 878
Qy      240 ValLeuValHISCyLeuAalaglyIleSerArgSerAalThrIleAalAalTy 259
Db      879 GTGCTGTGACATGTCAGCGCGGCTATCTCGCGTGGCCACCATCTGCTGCCCT 938
Qy      260 MetLyAapMetAapMetSerLeuAapGlnAalTYrArgPheVallyGlnlyAap 279
Db      939 ATGATGAAGAAACGGGTGAGGCTGAGAGGCTTCTGAGTTGTTAAGAGGCGC 998
Qy      280 ThrIleSerProAanPheAanPheLeuGlyGlnLeuAapTYrGlnlyAap 298
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Db      999  ATCATCTCGCCAACTTCAGAGGCGAGCTCTGCACTTGGATTCAGATCCAGGTG 1055

RESULT 15
US-09-736-457-803
; Sequence 803, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Mang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478615
; CURRENT APPLICATION NUMBER: US/09/736,457
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-803

Alignment Scores:
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Score:          425.00      Matches:      99
Percent Similarity: 53.85%      Conservative: 62
Best Local Similarity: 33.11%      Mismatches: 116
Query Match:    27.17%      Indels:      22
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QY      39  Thrsers1lleuglualailleanileanycyserylslseumetylaryargleu 58
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QY      59  GlnGlnAspIyValleuulethrlnleuule-----GlnHisSerAlaIyHislys 76
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QY      77  ValAspIleAspCysSerGlnIyValIyTyrAspGlnSerSerGlnAspValAla 96
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QY      97  SerIleSerSerAspCysAspIeuthrValIleuuleuglyIyLeuGlnIySerPhe--- 115
Db      402  AGCCTCGCGAGGACGACGACGCGTGCCTGCGTGCAGGCGGCGCTGCGCGCGACGCGAG 461

QY      116  ---AsnSerValHisleuIeulaglIyIyPheAlaglIyPheSerArgCysPheProGly 134
Db      462  CGCACCGACATCGCTGCTCAAAAGCGGCTATGAGAGTTCCTCCGAGTACCCAGAA 521

QY      135  LeuCysGlnGlyIySerThrIeu-----ValProThrCysIleSer 148
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QY      149  GlnPro-----CysIeuProValAla-----AsnIleGlyPro 159
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Qy	200	PhelIleProGluSerHisPhe	LeuLysValProValAsnAspSerPhe	CysGluTyIle
		:::	:::	:::
Db	759	TTTGAAAGGACATCATAGTAC	ACAAGTCATCCAGTGAAGATTAC	CAACAGGCCGACATC
Qy	220	LeuProTrpLeuAspLysSer	ValAspPheIleGluTySalaty	SalAsnAsnGlyCys
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Db	819	AGCTCTGTTTCATGGAAC	CCATAGATTCATCGCCGGAAGGAC	CTGCCCGGGCGC
Qy	240	ValLeuValHisGlySerLeu	IleGlyLeuSerArgSerAla	ThrIleAlaIleAlaTyIle
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Qy	260	MetLysArgMetAspMet	SerLeuAspGluAlaTy	ArgPheValIysGluTyArgPro
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Db	939	ATGATGAAAGAACGGGTG	AGCTGGAGGAGGCGCTTCGATTC	CGTTAAGCAGCGCGCGAGC
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Search completed: February 14, 2005, 11:12:22
Job time : 149.355 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 14, 2005, 10:56:55 ; Search time 403.187 Seconds
(without alignments)
4419.632 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 5378673 seqs, 2950229984 residues
Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -USER=US10029345.ccgcn_1.1.879 @runcat_09022005_091209_25846
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Database : Published Applications_NA.*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
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2	1552	99.2	1998	US-10-377-072-27	Sequence 27, Appl1
3	1552	99.2	1998	US-10-377-072-27	Sequence 27, Appl1
4	1552	99.2	2071	US-10-072-012-257	Sequence 257, Appl1
5	1552	99.2	2732	US-10-168-506-2	Sequence 2, Appl1
6	1552	99.2	3059	US-10-257-026-1	Sequence 1, Appl1
7	1552	99.2	3496	US-09-964-277-1	Sequence 1, Appl1
8	1552	99.2	3521	US-10-370-715B-261	Sequence 261, Appl1
9	1552	99.2	3544	US-09-816-494-1	Sequence 1, Appl1
10	1552	99.2	3544	US-10-377-072-25	Sequence 25, Appl1
11	1552	99.2	3544	US-10-377-072-25	Sequence 25, Appl1
12	1552	99.2	3625	US-10-425-114-26234	Sequence 26234, Appl1
13	1552	99.2	3766	US-10-343-357-17	Sequence 17, Appl1
14	1552	99.2	4790	US-10-648-593-115	Sequence 115, Appl1
15	1552	99.2	5145	US-10-357-930-20824	Sequence 20824, Appl1
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17	1552	99.2	5145	US-10-357-930-21071	Sequence 21071, Appl1
18	1552	99.2	5145	US-10-357-930-21083	Sequence 21083, Appl1
19	1552	99.2	5145	US-10-357-930-21303	Sequence 21303, Appl1
20	1552	99.2	5145	US-10-357-930-21307	Sequence 21307, Appl1
21	1552	99.2	5145	US-10-357-930-22820	Sequence 22820, Appl1
22	1552	99.2	5145	US-10-357-930-26669	Sequence 26669, Appl1
23	1552	99.2	5145	US-10-357-930-26815	Sequence 26815, Appl1
24	1552	99.2	5145	US-10-357-930-26912	Sequence 26912, Appl1
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28	1552	99.2	5145	US-10-357-930-28675	Sequence 28675, Appl1
29	1545	98.7	2962	US-10-094-749-673	Sequence 673, Appl1
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31	1504.5	96.2	2200	US-10-072-012-255	Sequence 255, Appl1
32	1194.5	76.4	3332	US-09-964-277-20	Sequence 20, Appl1
33	985	63.0	2453	US-10-005-858-1	Sequence 1, Appl1
34	943	60.3	2476	US-10-220-120-28	Sequence 28, Appl1
35	837	55.5	2039	US-10-072-012-265	Sequence 265, Appl1
36	724	46.3	418	US-10-357-930-11243	Sequence 11243, Appl1
37	724	46.3	461	US-10-357-930-12416	Sequence 12416, Appl1
38	724	46.3	461	US-10-357-930-11000	Sequence 11000, Appl1
39	724	46.3	461	US-10-357-930-11346	Sequence 11346, Appl1
40	698	44.6	427	US-10-357-930-10878	Sequence 10878, Appl1
41	635	40.6	419	US-10-357-930-12060	Sequence 12060, Appl1
42	634.5	40.6	422	US-10-357-930-2074	Sequence 2074, Appl1
43	602	38.5	345	US-10-357-930-2067	Sequence 2067, Appl1
44	602	38.5	346	US-10-357-930-11236	Sequence 11236, Appl1
45	602	38.5	377	US-10-357-930-12409	Sequence 12409, Appl1

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patient NO. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR APPLICATION NUMBER: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

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Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0
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QY 21 SerGlyThrGluLeuValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
Db 61 AGTGGAAACGGAAGAAAGTGTGCTGAATGTAGTACCGGCTTTGTGGAAATACATATCATCC 120
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleuMetIleuMetIleuArgLeuGlnGln 60
Db 121 CACATTTTGGAAAGCCCTTAATATCACTCTCCAACTTATGAGCGAAGTTGGAAACAG 180
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Db 181 GACAAAGTGTATATACAGAGCTCATCCAGATTGAGCGAAACATPAGGTTGACATTGAT 240
QY 81 CysSerGlnLeuValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 241 TGCAGTCAGAAAGGTGTAGTTTACGATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCCA 300
QY 101 AspCysPheLeuThrValLeuLeuGluLeuGluLeuSerPheAsnSerValHisIleu 120
Db 301 GACTGTTTCTACCTGTAATCTCTGGGTAACTGGAGAAGCTTCAACTCTTTCACTG 360
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuGlyGluIleYsSer 140
Db 361 CTTCGAGGGGTTGCTGAGTTCTCTCGTTTCCCTGGCTCTGCGAAGAAATCC 420
QY 141 ThrIleuValProThrCysIleSerGlnProCysIleuProValAlaAsnIleGlyProThr 160
Db 421 ACTCTAGTCTCTACCTGCAATTCCTCAGCTTCTTACCTGTTGCCAACAATGGGCAACC 480
QY 161 ArgIleLeuProAsnLeuTyrIleuGlyCysGlnArgAspValLeuAsnIleGluLeu 180
Db 481 CGAATCTTCCCAATCTTATCTTGGCTGCCAGCAGATGCTCTCAACAGAGCTGATG 540
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProIlePheAspPhe 200
Db 541 CAGCAGAAATGGGATTTGTTATGTAAATGCCACAATATCCTGTCCAAAGCCTGACTTT 600
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluIleIleu 220
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QY 221 ProTleuAspIleSerValAspPheIleGluValAlaIleSerAsnGlyCysVal 240
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QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
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Db 901 CAGACT 906
RESULT 2
US-10-377-072-27
Sequence 27, Application US/10377072
Publication No. US20040009501A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Miyoung
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MP103-0160NM1M
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
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SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27
Alignment Scores:
Pred. No.: 9,31e-193 Length: 1998
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
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US-10-029-345a-109_COPY_1_302 (1-302) x US-10-377-072-27 (1-1998)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValIleThrGluArgLeuValAlaLeuLeuGln 20
Db 1 ATGGCCCATGAGATGATGTAAGTCAAAATGTTACTGAGAAGTTGGCTCTGCTGGAA 60
QY 21 SerGlyThrGluLeuValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
Db 61 AGTGGAAACGGAAGAAAGTGTGCTGAATGTAGTACCGGCTTTGTGGAAATACATATCATCC 120
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleuMetIleuMetIleuArgLeuGlnGln 60

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DB 901 CAGACT 906
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US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US2004015721A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logsen, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Mlyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP103-0180NMIM
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; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
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; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1998)
US-10-377-072-27
Alignment Scores:
Pred. No.: 9,31e-193 Length: 1998
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0
US-10-029-345a-109_copy_1_302 (1-302) x US-10-377-072-27 (1-1998)
QY 1 MetAlaHisGluMetIleGlyThrcGlnIleValThrGluArgLeuValAlaSerleuGln 20
DB 1 ATGGCCCATGAGATGATGGAACCTCAATTTGATGAGAGGTTGGCTCTGCTGGA 60
QY 21 SerGlyThrGluValleuileuileasphserargProphalGluTyraanthrser 40
DB 61 AGTGAACGAAAGAGTCTGCTATTAATAGCCGCAATTTGTGAATACATTCATCC 120
QY 41 HisileuGlnu1aileasnileasnCyseerlyseuMetlysarargleuGln 60
DB 121 CACATTGGAGACCATTAATATCAAGCTCCAAAGCTTATGAGAGAGTTGCAACAG 180
QY 61 Aaplysvallleuilethgluleuileglnhiseralalyahlyvalaspiileap 80
DB 181 GACAAAGTTAATTACAGAGCTCATCCAGCACTTACGAAACATTAAGTTGACTTAT 240
QY 81 Cysserglnlyvalvalvaltyraapginserserglnaapvalalaserleuser 100
DB 241 TGCACTCGAAGAGTTGATGTTTACATCAAAAGCTCCAAAGATGTCCTCTCTCTCA 300
QY 101 AapCypheluthrvalleuileuglylyseuglylyserphesanserValhisleu 120
DB 301 GACTGTTTCTCAGTCACTCTGAGTAACTGAGAGAGAGTTCAACTCTTCACTCAG 360
QY 121 leu1aaglyglyphalaglupheserargCyphneproglyleuCyegluglyysser 140
DB 361 CTGGAGAGGAGTTGCTGAGAGTTCTCTGTTTCTCTGAGGCTCTGAGAAAGAAATCC 420
QY 141 ThrleuValProthrCyeliserglnProCyseuProvalAlaasnileglyProthr 160
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Db 421 ACTCTAGTCCCTACGATGCTTCTGACCTTGCTTCCGTGGCCAACTTGGGCCAAC 480
Qy 161 Arg11LeuProAsnLeuTyrLeuGlyCySGlnArgAspValLeuAsnLysGluLeu 180
Db 481 CGAATCTTCCCAATCTTATCTTGCTGCTCCAGCGAGATGCTCTCAACAGAGCTGAG 540
Qy 181 GlnGlnAsnGly11LeuGlyTyrVal1LeuAsnAlaSerTyrThrCyAspProLysProAspPhe 200
Db 541 CAGCGAATGGGATGCTTATGCTTAAATGCCAGAAATCCTGCTCCAAAGCTGACTTT 600
Qy 201 11eProGlnSerHisPheLeuArgVal1ProValAsnAspSerPheCySGlnLys11Leu 220
Db 601 ATCCCGAGCTCATCTTCTCGCTGCTGCTGGAAGAAGACGCTTTGTGAGAAATTTTG 660
Qy 221 ProTProLysAspLysSerValAspPhe11LeuGlyVal1LeuLysAlaSerAsnGlyCyVal 240
Db 661 CCGTGGTGGACAAATCAGTATGATTCATGATGAGAAAGAAAGCCCTCCAAATGATGTGT 720
Qy 241 LeuValHisCyLeuVal1LeuGly11LeuSerArgSerAlaThr11LeuAla11LeuTyr11LeuMet 260
Db 721 CTAGTGCATGTTTACGTGGATCTCCCGCTCCGCCACATGCTATGCTTACATCAGT 780
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheVal1LysGluLysArgProThr 280
Db 781 AAGAGAGTGCATGCTTATGATGAGCTTACAGATTGTGAAGAAAGAAAGACCTACT 840
Qy 281 11eSerProAsnPheAsnPheLeuGlyGlnLeuLysAspTyrGlnLysVal1LysAsn 300
Db 841 AATCTCCAACTTCAATTTCTGGGCGCAACTCTGAGTACTGAGAAAGAAATTAAGAAC 900
Qy 301 GlnThr 302
Db 901 CAGACT 906

RESULT 4
US-10-072-012-257
; Sequence 257, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spyrek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patkurajan, Weera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Futak, Katarzyna
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine B.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
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; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-257

Alignment Scores:
Pred. No.: 9,89e-193 Length: 2071
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Mismatches: 1
Best Local Similarity: 99.34% Indels: 0
Query Match: 99.23% Gaps: 0
DB: 17

US-10-029-345a-109_copy_1_302 (1-302) x US-10-072-012-257 (1-2071)
Qy 1 MetAlaHisGluMet11LeuGlyThrGln11LeuVal1ThrGluArgLeuVal1AlaLeuGlu 20
Db 61 ATGGCCCATGAGATGATGGAACCAATGTTACTGAGAGTGGGCTGCTGGAA 120
Qy 21 SerGlyThrGluLysVal1LeuLeu11eAspSerArgProPheVal1GluTyrAsnThrSer 40
Db 121 AGTGAACGGAAGAAAGCTGCTTATGATGACCGGCAATTTGTGAAATTCATACATCC 180
Qy 41 His11LeuGlnAla11LeuAsn11eAsnCySerLysLeuMetLysArgArgLeuGln 60
Db 181 CACATTTTGAAGGACATTATATCACTGCTCCAAAGTTATGAAGCAAGTTGCAACAG 240
Qy 61 AspLysVal1Leu11eThrGluLeu11eGlnHisSerAlaYsn11LysVal1Asp11eAsp 80
Db 241 GACAAAGTTAATATACAGAGCTCATCCAGCATTCAGCGAAACATAGTTGACATTGAT 300
Qy 81 CysSerGlnLysVal1Val1TyrAspGlnSerSerGlnAspVal1AlaSerLeuSerSer 100
Db 301 TGCAGTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy 101 AspCyPheLeuThrVal1LeuLeuGlyLysLeuGlnLysSerPheAsnSerVal1HisLeu 120
Db 361 GACTGTTTCTCACTGATCTTCTGGGTAACCTGGAAGAGCTTCAACTGTTCACTG 420
Qy 121 LeuAlaGly11LeuHisGlu11eAspSerArgCyPheProGlyLeuGlyGlyLysSer 140
Db 421 CTTCAGAGTGGGTTGTGTGATCTCTCGTTGTTCCCTGCGCTGTGAGAAATATCC 480
Qy 141 ThrLeuVal1ProThrCys11eSerGlnProCysLeuProVal1AlaAsn11LeuGlyProThr 160
Db 481 ACTCTAGTCCCTACGATGCTTCTGAGCTTGTCTTCTGCTTCTGCTTCTGCTTCTG 540
Qy 161 Arg11LeuProAsnLeuTyrLeuGlyCySGlnArgAspVal1LeuAsnLysGluLeu 180
Db 541 CGAATCTTCCCAATCTTATCTTGCTGCTCCAGCGAGATGCTCTCAACAGAGCTGAG 600
Qy 181 GlnGlnAsnGly11LeuGlyTyrVal1LeuAsnAlaSerTyrThrCyAspProLysProAspPhe 200
Db 601 CAGCGAATGGGATGCTTATGCTTAAATGCCAGAAATCCTGCTCCAAAGCTGACTTT 660
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Qy 201 ILeProgiuSerHisPheLeuArgValProValAsnSerPheCysGluLysIleLeu 220
Db 661 ATCCCGAGTCTCATTTCTGGCTGCTGCTGGAATGACAGCTTTTGTGAGAAATTTTG 720
Qy 221 ProTripleuAspLysSerValAspPheIleGluLysAlaLysSerAsnGlyCysVal 240
Db 721 CCGGTGTGGACAAATCAGTATTCATTGAGAAAGCAAAAGCTCCAAATGAGATGTT 780
Qy 241 LeuValHisCysPheAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 781 CTAGTCACTGTTTATGCTGGAGTCTCCGCTCCGACCATGCTATGCTTACATCAG 840
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr 280
Db 841 AAGGAGATGACATCTTTTATGATGACCTTACAGATTTGTGAAGAAAAAGACTTACT 900
Qy 281 ILeSerProAsnLysPheAsnLysGluLysLeuAspTyrGluLysIleLysAsn 300
Db 901 ATATCTCCAAACTTCAATTTTCTGGCCCAACTCTGACATATGAGAAAGATTAAAGAC 960
Qy 301 GlnThr 302
Db 961 CAGACT 966

RESULT 5

US-10-168-506-2
; Sequence 2, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MAYHE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSHANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168,506
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-168-506-2

Alignment Scores:

Pred. No.: 1,57e-192 Length: 2732
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservatve: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 17 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-168-506-2 (1-2732)

Qy 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 538 ATGGCCCATGAGATGATTTGGAATCTAATTTGTTACTGAGAGGTGGCTCTGCTGGAA 597
Qy 21 SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
Db 598 AGTGAAGAGAAAAGCTGCTGTAATGATAGCGGCATTTGTGAATTAACAATCATCC 657
Qy 41 HisIleLeuGluAlaIleAsnIleAsnCysSerLysPheMetLysArgArgLeuGln 60
Db 658 CACATTTTGAAGACCATTAATCACTGCTCCAAAGCTTATGAAAGGTTGCAACAG 717
Qy 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysIleValAspIleAsp 80

Db 718 GACAAAGTAAATTACAGAGCTCATCCAGATTCAGCGAAACATTAAGTTGACATTGAT 777
Qy 81 CysSerGluLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 778 TGCAGTCAGAAAGGTGATGTTACATCAAGAGCTCCAAAGATGTGCTCTCTCTTCA 837
Qy 101 AspCysPheLeuThrValLeuLeuGluLysLeuGluLysSerPheAsnSerValHisLeu 120
Db 838 GACTGTTTTCACCTGATCTTCTGGTAAATCGAAGAGACTTCACTGTTTACCTG 897
Qy 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db 898 CTGCAAGGTGGATTGCTGAGATTCCTGTTGTTTCCCTGGCCCTGTGAAGAAATCC 957
Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 958 ACTTATGTCCTTACCTGATTCGAGCTTGTCAAGCTTGTACCTGTTCCAAACATTTGGGCAAC 1017
Qy 161 ArgIleLeuProAsnLeuTyrLeuGluLysGlnArgAspValLeuAsnLysGluLeuIle 180
Db 1018 CGAATCTTCCCAATCTTATCTTGGCTGCCAGAGATGCTTCAACAAGAGCTGATG 1077
Qy 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
Db 1078 CAGAGAGATGGGATTTGTTATGTTAATGCAAGCAATACCTGTCCAAAGCTGACTTT 1137
Qy 201 ILeProgiuSerHisPheLeuArgValProValAsnSerPheCysGluLysIleLeu 220
Db 1138 ATCCCGAGTCTCATTTCTGCTGCTGCTGCTGATGACACTTTTGTAGAAATTTTG 1197
Qy 221 ProTripleuAspLysSerValAspPheIleGluLysAlaLysSerAsnGlyCysVal 240
Db 1198 CCGGTGTGGACAAATCAGTATTCATTGAGAAAGCAAAAGCTCCAAATGAGATGTT 1257
Qy 241 LeuValHisCysPheAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1258 CTAGTCACTGTTTATGCTGGAGTCTCCGCTCCGACCAATGCTATGCTTACATCAG 1317
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr 280
Db 1318 AAGGAGATGACATGCTTTTATGATGACACTTACAGATTTGTGAAGAAAAAGACTTACT 1377
Qy 281 ILeSerProAsnLysPheAsnLysGluLysLeuAspTyrGluLysIleLysAsn 300
Db 1378 ATATCTCCAAACTTCAATTTTCTGGCCCAACTCTGACATATGAGAAAGATTAAAGAC 1437
Qy 301 GlnThr 302
Db 1438 CAGACT 1443

RESULT 6

US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US2004008659A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDS
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:

Pred. No.: 1,9e-192 Length: 3059
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 17 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-257-026-1 (1-3059)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValIleThrGluArgLeuValAlaLeuGlu 20
DB 127 ATGGCCCATGAAATGATTTGAACTCAATTTGTTACTGAGAGGTGGTGGCTGTGGTGA 186
QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 187 AGTGAACCGAAGAAAGTGTCTGCTAAATTGATGACCGGCACTTTGGGAATACAAATCATCC 246
QY 41 HisIleLeuGluValAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 60
DB 247 CACATTTTGGAAAGCAATTAATATCAAGCTCCCAAGCTTAATGAGGAAAGTTGCAACAG 306
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaValHisIleValAspIleAsp 80
DB 307 GACAAAGGTAAATTAACAGAGCTCATCCAGCTTCAAGCAACATTAAGGTGACATTAAT 366
QY 81 CysSerGlnValValValValValValValValValValValValValValValValVal 100
DB 367 TGCAGTCAGAAAGTTGATGTTACGATCAAGCTCCCAAGATGTTGCCCTCTCTCTTCA 426
QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGlyValLeuGlyValLeuGlyValSer 120
DB 427 GACTGTTTCTCAGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGlyGlyValSer 140
DB 487 CTGGAGGTGGGTTGCTGAGTCTCTGCTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 547 ACTCAAGTCCCACTGATCTTCTCAGCTTCTCAAGCTTCTCAAGCTTCTCAAGCTTCTCA 606
QY 161 ArgIleLeuProAsnLeuThrLeuGlyCysGlnAspValLeuAsnIleGlyLeuIle 180
DB 607 GCAATTTTCCCAATCTTAATCTTGTGCGCCAGCAAGTGTCTTCAAGCAAGTGTGATG 666
QY 181 GlnGlnAsnGlyIleGlyThrValLeuAsnIleAsnIleAsnIleAsnIleAsnIleAsn 200
DB 667 CAGCAGATGGGATTTGTTATGTGTAAATGCCAGCAATACCTGTCCAAAGCTGACTTT 726
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlnIleLeu 220
DB 727 ATCCCGAGTCTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786
QY 221 ProThrLeuAspIleValSerValAspPheIleGlyValAlaValAlaValAlaValAla 240
DB 787 CCGGTGTGCAATATCAATGATTTCAATGAGAAAGCAAGCTCCAAAGGATGTGT 846
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIle 260
DB 847 CTATGTGACCTTTTATAGCTGGATCTCCGCTCCGCAACATCGCTATGCTTACATCATG 906
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyraArgPheValLysGluValArgProThr 280
DB 907 AAGGAGTGAACATGTCTTTAGATGAGCTTACAGATTTGTGAAGAAAGAAAGCACTACT 966
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyraGlyValLysIleLeuAsn 300
DB 967 ATAATCTCAAACTCAATTTTCTGCGCAACTCTGCACTATGAGAAAGAAATTAAGAAC 1026
QY 301 GlnThr 302
DB 1027 CAGACT 1032

RESULT 7
US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucie, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125,434
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Alignment Scores:
Pred. No.: 2,38e-192 Length: 3496
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-964-277-1 (1-3496)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValIleThrGluArgLeuValAlaLeuGlu 20
DB 562 ATGGCCCATGAGATGATTTGAACTCAATTTGTTACTGAGAGGTGGTGGCTGTGGTGA 621
QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 622 AGTGAACCGAAGAAAGTGTCTGCTAAATTGATGAGCGGCATTTGGGAATCAATACATCC 681
QY 41 HisIleLeuGluValAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 60
DB 682 CACATTTTGGAAAGCAATTAATTAATCACTGCTCCAGCTTATGAGCAAGAGTTGCAACAG 741
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaValHisIleValAspIleAsp 80
DB 742 GACAAAGTAAATTAACAGAGCTCATCCAGATTCAGCGAAACATTAAGTTGACATTAAT 801
QY 81 CysSerGlnValValValValValValValValValValValValValValValValVal 100
DB 802 TGCAGTCAAGAGTTGATGTTACGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 861
QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGlyValLeuGlyValLeuGlyValSer 120
DB 862 GACTGTTTCTCACTGATCTTGGGTAACTGGAAGAGCTTCAACTGTCTTCACTG 921
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGlyValSer 140
DB 922 CTGGAGGTGGGTTGCTGAGTCTCTCGTGTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 982 ACTTATGTCCCACTGATCTTCAAGCTTCTGAGCTTCTACCTGTTCGCAACATTTGGCAACC 1041
QY 161 ArgIleLeuProAsnLeuThrLeuGlyCysGlnArgAspValLeuAsnIleGlyLeuIle 180
DB 1042 CGAATCTTCCCAATCTTTATCTTGGCTGCAAGAGATGTCTCTCAAGAGAGCTGATG 1101
QY 181 GlnGlnAsnGlyIleGlyThrValLeuAsnIleAsnIleAsnIleAsnIleAsnIleAsn 200
DB 1102 CACAGAAATGGGATTTGTTATGTGTAAATGCCAGCAATACCTGTCCAAAGCTGACTTT 1161
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlnIleLeu 220
DB 1162 ATCCCGAGTCTCAATTTCTGCGGTGCTGTGTAATGACAGCTTTTGTGAGAAATTTTG 1221

QY 221 ProtripleuAspLyseSerValAspPhe11eg1uLyseValAspSerAsn1yCyVal 240
DB 1222 CGGTGTTGGAACAATCATAGATTTCATTGAGAAAGCAAGCCTCCAAATGATGCTT 1281
QY 241 LeuValHisCyLeuValAG1y11eSerArgSerAlaThr11eAla11eAla1yTr11eMet 260
DB 1282 CTAGGCACTGTTTGTGGGATCTCCGCTCCGACCACTGCTATGCTTACCTACATG 1341
QY 261 LysArgMetAspMetSerLeuAspG1uAlaTyraArgPheVal1y8G1uLysArgProThr 280
DB 1342 AAGAGATGACATCTCTTACATGAGCTTACAGATTGTGAAAGAAAAAGACCTTCT 1401
QY 281 I1eSerProAsnPheAsnPheLeuG1yG1uLeuAspTyrg1uLysAla1y1eLysAsn 300
DB 1402 ATATCTCAACTTCAATTTCTGCGCAACTCTCGACTATGAGAAAGATTAAAGAAC 1461
QY 301 GlnThr 302
DB 1462 CAGACT 1467
RESULT 8
US-10-370-715B-261
; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docker Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO: 261
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-261
Alignment Scores:
Pred. No.: 2,41e-192 Length: 3521
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0
US-10-029-345A-109_COPY_1_302 (1-302) x US-10-370-715B-261 (1-3521)
QY 1 MetAlaHisGluMet11eg1yThri11eVal1ThriG1uAglLeuValAlaLeuLeuGlu 20
DB 564 ATGGCCCATGAGATCATTTGAACCTCAAAATTGTACTGAGAGGTTGGTGGCTCTGGA 623
QY 21 SerGlyThrG1uLyseValLeuLeu1eAspSerArgPhePheValG1uTyraAsnThrSer 40
DB 624 AGTGAACGGAAGAGCTGCTCTATTAATACCCGCAATTTGTGAAATACATACATCC 683
QY 41 His11eLeuG1uAla11eAsn11eAsnCyser1yLeuMet1yArgArgLeuG1u 60
DB 684 CACATTTTGAAGCCATTAATCACTGCTCCAGCTTAAGAGCAAGGTTGCAACAG 743
QY 61 AspLyseValLeu11eThriG1uLeu11eG1uHisSerAla1yHisAla1yAsp11eAsp 80
DB 744 GACCAAGGTATTAATTAAGAGCTCATTCAGCACTTACGGAACATTAAGGTTGACATTTGAT 803
QY 81 CysSerG1uLyseValVal1y1yAspG1uSerSerG1uAspValAla1eSerLeuSerSer 100

DB 804 TGCACTGAGAAAGTGTGTAGTTACGATCAAGACTCCCAAGATGTTGCCCTCTCTTCA 863
QY 101 AspCysePheLeuThrValLeuLeuG1yLyseG1uLyseSerPheAsnSerValHisLeu 120
DB 864 GACTGTTTTCACCTGATCTTCTGGGTAACTGGAGAAAGACTTCAACTCTGTTACCTG 923
QY 121 LeuAlaG1yG1uPheAlaG1uPheSerArgCysePheProG1yLeuCyG1uG1yLysSer 140
DB 924 CTTCAGAGTGGGTTTGTGCAATTTCTCTGTTTCTTCCCTGGCCCTCTGAGAGAAATCC 983
QY 141 ThrLeuValProThrCyse11eSerG1uProCyseLeuProValAlaAsn11eg1yProThr 160
DB 984 ACTCTAGTCCCTTACCTGATTTCTTCAAGCTTCTTACCTGTTGCCAATGTTGGGCAACC 1043
QY 161 Arg11eLeuProAsnLeuTyrg1uG1uArg1uArgAspValLeuAsn1yG1uLeu11e 180
DB 1044 CGAATTTCTCCCAATCTTATCTTGGCTGCCAGCAAGATGCTTCACAAAGAGCTGATG 1103
QY 181 G1uG1uAsnG1y11eg1yTyraValLeuAsnAlaSerTyThrCyseProLyseProAspPhe 200
DB 1104 CAGCAAGATGGAGTTGTTATGTGTTAAATGCCAATACCTGTCCAAAGCTTACCTTT 1163
QY 201 I1eProG1uSerHisPheLeuArgValProValAsnAspSerPheCyseG1uLyse11eLeu 220
DB 1164 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACACTTTTGTGAGAAATTTTG 1223
QY 221 ProtripleuAspLyseSerValAspPhe11eg1uLyseValAspSerAsn1yCyVal 240
DB 1224 CGGTGTTGGAACAATCATAGATTTCATTGAGAAAGCAAGCCTCCAAATGATGCTT 1283
QY 241 LeuValHisCyLeuValAG1y11eSerArgSerAlaThr11eAla11eAla1yTr11eMet 260
DB 1284 CTAGTGCATCTTTAGCTGGAGATCTCCGCTCCGACCACTGCTATGCTTACCTACATG 1343
QY 261 LysArgMetAspMetSerLeuAspG1uAlaTyraArgPheVal1y8G1uLysArgProThr 280
DB 1344 AAGAGATGACATGCTTGTGAGAGCTTACAGATTGTGAAAGAAAAAGACCTTACT 1403
QY 281 I1eSerProAsnPheAsnPheLeuG1yG1uLeuAspTyrg1uLysAla1y1eLysAsn 300
DB 1404 ATATCTCAACTTCAATTTCTGCGCAACTCTCGACTATGAGAAAGATTAAAGAAC 1463
QY 301 GlnThr 302
DB 1464 CAGACT 1469
RESULT 9
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1
Alignment Scores:
Pred. No.: 2,43e-192 Length: 3544

Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-816-494-1 (1-3544)

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OY 1 MetAlaHISGLuMetILEGlyThrGlnILEValThrGluArgLeuValAlaLeuEnglu 20
DB 589 ATGGCCCATGATGATGATGGAATCTCAATTTGTTACTGAGAGGTTGGCTCTGCTGGAA 648
OY 21 SerGlyThrGluLysValLeuLeuILEaspSerArgProPheValGluTyraAnthSer 40
DB 649 AGTGGAAACGAAAAAGTGTCTTAATTGATGACCGGCGCATTTGTGGAATACATCATCC 708
OY 41 HisILEuGluAlaILEasnILEasnCySerIySLeuMetIyArgArgLeuGlnGln 60
DB 709 CACATTTTGGAGCCATTAAATATCACTCTCCAGCTTATGAGCGAAGTTGCAACAG 768
OY 61 AspLysValLeuILEThrGluLeuILEGlnHISSerAlaLysHISLysValAspILEasp 80
DB 769 GACAAAGTTTAATTACAGAGCTCATCCAGCTTACAGCAACATAGGTTACATTTGAT 828
OY 81 CySSerGlnLysValValValIyTyraSpGlnSerSerGlnAspValAlaSerLeuSer 100
DB 829 TGCAGTTCAGAAAGTTGATGATTACGATCAAGCTCCCAAGATGTTGCCCTCTCTTCA 888
OY 101 AspCySPheLeuThrValLeuEngluLysILEuGluLysSerPheAsnSerValHISLeu 120
DB 889 GACTGTTTCTACGTACTCTTGAGTAACTGGAGAAAGGCTTCAACTGTGTTACCTG 948
OY 121 LeuAlaGlyLysPheAlaGluPheSerArgCySPheProGlyLeuCyGluGlyLysSer 140
DB 949 CTGAGAGGTGGTGTGCTGAGTCTCTCTGTTTCTCTGCTGCTGCTGAGGAAATCC 1008
OY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnILEGlyProThr 160
DB 1009 ACTCTAGTCCCTACCTGATCTCTGAGCTTCTTACCTGTTGCCAATGGGCAACC 1068
OY 161 ArgILEuProAsnLeuTyrlenGlyCySGlnArgAspValLeuAsnLysGluLeuILE 180
DB 1069 GCAATCTTCCCAATCTTATCTTGCTGCCAGCAGAGATGTCCTCAACAGAGGCTGATG 1128
OY 181 GlnGlnAsnGlyILEGlyTyrlValLeuAsnAspSerTyrlThrCysProLysProAspPhe 200
DB 1129 CAGCAGATGGGATGGTTATGTTATGTTAAATGACCAATACCTGTCCAAGCTGACTTT 1188
OY 201 ILEProGluSerHISPheLeuArgValProValAsnAspSerPheCySGluLysILEu 220
DB 1189 ATCCCCGAGTCTCATTTCTCGTGTGCTGATGACAGCTTTTGAGAAAAATTTTG 1248
OY 221 ProTrpLeuAspLysSerValAspPheILEGlyLysAlaLysAspSerHISCyVal 240
DB 1249 CCGGTGTGGCAAAATCGATGATTTCATGAGAAAGAAAGCCCTCCAAATGAGATGTTT 1308
OY 241 LeuValHISCySLeuAlaGlyILESerArgSerAlaThrILEAlaILEAlaTyrlMet 260
DB 1309 CTAGTGCACTGTTTATGCTGGATCTCCGCTCCGCAACATCGCTATGCTTACATCAG 1368
OY 261 LysArgMetAspMetSerLeuAspGluAlaTyraArgPheValLysGluLysArgProThr 280
DB 1369 AAGGAGATGACATGCTTTAGATGAACTTACAGATTTTGGAAGAAAAAGACTTACT 1428
OY 281 ILESerProAsnPheAsnPheLeuGlyLysILEuLeuAspTyrlGluLysILELysAsn 300
DB 1429 ATATCTCCAAACTCAATTTCTGGGCCCACTCCGACATGAGTATGAGAAAGATTAAGAAC 1488
OY 301 GlnThr 302
DB 1489 CAGACT 1494
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RESULT 10

US-10-377-072-25

; Sequence 25, Application US/10377072
; Publication No. US20040009501A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

; APPLICANT: Curtis, Roy A.J.

; APPLICANT: Logan, Thomas Joseph

; APPLICANT: Glucksmann, Maria A.

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Williamson, Mark J.

; APPLICANT: Rudolph-Owen, Laura A.

; APPLICANT: Chun, Miyoung

; APPLICANT: Tsai, Fong-Ying

; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,

; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES

; TITLE OF INVENTION: AND USES THEREFOR

; FILE REFERENCE: MP103-0180NMIM

; CURRENT APPLICATION NUMBER: US/10/377, 072

; PRIOR FILING DATE: 2003-02-27

; PRIOR APPLICATION NUMBER: US 09/895,860

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/215,370

; PRIOR FILING DATE: 2000-06-29

; PRIOR APPLICATION NUMBER: US 09/723,806

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 60/187,455

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 09/843,297

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 60/199,801

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: US 09/861,801

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: US 60/205,508

; PRIOR FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: US 09/816,494

; PRIOR FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: US 09/815,419

; PRIOR FILING DATE: 2001-03-22

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 3544

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (589) ... (2586)

US-10-377-072-25

Alignment Scores:

Pred. No.: 2,43e-192 Length: 3544

Score: 1552.00 Matches: 300

Percent Similarity: 99.67% Conservative: 1

Best Local Similarity: 99.34% Mismatches: 1

Query Match: 99.23% Indels: 0

DB: Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-377-072-25 (1-3544)

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OY 1 MetAlaHISGLuMetILEGlyThrGlnILEValThrGluArgLeuValAlaLeuEnglu 20
DB 589 ATGGCCCATGATGATGGAATCTCAATTTGTTACTGAGAGGTTGGCTCTGCTGGAA 648
OY 21 SerGlyThrGluLysValLeuLeuILEaspSerArgProPheValGluTyraAnthSer 40
DB 649 AGTGGAAACGAAAAAGTGTCTTAATTGATGACCGGCGCATTTGTGGAATACATCATCC 708
OY 41 HisILEuGluAlaILEasnILEasnCySerIySLeuMetIyArgArgLeuGlnGln 60
DB 709 CACATTTTGGAGCCATTAAATATCACTCTCCAGCTTATGAGCGAAGGTTGCAACAG 768
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DB	SEQ ID NO	LENGTH	SCORE	PERCENT SIMILARITY	BEST LOCAL SIMILARITY	QUERY MATCH	GAPS
Prior Filing Date: 2001-06-29							
Prior Application Number: US 60/215,370							
Prior Filing Date: 2000-06-29							
Prior Application Number: US 09/723,806							
Prior Filing Date: 2000-11-28							
Prior Application Number: US 60/187,455							
Prior Filing Date: 2000-03-07							
Prior Application Number: US 09/843,297							
Prior Filing Date: 2001-04-25							
Prior Application Number: US 60/199,801							
Prior Filing Date: 2000-04-26							
Prior Application Number: US 09/861,801							
Prior Filing Date: 2001-05-21							
Prior Application Number: US 60/205,508							
Prior Filing Date: 2000-05-19							
Prior Application Number: US 09/816,494							
Prior Filing Date: 2001-03-23							
Prior Application Number: US 09/815,419							
Prior Filing Date: 2001-03-22							
Remaining Prior Application data removed - See File Wrapper or PALM.							
NUMBER OF SEQ ID NOS: 114							
SOFTWARE: FastSeq for Windows Version 4.0							
SEQ ID NO 25							
LENGTH: 3544							
TYPE: DNA							
ORGANISM: Homo Sapiens							
FEATURE:							
NAME/KEY: CDS							
LOCATION: (589) ... (2586)							
US-10-377-072-25							
Alignment Scores:							
Pred. No.:	2,43e-192	Length:	3544				
Score:	1552.00	Matches:	300				
Percent Similarity:	99.67%	Conservative:	1				
Best Local Similarity:	99.34%	Mismatches:	1				
Query Match:	99.23%	Indels:	0				
DB:	18	Gaps:	0				
US-10-029-345A-109_COPY_1_302 (1-302) x US-10-377-072-25 (1-3544)							
QY	1	MetValHisGluMetIleGlyThrGlnIleValThrGluValAlaLeuLeuGlu	20				
DB	589	ATGGCCCATGAGATGATGGAACTCAATTTGTCTGAGAGTGGTGGCTTGGTGGAA	648				
QY	21	SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTrpAsnThrSer	40				
DB	649	AGTGGAAACGAAAGAGTCTCTAATGATGACCGCCATTGTGGAAATACATATATCC	708				
QY	41	HisIleLeuGluAlaIleAsnIleAsnCySerIleValMetIleArgArgLeuGln	60				
DB	709	CACATTTTGGAGCCATTATATCATCACTGCCAAGCTTATGAAACGAAAGTTGCAACAG	768				
QY	61	AspIleValLeuIleThrGluLeuIleGlnHisSerAlaIleValIleAspIleAsp	80				
DB	769	GACAAATGTTAATTACAGACCTCATCCAGATTCAACGAAACAAATAGATTGACATTGAT	828				
QY	81	CysSerGlnValValIleValIleAspGlnSerSerGlnAspValAlaSerLeuSerSer	100				
DB	829	TGCGATCAGAGGTGTGATGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA	888				
QY	101	AspCyAspHeuThrValLeuLeuGlyValLeuGluIleValSerPheAsnSerValHisLeu	120				
DB	889	GACTGTTTCTCACTGATCTCTGGGTAACTGGAGAGAGACTTCACTCTGTTCACCTG	948				
QY	121	LeuAlaIleGlyPheAlaGluPheSerArgCysPheProGlyIleuCyGluGlyIleSer	140				
DB	949	CTTGCAGATGGGTGTGCTGAGTTCTCTCGTGTGTTCCCTTGCCCTTGGAAAGGAAATCC	1008				
QY	141	ThrIleuValProThrCysIleSerGlnProCysIleuProValAlaAsnIleGlyProThr	160				
DB	1009	ACTCTATCTCCCTACCTGATTTCTCAGGCTTCTTACTCTGTTCACCAATTTGGGCCAAC	1068				

Qy 161 Arg11eLeuProAsnLeuTyrLeuGlyCysGlnAArgAspValLeuAsnLysGluLeu 180
|||
Db 1069 CGAATTCCTCCAACTTTATCTTGTGGCTGCCAGCAGATGCTCTCAACAAGAGCTGATG 1128
|||
Qy 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnLysSerTyrThrCysProLysProAspPhe 200
|||
Db 1129 CAGCAGATGGGATGTGTTATGTGTTAAATGCGACCAATACCTGTCCAAAGCCTGACTTT 1188
|||
Qy 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
|||
Db 1189 ATCCCGAGTCTCAATTCCTGCGTGTGCTGGAATGACAGCTTTTGAGAAAATTTTG 1248
|||
Qy 221 ProTLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240
|||
Db 1249 CCGTGTGGACCAATCAGTGAATTCATTTGAGAAAGAAAGCCCTCCAAATGAGTGT 1308
|||
Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
|||
Db 1309 CTAGTGCACGTGTTAGCTGGGATCTCCGCTCCGACCATGCTATGCGCTACATCATG 1368
|||
Qy 261 LysArgMetAspMetSerLeuAsnGluAlaTyrArgPheValLysGluLysArgProThr 280
|||
Db 1369 AAGGAGATGACATGCTTTTATGATGAACTTACAGATTTGGAAGAAAGAAAGACTTACT 1428
|||
Qy 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysAsn 300
|||
Db 1429 ATATCTCCAAACTTCAATTTCTGGGCCCACTCCCTGAGCTATGAGAAAGATTAGAAC 1488
|||
Qy 301 GlnThr 302
|||
Db 1489 CAGACT 1494
|||

RESULT 12

US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
; US-10-425-114-26234

Alignment Scores:

Pred. No.: 2,53e-192 Length: 3625
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 17 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-425-114-26234 (1-3625)

Qy 1 MetAlaHisGluMetIleGlyTyrGlnIleValIThrGluArgLeuValAlaLeuLeuGln 20
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Db 692 ATGCCCATGAGATGATTGGAACCTCAATTTTACTGAGAGGTTGGTGGCTCTGCGAA 751
|||
Qy 21 SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
|||

Db 752 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGCCCATTTGTGAATACATATCATCC 811
|||
Qy 41 H1811eLeuGluAlaIleAsnIleAsnGlySerIleLeuMetLysArgArgLeuGln 60
|||
Db 812 CACATTTGGAAAGCCATTAAATATCAACTGCTCCAGGCTTAAGAGCGAAGGTTGCAACAG 871
|||
Qy 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
|||
Db 872 GACAAAGTTTAATTAACAGACTCATCCAGATTCACGGAACAATAAGCTTGACATTGAT 931
|||
Qy 81 CysSerGlnLysValIleValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSer 100
|||
Db 932 TGCACTGAGAAAGTTGATGATTAAGATCAAGCAAGCTCCCAAGATGTGCTCTCTCTCA 991
|||
Qy 101 AspCysPheLeuThrValIleLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
|||
Db 992 GACTGTTTCTCAGCTGATCTTCTGGTAACTGGAGAAAGACCTTCACTGTTACCTG 1051
|||
Qy 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuCysGluLysLysSer 140
|||
Db 1052 CTTCGAGGTGGGTTTGGCTGAGTTCTCTCGTTGTTCCCTGGCTCTGTGAAGAAATCC 1111
|||
Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
|||
Db 1112 ACTCTAGCCCTTACCTGCATTTCTCAGCCTTGCTTACCTGTGCGCAATGGGCGCAACC 1171
|||
Qy 161 Arg11eLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeu 180
|||
Db 1172 CGAATTCCTCCAACTTTATCTTGTGGCTCCAGCAGAAATGCTCAACAAGAGCTGATG 1231
|||
Qy 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnLysSerTyrThrCysProLysProAspPhe 200
|||
Db 1232 CAGCAGATGGGATGTGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 1291
|||
Qy 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
|||
Db 1292 ATCCCGAGTCTCAATTCCTGCGTGTGCTGGAATACAGCTTTGTGAAAATTTTG 1351
|||
Qy 221 ProTLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240
|||
Db 1352 CCGTGTGGACCAATCAGTGAATTTCAATTGAGAAAGAAAGCTCCAAATGAGTGTGT 1411
|||
Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
|||
Db 1412 CTATGACATGTTTATGCTGGAGATCTCCGCTCCGACCAATCGCTATCGCTCATCATG 1471
|||
Qy 261 LysArgMetAspMetSerLeuAsnGluAlaTyrArgPheValLysGluLysArgProThr 280
|||
Db 1472 AAGAGATGACATGCTTTATGATGAACTTACAGATTTGTGAAGAAAGAAAGCTTACT 1531
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Qy 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLysAsn 300
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Db 1532 ATATCTCCAAACTTCAATTTCTGGGCCCACTCCTGAGCTATGAGAAAGATTAGAAC 1591
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Qy 301 GlnThr 302
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Db 1592 CAGACT 1597
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RESULT 13

US-10-343-357-17
; Sequence 17, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCTE GENOMICS, INC.; TANG, Y.Tom
; APPLICANT: ELLIOTT, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; TRIBOULET, Catherine M.
; APPLICANT: LU, Dyrus Alina M.; TRIBOULET, Catherine M.
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Marian R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Daniel B.; CHAWLA, Narinder K.

```

APPLICANT: KEARNEY, Liam
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFERENCE: PI-0173 PCT
CURRENT APPLICATION NUMBER: US/10/343,357
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: PCT/US01/23716
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,679
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/223,272
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/224,309
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 60/226,728
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/229,254
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/231,366
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO: 17
LENGTH: 3766
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CB1
US-10-343-357-17

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Alignment Scores:
Pred. No.: 2,69e-192 Length: 3766
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conserved: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0
DB: 17

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US-10-029-345a-109_copy_1_302 (1-302) x US-10-343-357-17 (1-3766)

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QY 1 MetAlahisglumetiieglyThrglnilevalThrgluargluvalaleuenglun 20
DB 538 ATGCCCATGAGATGATGGAATCAATTTGACTGAGAGGTGGCTGCTGGAA 597
QY 21 SerGlyThrGluValValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 598 AGTGAACGGAAGAGTCTCTAATTGATGACCGGCAATTTGGAAATACATCATCC 657
QY 41 HisIleuGlualaleaenlleasnleasnCyserlysluemetlysluarglengln 60
DB 658 CACATTTGGAAAGCATTAATATCACTGCTCCAGCTTATGAGCGAAGGTTGCAACG 717
QY 61 AsplyValLeuIleThrglnleuIleGlnHisSerAluYshIlyValAspIleAsp 80
DB 718 GACAAAGTGAATTAATACAGACTCATCCAGCATTCAGGAAACATTAAGTGAATGAT 777
QY 81 CysSerGlnlyValValValValValValValValValValValValValValVal 100
DB 778 TGCAAGTCGAAGGTGTGATTGATGATCAAGCTCCCAAGATGTTGCCCTCTCTCTCA 837
QY 101 AspCysPheLeuThrValLeuLeuGllysluenglulysSerPheAsnSerValHisLeu 120
DB 838 GACGTTTTCTCACTGTCCTCTGAGTAACTGAGAAAGACCTTCACTGTCACCTG 897
QY 121 LeuAlaGlyIlePheAlaGlnPheSerArgCysPheProGlyLeuCyseGlnGlyLysSer 140
DB 898 CTTCAGAGTGGGTTTGTGAGAGTCTCTGTTGTTTCCCTGGCTCTGGAAGAAATCC 957
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 958 ACTCTAGCTCCTACCTGCAATTTCTCAGCTTGTGCTTAAGCTGTTGCCAATATTGGCAACC 1017
QY 161 ArgIleuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnlyGlnLeuIle 180

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DB 1018 CGAATTTCCCAATCTTATCTTGCTGCCAGCAGATGCTCTCAACAGAGCTGATG 1077
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnIleSerTyrThrCysProlyProAspPhe 200
DB 1078 CAGCAAGATGGATGTGTTAATGTGTTAAATGACACCAATACCTGTGCCAAAGCTTACATT 1137
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnlysluLeu 220
DB 1138 ATCCCGAGTCTCATTTCTGCTGCTGCTGCTGATGACAGCTTTTGGAGAAATTTTG 1197
QY 221 ProTyrLeuAspLysSerValAspPheIleGlnlysluAlaIleSerAsnGlyCysVal 240
DB 1198 CGGTGTGGACAATCAATGATGATTTCAATTGGAAGCAAAAGCTCCCAATGATGTGT 1257
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 1258 CTAGTCACTGTTAAGCTGGGATCTCCCGCTCCGACCATGCTATGCTTACATCATG 1317
QY 261 LysArgMetAspMetSerLeuAspGlnAlaTyrArgPheVallysluLysArgProThr 280
DB 1318 AAGAGATGACATGCTTTTGAATGAACTTACAGATTTTGGAAAGAAAGAACTTACT 1377
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnlysluLysIleLysAsn 300
DB 1378 ATATCTCAAACTTCAATTTCTGCGGCACTCTGCACTATGAGAGATTAAGAAC 1437
QY 301 GlnThr 302
DB 1438 CAGACT 1443

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RESULT 14

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US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:

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; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

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Alignment Scores:

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Pred. No.: 4.03e-192 Length: 4790
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conserved: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0
DB: 18

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US-10-029-345a-109_copy_1_302 (1-302) x US-10-648-593-115 (1-4790)

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QY 1 MetAlahisglumetiieglyThrglnilevalThrgluargluvalaleuenglun 20
DB 184 ATGCCCATGAGATGATGGAATCAATTTGACTGAGAGGTGGCTGCTGGAA 243
QY 21 SerGlyThrGluValValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 244 AGTGAACGGAAGAGTCTCTAATTGATGACCGGCAATTTGGAAATACATCATCC 303
QY 41 HisIleuGlualaleaenlleasnleasnCyserlysluemetlysluarglengln 60

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Db 304 CACATTTTGGAGCCATTATATCACTGCTCCAAAGCTTATGAAAGGTTGCAAG 363
Qy AsplysValleuileThrgluLeuileglnHisSerAlaIysHisIleValAsp11leAsp 80
Db 364 GACAAAGGTATATATACAGAGCTCATCCAGCAATTCAGCAAAACAATAGGTGACATTTAT 423
Qy CysSerGlnIysValIvalValTyraSpGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 424 TGCAATCAGAAAGTTGATGTTACATCAAACTCCAAAGATGTTGCTCTCTCTCTCA 483
Qy AspCysPheLeuThrValleuLeuGlyIysLeuGlnIysSerPheAsnSerValHisIleu 120
Db 484 GACTGTTTCTCACAGTACTCTCTGGTAAACTGGAGAAAGCTTCAACTCTGTTCACTG 543
Qy LeuAlaGlyIysPheAlaGlnPheSerArgCysPheProGlyLeuCysGlnGlyIysSer 140
Db 544 CTTCAGAGTGGGTGCTGAGTCTCTGTTGTTTCCCTGGGCTCTGGAGAAATCC 603
Qy ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 604 ACTTAGTCCCTACTGATTTCTCAGCTTGTCTTACTGCTTGCACAACTTGGGCAAC 663
Qy ArgIleLeuProAsnLeuTyrlleuGlyCysGlnAlaGspValLeuAsnIleGlyLeu 180
Db 664 CGAATTTCTCCCAATCTTATCTTGCTGCCAGCAGATGCTCTCAACAAGAGCTGAT 723
Qy GlnGlnAsnGlyIleGlyTyraValleuAsnAlaSerTyrrThrCysProIysProAspPhe 200
Db 724 CAGCAAAATGGGATTTGTTATGTTAAATGCAACAATACCTGTGCCAAAGCTGACTTT 783
Qy IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnIysIleLeu 220
Db 784 ATCCCGAGTCTCATTTCTGCTGGTGGCTGAGATGACAGTTTGTGAGAAATTTTG 843
Qy ProTrpLeuAspIysSerValAspPheIleGlyIysAlaIysAlaSerAsnGlyCysVal 240
Db 844 CCGGTGTGGCAATCATGATTTCTGATGAAAGCAAAAGCTCCAAATGATGTGTT 903
Qy LeuValHisCysIleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrlleu 260
Db 904 CTAGTGACGTGTTTACTGAGATCTCCGCTCCGCAACATGCTATGCTCTACACTG 963
Qy LysArgMetAspMetSerLeuAspGlnAlaTyraPheValIysGlnIysArgProThr 280
Db 964 AAGAGGATGACAGTCTTTAGATGAACTTACAGATTTGTGAAAGAAAGAAAGCTACT 1023
Qy IleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspTyrglnIysIleIysAsn 300
Db 1024 ATATCTCCAAACTTCAATTTCTGGGCCAACTCTGACTATGAGAGAGATTAAGAAC 1083
Qy GlnThr 302
Db 1084 CAGACT 1089

RESULT 15
US-10-357-930-20824
: Sequence 20824, Application US/10357930
: Publication No. US20040259086A1
: GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Endegren, Wilson
: APPLICANT: Mohan, John
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
: TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
: TITLE OF INVENTION: HUMAN PROSTATE CANCER
: FILE REFERENCE: KRI-007BCN
: CURRENT APPLICATION NUMBER: US/10/357, 930
: PRIOR FILING DATE: 2003-02-04
: PRIOR APPLICATION NUMBER: 09/785, 276
: PRIOR FILING DATE: 2003-02-16
: PRIOR APPLICATION NUMBER: 60/183, 319
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: 60/189, 862

Qy PRIOR FILING DATE: 2000-03-16
Qy PRIOR APPLICATION NUMBER: 60/207, 454
Qy PRIOR FILING DATE: 2000-05-25
Qy PRIOR APPLICATION NUMBER: 60/211, 314
Qy PRIOR FILING DATE: 2000-06-09
Qy PRIOR APPLICATION NUMBER: 60/219, 007
Qy PRIOR FILING DATE: 2000-07-18
Qy PRIOR APPLICATION NUMBER: 60/255, 281
Qy NUMBER OF SEQ ID NOS: 62232
Qy SOFTWARE: FastSeq for Windows Version 4.0
Qy SEQ ID NO 20824
Qy LENGTH: 5145
Qy TYPE: DNA
Qy ORGANISM: Homo sapiens
Qy FEATURES:
Qy NAME/KEY: misc.feature
Qy LOCATION: 1, 5144, 5145
Qy OTHER INFORMATION: n = A,T,C or G
Qy US-10-357-930-20824

Alignment Scores:
Pred. No.: 4,546-192 Length: 5145
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 18 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-357-930-20824 (1-5145)

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Qy 21 SerGlyThrGlnIysValleuLeuIleAspSerArgProPheValGlnTyraSerThrSer 40
Db 649 AGTGAACGGAAGAAAGTGTGCTATGATGATGATGATGATGATGATGATGATGATGAT 708
Qy 41 HisIleLeuGlnAlaIleAsnIleAsnCysSerIysLeuMetIysArgIleGlnGln 60
Db 709 CACATTTTGGAAAGCATTAATATCACTGCTCCAAAGCTTGTGAAGCAAGGTGCAACAG 768
Qy AspIysValleuIleThrgluLeuileglnHisSerAlaIysHisIleValAsp11leAsp 80
Db 769 GACAAAGTATATATACAGAGCTCATCAGCATTCAGCGAAACATTAAGTTGACATTTGAT 828
Qy CysSerGlnIysValIvalValTyraSpGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCACTCAGAAAGTTGATGTTTACATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 888
Qy AspCysPheLeuThrValleuLeuGlyIysLeuGlnIysSerPheAsnSerValHisIleu 120
Db 889 GACTGTTTCTCACAGTACTCTCTGGTAAACTGGAGAAAGCTTCAACTCTGTTCACTG 948
Qy LeuAlaGlyIysPheAlaGlnPheSerArgCysPheProGlyLeuCysGlnGlyIysSer 140
Db 949 CTTCAGAGTGGGTGCTGAGTCTCTGTTGTTTCCCTGGGCTCTGTGAAAGAAATCC 1008
Qy ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTTAGTCCCTACTGATTTCTCAGCTTGTGCTTACTGCTTGCACAACTTGGGCAAC 1068
Qy ArgIleLeuProAsnLeuTyrlleuGlyCysGlnAlaGspValLeuAsnIleGlyLeu 180
Db 1069 CGAATTTCTCCCAATCTTATCTTGCTGCCAGCAGATGCTCTCAACAAGAGCTGAT 1128
Qy GlnGlnAsnGlyIleGlyTyraValleuAsnAlaSerTyrrThrCysProIysProAspPhe 200
Db 1129 CAGCAAAATGGGATTTGTTATGTTAAATGCAACAATACCTGTGCCAAAGCTGACTTT 1188
Qy IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnIysIleLeu 220

Db	1189	ATCCCGGAGTCTCAATTCCTCGGTGCTGCTGATGACAGCTTTTGGAGAAATTTTG	1248
Qy	221	ProtripleuaplysServaIaSpPheIleGluIysAlaIysAlaSerAngIyCysVal	240
Db	1249	CCGGTGTTGGCAAAATCAGTAGATTTCATTAGAAAGCAAAAGCCTCCAAATGAGTGT	1308
Qy	241	LeuValHisCybLeuValagIyIleSerArgSerAlaThrIleAlaIleAlaTyrlleMet	260
Db	1309	CTAGGCACTGTTTAGTGTGGGATCTCCGGCTCCGGCACCATCGCTATCGCTTACATATG	1368
Qy	261	LysArgMetAspMetSerLeuAspGluAlaTyrlArgPheValIysGluIysArgProThr	280
Db	1369	AAGAGGATGGACATGCTTTTAGATGAGACCTTACAGATTGTGAAAGAAAAGACCTACT	1428
Qy	281	IleSerProAsnPheAsnPheLeuGlyGluIleuLeuAspTyrgluIyIysIleLysAsn	300
Db	1429	ATATCTCAAACCTTCATTTTCTGGGGCAACTCCTCGACTATGAGAGAAAGATTAAAGAC	1488
Qy	301	GlnThr 302	
Db	1489	CAGACT 1494	

its rye drink (uspio)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 12:12:08 ; Search time 45 Seconds
(without alignments)
1103.147 Million cell updates/sec

Title: US-10-029-345A-109
Perfect score: 665
Sequence: 1 MAHEMIGQIVTERLVALL.....LGKVGSGSSFGSMETIEVS 665

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 50

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472	71.0	665	4	US-09-816-494-2

ALIGNMENTS

RESULT 1
US-09-816-494-2
; Sequence 2, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR APPLICATION NUMBER: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-816-494-2

Query Match 71.0%; Score 472; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	194	TCPEKDFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKSNGCVLHCLAGISRSAT	253
DB	194	TCPEKDFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKSNGCVLHCLAGISRSAT	253
QY	254	IAIAYIMRMDMSLDEAVRPVYKRPPTISPNPNFGLLDYKKTIKNOTGASGPKLKL	313
DB	254	IAIAYIMRMDMSLDEAVRPVYKRPPTISPNPNFGLLDYKKTIKNOTGASGPKLKL	313
QY	314	LHLEKPNPVPVAVSEGGKSETPPLSPCADSATSSAAGQRPVHPASVSPSPVQSLLED	373
DB	314	LHLEKPNPVPVAVSEGGKSETPPLSPCADSATSSAAGQRPVHPASVSPSPVQSLLED	373
QY	374	SPLVQALSGHLISADRLSDSNLKRSPSLDIKSVSYASMAASLHGFSSEDALEYKPS	433
DB	374	SPLVQALSGHLISADRLSDSNLKRSPSLDIKSVSYASMAASLHGFSSEDALEYKPS	433
QY	434	TLIDGTNKLQCPSPVQELSEQTPETSPDKEASIPKLTQAPSDSQSKRLHSVRTSSSG	493
DB	434	TLIDGTNKLQCPSPVQELSEQTPETSPDKEASIPKLTQAPSDSQSKRLHSVRTSSSG	493
QY	494	TAQRSLSPILHRSGSVEDNHYHTSFLFGISTSQOHLTKSAGLKKMHSDIILAPQSTPBL	553
DB	494	TAQRSLSPILHRSGSVEDNHYHTSFLFGISTSQOHLTKSAGLKKMHSDIILAPQSTPBL	553
QY	554	TSSWYFATESHSHFYASAIYGGASAYVSCQLPTCGDQVYSVRRQKPSDRADSRSM	613
DB	554	TSSWYFATESHSHFYASAIYGGASAYVSCQLPTCGDQVYSVRRQKPSDRADSRSM	613
QY	614	HEESPFEKQFRRSCQMEFGSISMEENSRBELGKVGSGSSFGSMETIEVS 665	
DB	614	HEESPFEKQFRRSCQMEFGSISMEENSRBELGKVGSGSSFGSMETIEVS 665	

Search completed: February 9, 2005, 12:29:30
Job time : 45 secs

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Db      1799  GGCGAAGCCAGATGACAGAGCTGACTCGCCGCGAGACTGGCATGAAGAGAGCCCTTTGG
Qy      620  TuluSgInpHelysArgpSerCySgInMetGluPhegiYgiuSerIleMetSerGluuA
Db      1859  AAAAGCAGTTTAAAGCGAAGAGCTGCCAAATGGAAATTGGAGAGACATCATGTCCAGAA
Qy      640  snArgSerArgGluGluLeuGluYlyValGlySerGlnSerPheSerGlySerMetG
Db      1919  AAGGTCACGGGAAGAGCTGGGGGAAGTGGGAGTCAAGTCTAGCTTTTCGGGACAGATGG
Qy      660  IuileIleGluValSer 665
Db      1979  AAATCATTTGAGGCTCTCC 1995

RESULT 2
US-09-816-494-1
/ Sequence 1, Application US/09816494
/ Patent No. 6664089
/ GENERAL INFORMATION:
/ APPLICANT: Meyers, Rachel A.
/ TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
/ FILE REFERENCE: 10448-030002
/ CURRENT APPLICATION NUMBER: US/09/816,494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 60/191,858
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 3544
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (589)...(2583)
US-09-816-494-1

Alignment Scores:
Pred. No.: 0
Score: 472.00 Length: 3544
Percent Similarity: 99.40% Matches: 663
Best Local Similarity: 99.40% Conservative: 0
Query Match: 70.98% Mismatches: 2
DB: 4 Indels: 4
Gaps: 0

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Qy      1  MetAlaHieGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
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Qy      21  SerGlyThrGluYsValLeuLeuIleAspSerArgProPheValGluYrAsnThrSer 40
Db      649  AGTGAAGAGGAAAAAGCTGCTGATTTGAGAGCCGCGCATTTGTGGAAATACATCATCC 70
Qy      41  HisIleLeuGluAlaIleAsnIleAsnCySerYsLeuMetYsArgArgLeuGlnGln 60
Db      709  CACATTTTGAAGCCATTAATATCAACTCTCTCCAGCTTATGAGGAAAGTTGCAACG 76
Qy      61  AspYsValLeuIleThrGluLeuIleGlnHisSerAlaYsHisYsValAspIleAsp 80
Db      769  GACAAAGTGTATTTACAGAGCTCATCCAGCATTCAGAGGAAACATTAAGTTGACATGAT 82
Qy      81  CysSerGluYsValYsValYrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db      829  TGCAGTCAGAGAGGTTGATTTATTCATCAATCAAGAGTCCCAAGATGTGCTCTCTTCA 88
Qy      101  AspCyPheLeuThrValLeuLeuGluYlySerGluYsSerPheAsnSerValHisLeu 120
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121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyCysGluGlyLysSer 140
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Qy 141 ThrLeuValProThrCysAlaSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db ACTGAGGCCCTACCTGATCTCTCAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
Qy 161 ArgIleLeuProThrLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 180
Db CGAATCTCTCCAACTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
Qy 181 -GlnGlnGlnGlyIleGlyIleValLeuAsnAlaSerTyr-ThrCysProLysProAsp 200
Db GCAGAGAAATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 1186
Qy 200 heileProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluGlyIle 220
Db TTATCCCGAGCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246
Qy 220 euProTLeuAspLysSerValAspPheIleGlyLeuAlaLysAlaSerGlyCysGly 240
Db TGCCGTGGTGGACAAATCAGTATGATTTGATGAGAAAGCAAAAGCTCCATGATGATG 1306
Qy 240 allLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
Db TTCTAGTCACTGTTAGTGGATCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 1366
Qy 260 eLyArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgPro 280
Db TGAAGAGATGAGCAATGCTTTAGATGAGCTTACAGATTTGAGAGAGAGAGAGAGAGAGAG 1426
Qy 280 hriLysSerProAsnPheAsnPheLeuGlyGlyLeuLeuLeuLeuLeuLeuLeuLeuLeu 300
Db CTATATCTCCAACTTCAATTTCTGCGGCAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1486
Qy 300 sngInThGlyAlaSerGlyProLysSerLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 320
Db ACCAGACTGAGACATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1546
Qy 320 sngIuProValProAlaValSerGluGlyGlyGlyLysSerGlnThrProLysSerProp 340
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Qy 340 roCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSer 360
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Qy 360 alProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 380
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Qy 380 euSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSer 400
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Qy 400 heSerLeuAspLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGly 420
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Qy 500 euSerProLeuHisArgSerLysSerValGluAspArgTyrHisPheSerLeuPheG 520
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Db GCCTTCCAGAGCCAG 2206
Qy 540 LysSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPhe 560
Db 2207 ACTGGAATATCTGGCCCCCAGAGCTCTACCCCTCCCTGACAGAGAGAGAGAGAGAGAG 2266
Qy 560 LathGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyr 580
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Db 2327 CTGCTACAGCTGAGCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2386
Qy 600 rGlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGlyGluSerProphe 620
Db 2387 GGCAGAGCCAGTACAG 2446
Qy 620 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGlu 640
Db 2447 AAAAGCACTTTAAAGCAG 2506
Qy 640 sArgSerArgGlnGluGlyLysValGlyLysSerGlnSerSerSerSerSerSerSerSer 660
Db 2507 ACAGGTCAAGGAG 2566
Qy 660 LysIleIleGluValSer 665
Db 2567 AAATCATGAGGTCTCC 2583

Search completed: February 14, 2005, 14:08:29
Job time : 298 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using SW model

Run on: February 9, 2005, 12:25:39 ; Search time 135 Seconds
(without alignments)
1604.386 Million cell updates/sec

Title: US-10-029-345a-109

Perfect score: 665
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Gapop 60.0 , Gapext 60.0

Searched: 1373511 seqs, 325702437 residues

Word size : 50

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Post-processing: Listing first 1000 summaries

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20: /cgn2_6/ptodata/1/pubpaa/US66_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	472	71.0	517	US-09-964-277-21	Sequence 21, Appl1
2	472	71.0	665	US-09-816-494-2	Sequence 2, Appl1
3	472	71.0	665	US-09-864-277-2	Sequence 2, Appl1
4	472	71.0	665	US-10-094-749-2312	Sequence 2312, Ap
5	472	71.0	665	US-10-377-072-26	Sequence 26, Appl1
6	472	71.0	665	US-10-072-012-680	Sequence 680, App
7	472	71.0	665	US-10-072-012-681	Sequence 681, App
8	472	71.0	665	US-10-168-506-14	Sequence 14, Appl1
9	472	71.0	665	US-10-343-357-7	Sequence 7, Appl1
10	472	71.0	665	US-10-257-026-2	Sequence 2, Appl1
11	472	71.0	665	US-10-648-593-240	Sequence 240, App
12	472	71.0	665	US-10-648-593-247	Sequence 247, App
13	472	71.0	665	US-10-377-072-26	Sequence 26, Appl1

14	472	71.0	690	US-10-072-012-679	Sequence 679, App
15	472	71.0	690	US-10-072-012-703	Sequence 703, App
16	472	71.0	690	US-10-425-114-54204	Sequence 54204, A
17	394	59.2	680	US-10-072-012-256	Sequence 256, App
18	304	45.7	662	US-10-072-012-258	Sequence 258, App
19	258	38.8	672	US-10-296-115-1259	Sequence 1259, Ap
20	152	22.9	15	US-10-108-260A-4872	Sequence 4872, Ap
21	108	16.2	155	US-09-964-277-7	Sequence 7, Appl1
22	67	10.1	660	US-10-072-012-682	Sequence 682, App
23	64	9.6	677	US-10-072-012-683	Sequence 683, App
24	56	8.4	88	US-09-764-853-578	Sequence 578, App

ALIGNMENTS

RESULT 1
US-09-964-277-21
; Sequence 21, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucite, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-21

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	106	IAIAYIMKMDMSLDEAYRFEVKEKPTSPNENPLGQLLDYERKIKNOTGASGPKSKTL	165
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DB	166	LHLKRNBPVPAVSEGGQKSETPPLSPPCADSATSEAAQGPVHPASVPSPVQPSLTD	225
QY	374	SPLVQALSGHLISADRLBDSNKLKRSFSLDKSVSYASMAASLHGFSSEDALEYKPS	433
DB	226	SPLVQALSGHLISADRLBDSNKLKRSFSLDKSVSYASMAASLHGFSSEDALEYKPS	285
QY	434	TLIDGTNKLCOFSPVQELSEQTPETSPOKEASIRKULOTARPDSQSKRLSVRSSSG	493
DB	286	TLIDGTNKLCOFSPVQELSEQTPETSPOKEASIRKULOTARPDSQSKRLSVRSSSG	345
QY	494	TAORSILSPILHSGSVEDVYHTSFLFGLSTSQOHLTKSAGLKGWHSIILAPOTSTPL	553
DB	346	TAORSILSPILHSGSVEDVYHTSFLFGLSTSQOHLTKSAGLKGWHSIILAPOTSTPL	405
QY	554	TSSWTFATESHSPYASAIYGGASASVAYSCQLPTCGQVYSVRRQKPSDRADSRSG	613
DB	406	TSSWTFATESHSPYASAIYGGASASVAYSCQLPTCGQVYSVRRQKPSDRADSRSG	465
QY	614	HESEFPEQFKRSCOMEGESIMSENSRELKGVGSSGSSFGSMETIEVS 665	
DB	466	HESEFPEQFKRSCOMEGESIMSENSRELKGVGSSGSSFGSMETIEVS 517	

RESULT 2

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US-09-816-494-2
; Sequence 2, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-816-494-2
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Query Match 71.0%; Score 472; DB 9; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 314 LHLEKNEPVPVAVSSEGGOKSETPLSPCADATSEAAQORVHPASVSVSVQPSLLED 373
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DB 374 SPLVQALSGHLISADRLSDSNKLRKSFSLDIKSVSYASMAASLHGFSSSEDALEYKPS 433
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DB 434 TTLDTGNKLCQFSPVQELSEOTPEPTSPDKKEASIPKQLQTPARPSDSQKRLHSVRTSSG 493
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RESULT 3

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US-09-964-277-2
; Sequence 2, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125,434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-964-277-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 254 IAIAYIMKRMDSLDEAARFVYKERTPTISPNFNFGOLDYEKKIKNOTGASGPKSKLKL 313
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DB 314 LHLEKNEPVPVAVSSEGGOKSETPLSPCADATSEAAQORVHPASVSVSVQPSLLED 373
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DB 374 SPLVQALSGHLISADRLSDSNKLRKSFSLDIKSVSYASMAASLHGFSSSEDALEYKPS 433
QY 434 TTLDTGNKLCQFSPVQELSEOTPEPTSPDKKEASIPKQLQTPARPSDSQKRLHSVRTSSG 493
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DB 494 TAQRSLSPHRSQSVEDNYHTSFLFGLSTSQOHLTKSAGLGLKGMHSDILAPOTSTPSL 553
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DB 554 TSSWYFATESHSHFYSAIYGSASAYSACQOLPTCGOYYSVRRQKPSDRADSRSSW 613
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RESULT 4

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US-10-094-749-2312
; Sequence 2312, Application US/10094749
; Publication No. US20030229741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUTUKO
; APPLICANT: HITO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 08435/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 2312
 LENGTH: 665
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-094-749-2312

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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 5
 US-10-377-072-26
 Sequence 26, Application US/10377072
 Publication No. US20040009501A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals Inc.
 APPLICANT: Curtis, Rory A.J.
 APPLICANT: Logan, Thomas Joseph
 APPLICANT: Glucksmann, Maria A.
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Williamson, Mark J.
 APPLICANT: Rudolph-Owen, Laura A.
 APPLICANT: Chun, Myoung
 APPLICANT: Teal, Feng-Ying
 TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
 TITLE OF INVENTION: 36692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 FILE REFERENCE: MP103-0180NMIM
 CURRENT APPLICATION NUMBER: US/10/377,072
 CURRENT FILING DATE: 2003-02-27
 PRIOR APPLICATION NUMBER: US 09/895,860
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/215,370
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: US 09/723,806
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: US 60/187,455
 PRIOR FILING DATE: 2000-03-07
 PRIOR APPLICATION NUMBER: US 09/843,297
 PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 60/199,801
 PRIOR FILING DATE: 2000-04-26
 PRIOR APPLICATION NUMBER: US 09/861,801
 PRIOR FILING DATE: 2001-05-21
 PRIOR APPLICATION NUMBER: US 60/205,508
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/816,494
 PRIOR FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: US 09/815,419
 PRIOR FILING DATE: 2001-03-22
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 26
 LENGTH: 665
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-377-072-26

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 434 TTLDTGNKLCQPSVQELSEOTPEPSPDKEASIPKKIQTARPSDSQSKRLHSVTSSSG 493
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 494 TQRSLSLPLHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPSL 553
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 554 TSSWFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRQKPSDRADSRGW 613
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RESULT 6
 US-10-072-012-660
 Sequence 680, Application US/10072012
 Publication No. US20040033493A1
 GENERAL INFORMATION:
 APPLICANT: Tcheurev, Velizar
 APPLICANT: Spytek, Kimberly
 APPLICANT: Zernusen, Bryan
 APPLICANT: Patcurajan, Meera
 APPLICANT: Shinkets, Richard
 APPLICANT: Li, Li
 APPLICANT: Gangoli, Baha
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Anderson, David W.
 APPLICANT: Rastelli, Luca
 APPLICANT: Miller, Charles E.
 APPLICANT: Gerlach, Valerie

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; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimир Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 680
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-680

Query Match          71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPFIPESHFLRVPVNDSECEKILPMUDKSVDFIERAKASNGCVLVHCLAGISRAT 253
    |||||
DB 194 TCPKPFIPESHFLRVPVNDSECEKILPMUDKSVDFIERAKASNGCVLVHCLAGISRAT 253
    |||||

QY 254 IAIAYIMKEMDMSLDEAYR PVYKRPDTISPNENFLGQLLDYEKKIKNOTGASGPKSKLT 313
    |||||
DB 254 IAIAYIMKEMDMSLDEAYR PVYKRPDTISPNENFLGQLLDYEKKIKNOTGASGPKSKLT 313
    |||||

QY 314 LHEKNEVPAVSEGGOKSETPPLSPCCADSAISEAAGRPVPAVSPVQPSLLTD 373
    |||||
DB 314 LHEKNEVPAVSEGGOKSETPPLSPCCADSAISEAAGRPVPAVSPVQPSLLTD 373
    |||||

QY 374 SPLVQALSGILHSAADLEDSNKLKRSFSLDIKSVYSASMAASIHGFSSSEDALEYKKS 433
    |||||
DB 374 SPLVQALSGILHSAADLEDSNKLKRSFSLDIKSVYSASMAASIHGFSSSEDALEYKKS 433
    |||||

QY 434 TTLDTGNKLCOPSPVOELSEQTPETSPDYKEASIPKKTOTARPDSQSRLHSVTSSEG 493
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DB 434 TTLDTGNKLCOPSPVOELSEQTPETSPDYKEASIPKKTOTARPDSQSRLHSVTSSEG 493
    |||||

QY 494 TAORSLSLPLHRSQSVEDNYHTSFLRGLSTSOOHLTKSAGILGKGMHSDIILAPQSTPSL 553
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DB 494 TAORSLSLPLHRSQSVEDNYHTSFLRGLSTSOOHLTKSAGILGKGMHSDIILAPQSTPSL 553
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RESULT 7
US-10-072-012-681
; Sequence 681, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tcherny, Velizar
; APPLICANT: Spyrek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Bsha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 681
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-681

Query Match          71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 194 TCEPKDFPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
DB 194 TCEPKDFPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
QY 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLGOLLDYEEKIKNOGTGASGPKSKLX 313
DB 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLGOLLDYEEKIKNOGTGASGPKSKLX 313
QY 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSVPQPSLLBD 373
DB 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSVPQPSLLBD 373
QY 374 SPLVQALSGLHLSADRLSDSNLKRSPSLDIKSVSYSASMAASLHGFSSEDLLEYKXS 433
DB 374 SPLVQALSGLHLSADRLSDSNLKRSPSLDIKSVSYSASMAASLHGFSSEDLLEYKXS 433
QY 434 TLLDGTNKLCOFSPVOELSEQTPETSPDXEASIPKQLOTARPDSQSKRLHSVRTSSG 493
DB 434 TLLDGTNKLCOFSPVOELSEQTPETSPDXEASIPKQLOTARPDSQSKRLHSVRTSSG 493
QY 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOOHLTKSAGLGKWHSDIILAPQISTPST 553
DB 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOOHLTKSAGLGKWHSDIILAPQISTPST 553
QY 554 TSSWYFATESHPSYASAIYGSASAYSASCSQLPTCGQOYVSVRROKPSDRADRRSM 613
DB 554 TSSWYFATESHPSYASAIYGSASAYSASCSQLPTCGQOYVSVRROKPSDRADRRSM 613
QY 614 HESPEPKOFRKRSQCMERGESIMSENRSREELGKVGSGSSFSGSMELIEVS 665
DB 614 HESPEPKOFRKRSQCMERGESIMSENRSREELGKVGSGSSFSGSMELIEVS 665

RESULT 8

US-10-168-506-14
Sequence 14, Application US/10168506
Publication No. US20040053229A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY D.
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: HILL, RON
APPLICANT: FLANAGAN, PETER
TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
FILE REFERENCE: 038602/1351
CURRENT APPLICATION NUMBER: US/10/168,506
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: PCT/US00/34736
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-506-14

Query Match 71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCEPKDFPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
DB 194 TCEPKDFPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
QY 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLGOLLDYEEKIKNOGTGASGPKSKLX 313
DB 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLGOLLDYEEKIKNOGTGASGPKSKLX 313
QY 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSVPQPSLLBD 373
DB 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSVPQPSLLBD 373

DB 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSVPQPSLLBD 373
QY 374 SPLVQALSGLHLSADRLSDSNLKRSPSLDIKSVSYSASMAASLHGFSSEDLLEYKXS 433
DB 374 SPLVQALSGLHLSADRLSDSNLKRSPSLDIKSVSYSASMAASLHGFSSEDLLEYKXS 433
QY 434 TLLDGTNKLCOFSPVOELSEQTPETSPDXEASIPKQLOTARPDSQSKRLHSVRTSSG 493
DB 434 TLLDGTNKLCOFSPVOELSEQTPETSPDXEASIPKQLOTARPDSQSKRLHSVRTSSG 493
QY 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOOHLTKSAGLGKWHSDIILAPQISTPST 553
DB 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOOHLTKSAGLGKWHSDIILAPQISTPST 553
QY 554 TSSWYFATESHPSYASAIYGSASAYSASCSQLPTCGQOYVSVRROKPSDRADRRSM 613
DB 554 TSSWYFATESHPSYASAIYGSASAYSASCSQLPTCGQOYVSVRROKPSDRADRRSM 613
QY 614 HESPEPKOFRKRSQCMERGESIMSENRSREELGKVGSGSSFSGSMELIEVS 665
DB 614 HESPEPKOFRKRSQCMERGESIMSENRSREELGKVGSGSSFSGSMELIEVS 665

RESULT 9

US-10-343-357-7
Sequence 7, Application US/10343357
Publication No. US20040058341A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; TANG, Y.Tom
APPLICANT: ELIOTT, VICKI S.; RAMKUMAR, Jayalaxmi
APPLICANT: YAO, Monique G.; BUREFORD, Neil
APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
APPLICANT: GANDHI, Ameesha R.; ARVIZU, Chandra S.
APPLICANT: LEE, Ernestine A.; HAPALITA, April J.A.
APPLICANT: LU, Dying Aina M.; TRIBOULEY, Catherine M.
APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
APPLICANT: YUE, Henry; WARREN, Bridget A.
APPLICANT: NGUYEN, Damiel B.; CHAWLA, Nandinder K.
APPLICANT: KEARNEY, Liam
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFERENCE: PI-0173 PCT
CURRENT APPLICATION NUMBER: US/10/343,357
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: PCT/US01/23716
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,679
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/223,272
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/224,309
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 60/226,728
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/229,254
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/231,366
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CD1
US-10-343-357-7

Query Match 71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCEPKDFPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253

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Db 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Qy 254 IAIAYIMKMDMSLDEAYRFVYKEKRPRTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Db 254 IAIAYIMKMDMSLDEAYRFVYKEKRPRTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Qy 314 IHLKPNNEVPVAVSEGGQKSETPPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Db 314 IHLKPNNEVPVAVSEGGQKSETPPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Qy 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSEDALEYYKPS 433
Db 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSEDALEYYKPS 433
Qy 434 TTLDTGNKLCQFSPVOELSEQTPETSPDKBEASIPKKLQTARPSDSQSKRLHSVRTSSG 493
Db 434 TTLDTGNKLCQFSPVOELSEQTPETSPDKBEASIPKKLQTARPSDSQSKRLHSVRTSSG 493
Qy 494 TAOBSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPBL 553
Db 494 TAOBSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPBL 553
Qy 554 TSSWTFATESSHFYASAIYGGASAYSCGQLPTCGDQVYSVRRROKPSDRADSRBW 613
Db 554 TSSWTFATESSHFYASAIYGGASAYSCGQLPTCGDQVYSVRRROKPSDRADSRBW 613
Qy 614 HESPEKOPKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
Db 614 HESPEKOPKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
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RESULT 10

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US-10-257-026-2
; Sequence 2, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDM5
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-026-2
```

Query Match 71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Db 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Qy 254 IAIAYIMKMDMSLDEAYRFVYKEKRPRTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Db 254 IAIAYIMKMDMSLDEAYRFVYKEKRPRTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Qy 314 IHLKPNNEVPVAVSEGGQKSETPPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Db 314 IHLKPNNEVPVAVSEGGQKSETPPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Qy 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSEDALEYYKPS 433
Db 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSEDALEYYKPS 433
Qy 434 TTLDTGNKLCQFSPVOELSEQTPETSPDKBEASIPKKLQTARPSDSQSKRLHSVRTSSG 493
Db 434 TTLDTGNKLCQFSPVOELSEQTPETSPDKBEASIPKKLQTARPSDSQSKRLHSVRTSSG 493
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Qy 494 TAOBSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPBL 553
Db 494 TAOBSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPBL 553
Qy 554 TSSWTFATESSHFYASAIYGGASAYSCGQLPTCGDQVYSVRRROKPSDRADSRBW 613
Db 554 TSSWTFATESSHFYASAIYGGASAYSCGQLPTCGDQVYSVRRROKPSDRADSRBW 613
Qy 614 HESPEKOPKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
Db 614 HESPEKOPKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
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RESULT 11

```
US-10-648-593-240
; Sequence 240, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 240
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-240
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Query Match 71.0%; Score 472; DB 16; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Db 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Qy 254 IAIAYIMKMDMSLDEAYRFVYKEKRPRTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Db 254 IAIAYIMKMDMSLDEAYRFVYKEKRPRTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Qy 314 IHLKPNNEVPVAVSEGGQKSETPPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Db 314 IHLKPNNEVPVAVSEGGQKSETPPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Qy 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSEDALEYYKPS 433
Db 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSEDALEYYKPS 433
Qy 434 TTLDTGNKLCQFSPVOELSEQTPETSPDKBEASIPKKLQTARPSDSQSKRLHSVRTSSG 493
Db 434 TTLDTGNKLCQFSPVOELSEQTPETSPDKBEASIPKKLQTARPSDSQSKRLHSVRTSSG 493
Qy 494 TAOBSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPBL 553
Db 494 TAOBSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPBL 553
Qy 554 TSSWTFATESSHFYASAIYGGASAYSCGQLPTCGDQVYSVRRROKPSDRADSRBW 613
Db 554 TSSWTFATESSHFYASAIYGGASAYSCGQLPTCGDQVYSVRRROKPSDRADSRBW 613
Qy 614 HESPEKOPKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
Db 614 HESPEKOPKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
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RESULT 12
 US-10-648-593-247
 / Sequence 247, Application US/10648593
 / Publication No. US20040106132A1
 / GENERAL INFORMATION:
 / APPLICANT: Bristol-Myers Squibb Company
 / TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
 / INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
 / TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
 / FILE REFERENCE: D0273 NP
 / CURRENT APPLICATION NUMBER: US/10/648,593
 / CURRENT FILING DATE: 2003-08-26
 / PRIOR APPLICATION NUMBER: 60/406,385
 / PRIOR FILING DATE: 2002-08-27
 / NUMBER OF SEQ ID NOS: 557
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 247
 / LENGTH: 665
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-648-593-247

Query Match 71.0%; Score 472; DB 16; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	DB	Sequence	Score	DB	Length	Indels	Gaps
194	TCPKDPIFESHFLRVPNVDSFCCKILPWLKDSVDFIERAKASNGCVLVHCLAGISRAT	253					
194	TCPKDPIFESHFLRVPNVDSFCCKILPWLKDSVDFIERAKASNGCVLVHCLAGISRAT	253					
254	IAIAYIMKMDMSLDEAYRFVKEKRTISPNFNFLGQLLDYKIKINQVGAAGPSKLT	313					
254	IAIAYIMKMDMSLDEAYRFVKEKRTISPNFNFLGQLLDYKIKINQVGAAGPSKLT	313					
314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAAQGRPVHPASVPSVQPSLLED	373					
314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAAQGRPVHPASVPSVQPSLLED	373					
374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433					
374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433					
434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKLQOTAPPSOSQRLHSVRTSSG	493					
434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKLQOTAPPSOSQRLHSVRTSSG	493					
494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553					
494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553					
554	TSSWTFATESHFFYSASAIYGGASAYSCGQLPTCGQVYSVRRQKPSDRADSRRW	613					
554	TSSWTFATESHFFYSASAIYGGASAYSCGQLPTCGQVYSVRRQKPSDRADSRRW	613					
614	HEESPEKQFKRRSCOMERGESIMENRSREELGKVGSSQSPSGSMETIEVS	665					
614	HEESPEKQFKRRSCOMERGESIMENRSREELGKVGSSQSPSGSMETIEVS	665					

RESULT 13
 US-10-377-072-26
 / Sequence 26, Application US/10377072
 / Publication No. US20040157221A9
 / GENERAL INFORMATION:
 / APPLICANT: Millennium Pharmaceuticals Inc.
 / APPLICANT: Curtis, Rory A.J.
 / APPLICANT: Logan, Thomas Joseph
 / APPLICANT: Gluckmann, Maria A.
 / APPLICANT: Meyers, Rachel E.
 / APPLICANT: Williamson, Mark J.
 / APPLICANT: Rudolph-Owen, Laura A.
 / APPLICANT: Chun, Miyoung
 / APPLICANT: Teal, Fong-Ying

/ TITLE OF INVENTION: NOVEL, 25869, 25934, 26335, 50365, 21117,
 / TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 / TITLE OF INVENTION: AND USES THEREFOR
 / FILE REFERENCE: MP103-0180M1M
 / CURRENT APPLICATION NUMBER: US/10/377,072
 / CURRENT FILING DATE: 2003-02-27
 / PRIOR APPLICATION NUMBER: US 09/895,860
 / PRIOR FILING DATE: 2001-06-29
 / PRIOR APPLICATION NUMBER: US 60/215,370
 / PRIOR FILING DATE: 2000-06-29
 / PRIOR APPLICATION NUMBER: US 09/723,806
 / PRIOR FILING DATE: 2000-11-28
 / PRIOR APPLICATION NUMBER: US 60/187,455
 / PRIOR FILING DATE: 2000-03-07
 / PRIOR APPLICATION NUMBER: US 09/843,297
 / PRIOR FILING DATE: 2001-04-25
 / PRIOR APPLICATION NUMBER: US 60/199,801
 / PRIOR FILING DATE: 2000-04-26
 / PRIOR APPLICATION NUMBER: US 09/861,801
 / PRIOR FILING DATE: 2001-05-21
 / PRIOR APPLICATION NUMBER: US 60/205,508
 / PRIOR FILING DATE: 2000-05-19
 / PRIOR APPLICATION NUMBER: US 09/816,494
 / PRIOR FILING DATE: 2001-03-23
 / PRIOR APPLICATION NUMBER: US 09/815,419
 / PRIOR FILING DATE: 2001-03-22
 / Remaining Prior Application data removed - See file wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 114
 / SOFTWARE: FaeltSeq for Windows Version 4.0
 / SEQ ID NO 26
 / LENGTH: 665
 / TYPE: PRT
 / ORGANISM: Homo Sapiens
 US-10-377-072-26

Query Match 71.0%; Score 472; DB 16; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	DB	Sequence	Score	DB	Length	Indels	Gaps
194	TCPKDPIFESHFLRVPNVDSFCCKILPWLKDSVDFIERAKASNGCVLVHCLAGISRAT	253					
194	TCPKDPIFESHFLRVPNVDSFCCKILPWLKDSVDFIERAKASNGCVLVHCLAGISRAT	253					
254	IAIAYIMKMDMSLDEAYRFVKEKRTISPNFNFLGQLLDYKIKINQVGAAGPSKLT	313					
254	IAIAYIMKMDMSLDEAYRFVKEKRTISPNFNFLGQLLDYKIKINQVGAAGPSKLT	313					
314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAAQGRPVHPASVPSVQPSLLED	373					
314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAAQGRPVHPASVPSVQPSLLED	373					
374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433					
374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433					
434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKLQOTAPPSOSQRLHSVRTSSG	493					
434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKLQOTAPPSOSQRLHSVRTSSG	493					
494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553					
494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553					
554	TSSWTFATESHFFYSASAIYGGASAYSCGQLPTCGQVYSVRRQKPSDRADSRRW	613					
554	TSSWTFATESHFFYSASAIYGGASAYSCGQLPTCGQVYSVRRQKPSDRADSRRW	613					
614	HEESPEKQFKRRSCOMERGESIMENRSREELGKVGSSQSPSGSMETIEVS	665					
614	HEESPEKQFKRRSCOMERGESIMENRSREELGKVGSSQSPSGSMETIEVS	665					

RESULT 14

US-10-072-012-679
; Sequence 679, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Molenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 679
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-679
Query Match 71.0%; Score 472; DB 15; Length 690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 194 TCPKDFIPESHFLVAVNDSCFKILPMLDKSVDFIEKAKASNGCVLVHCLAGISRSAT 253
DB 219 TCPKDFIPESHFLVAVNDSCFKILPMLDKSVDFIEKAKASNGCVLVHCLAGISRSAT 278
QY 254 IAIATIMRMKMSLDEAVRFVYCKERTPTSPNPNFGQLLDYKAKIKNOTGASGPKSKL 313
DB 279 IAIATIMRMKMSLDEAVRFVYCKERTPTSPNPNFGQLLDYKAKIKNOTGASGPKSKL 338
QY 314 LHLKRNPEVPVAVSEGQKSEFTPLSPPCADSATSEAAQRPVHPASVSPSVQPSLLED 373

DB 339 LHLKRNPEVPVAVSEGQKSEFTPLSPPCADSATSEAAQRPVHPASVSPSVQPSLLED 398
QY 374 SPLVALSLGHLHSADRLDSDNKLKRSFSLDLIKSVSYASMSAASLHGFSSSBDALERYKPS 433
DB 399 SPLVALSLGHLHSADRLDSDNKLKRSFSLDLIKSVSYASMSAASLHGFSSSBDALERYKPS 458
QY 434 TTLDTGNLCOPSPVOELSEOTPEPSPDKEASIPKLIQTARPSDSQKRLHVSATSSSG 493
DB 459 TTLDTGNLCOPSPVOELSEOTPEPSPDKEASIPKLIQTARPSDSQKRLHVSATSSSG 518
QY 494 TAORSLSLPLKRSQVEDNHTSFLFGLSTSQOHLTKSAGLKGMSDILAPOTSTPSL 553
DB 519 TAORSLSLPLKRSQVEDNHTSFLFGLSTSQOHLTKSAGLKGMSDILAPOTSTPSL 578
QY 554 TSSWYFATESSHFYASAIYGGASASVAYSCSGLPTCGDOYVSVRROKPSDRADRSRW 613
DB 579 TSSWYFATESSHFYASAIYGGASASVAYSCSGLPTCGDOYVSVRROKPSDRADRSRW 638
QY 614 HESPEKQFKRRSCQMEFGESIMSENRSREBLKVGSSFSFGSMETIEVS 665
DB 639 HESPEKQFKRRSCQMEFGESIMSENRSREBLKVGSSFSFGSMETIEVS 690
RESULT 15
US-10-072-012-703
; Sequence 703, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Molenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 703
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-703

/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See file wrapper or PAM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 703
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-703

Query Match 71.0%; Score 472; DB 15; Length 690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKDPFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKASNCVTVHCLAGISRSAT 253
DB 219 TCPKDPFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKASNCVTVHCLAGISRSAT 278
QY 254 IAIAYIMRMDMSLDEAARFVYKERTPTSPNPNFGLLDYRKIKNOTGASGPKSKL 313
DB 279 IAIAYIMRMDMSLDEAARFVYKERTPTSPNPNFGLLDYRKIKNOTGASGPKSKL 338
QY 314 LHLKPNRPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPQSLIED 373
DB 339 LHLKPNRPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPQSLIED 398
QY 374 SPLVALSGHLISADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 433
DB 399 SPLVALSGHLISADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 458
QY 434 TTLDTGNTKLCQPSVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLSVRTSSG 493
DB 459 TTLDTGNTKLCQPSVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLSVRTSSG 518
QY 494 TPAORSLSPLRSGSVEDNYHTSPLFGLSTSQOHLTKSAGLKGWHSIILAPOTSTPBL 553
DB 519 TPAORSLSPLRSGSVEDNYHTSPLFGLSTSQOHLTKSAGLKGWHSIILAPOTSTPBL 578
QY 554 TSSWYFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRQKPSDRADSRSM 613
DB 579 TSSWYFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRQKPSDRADSRSM 638
QY 614 HESPEFKQFKRRSCOMERGESIMENRREELGKVGSSSFGSMETIEVS 665
DB 639 HESPEFKQFKRRSCOMERGESIMENRREELGKVGSSSFGSMETIEVS 690

RESULT 16

US-10-425-114-54204
/ Sequence 54204, Application US/10425114
/ Publication No. US2004003488A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhou, Yinhua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack B
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 54204
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB4119-028-H6_F11.pap
US-10-425-114-54204

Query Match 71.0%; Score 472; DB 15; Length 690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKDPFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKASNCVTVHCLAGISRSAT 253
DB 219 TCPKDPFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKASNCVTVHCLAGISRSAT 278
QY 254 IAIAYIMRMDMSLDEAARFVYKERTPTSPNPNFGLLDYRKIKNOTGASGPKSKL 313
DB 279 IAIAYIMRMDMSLDEAARFVYKERTPTSPNPNFGLLDYRKIKNOTGASGPKSKL 338
QY 314 LHLKPNRPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPQSLIED 373
DB 339 LHLKPNRPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPQSLIED 398
QY 374 SPLVALSGHLISADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 433
DB 399 SPLVALSGHLISADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 458
QY 434 TTLDTGNTKLCQPSVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLSVRTSSG 493
DB 459 TTLDTGNTKLCQPSVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLSVRTSSG 518
QY 494 TPAORSLSPLRSGSVEDNYHTSPLFGLSTSQOHLTKSAGLKGWHSIILAPOTSTPBL 553
DB 519 TPAORSLSPLRSGSVEDNYHTSPLFGLSTSQOHLTKSAGLKGWHSIILAPOTSTPBL 578
QY 554 TSSWYFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRQKPSDRADSRSM 613
DB 579 TSSWYFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRQKPSDRADSRSM 638
QY 614 HESPEFKQFKRRSCOMERGESIMENRREELGKVGSSSFGSMETIEVS 665
DB 639 HESPEFKQFKRRSCOMERGESIMENRREELGKVGSSSFGSMETIEVS 690

RESULT 17

US-10-072-012-256
/ Sequence 256, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchervet, Vellizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Patuturajan, Meera
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangoli, Esba
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier, Jr., Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Wolman, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grosse, William M.
/ APPLICANT: Alsbrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514

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; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 256
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-256

Query Match      59.2%; Score 394; DB 15; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 RFVKEKRPTISNPNFGLGLDYEEKIKKQGTASGPKSLKLLHLEKPNBPVPAVSEGGQ 331
DB 267 RFVKEKRPTISNPNFGLGLDYEEKIKKQGTASGPKSLKLLHLEKPNBPVPAVSEGGQ 346
QY 332 KSETLSPPCADSATSEAAQGRPVHPASVSVSVQPSLLEDSPLVQALSGHLSDADLE 391
DB 347 KSETLSPPCADSATSEAAQGRPVHPASVSVSVQPSLLEDSPLVQALSGHLSDADLE 406
QY 332 DSNKTKRPSLIDIKVSVYSASMAASLHGSSSEDALEYKPKETTLDTGNKLCQFSPVOEL 451
DB 407 DSNKTKRPSLIDIKVSVYSASMAASLHGSSSEDALEYKPKETTLDTGNKLCQFSPVOEL 466
QY 452 SEQTPETSPDKEEASIPKKLQTPAPSDSQSKRLHSVTRSSSGTAQRLSLPLHRSGVVD 511
DB 467 SEQTPETSPDKEEASIPKKLQTPAPSDSQSKRLHSVTRSSSGTAQRLSLPLHRSGVVD 526
QY 512 NYHTSFLFGLSTSQOHLTKSAGLKGWHSDDLAPQSTPSTLTSWYFATSSHFYSASA 571
DB 527 NYHTSFLFGLSTSQOHLTKSAGLKGWHSDDLAPQSTPSTLTSWYFATSSHFYSASA 586
QY 572 IYGSASYSAYSCSGLPTCGDOVYSVRROKPSDRADSRSMHEBSPFEKQPKRSCOME 631
DB 587 IYGSASYSAYSCSGLPTCGDOVYSVRROKPSDRADSRSMHEBSPFEKQPKRSCOME 646
QY 632 FGEISIMSENRSEELGKVGSSSFGSGMEIIEVS 665
DB 647 FGEISIMSENRSEELGKVGSSSFGSGMEIIEVS 680

RESULT 18
US-10-072-012-258
; Sequence 258, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: zeinusen, Bryan
; APPLICANT: Patnurajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
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; APPLICANT: Raastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grobse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-258

Query Match      45.7%; Score 304; DB 15; Length 662;
Best Local Similarity 100.0%; Pred. No. 1,4e-278;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 SVPSVQPSLLEDSPLVQALSGHLSDADLEDSNKKRPSLIDIKSVSASMAASLHGFS 421
DB 359 SVPSVQPSLLEDSPLVQALSGHLSDADLEDSNKKRPSLIDIKSVSASMAASLHGFS 418
QY 422 SSEDALLEYKPKETTLDTGNKLCQFSPVOELSEQTPETSPDKEEASIPKKLQTPAPSDSQS 481
DB 419 SSEDALLEYKPKETTLDTGNKLCQFSPVOELSEQTPETSPDKEEASIPKKLQTPAPSDSQS 478
QY 482 KRLHSVTRSSSGTAQRLSLPLHRSGVVDNYHTSFLFGLSTSQOHLTKSAGLKGWHS 541
DB 479 KRLHSVTRSSSGTAQRLSLPLHRSGVVDNYHTSFLFGLSTSQOHLTKSAGLKGWHS 538
QY 542 DILAPQSTPSTLTSWYFATSSHFYSASATYGSASYSAYSCSGLPTCGDOVYSVRRO 601
DB 539 DILAPQSTPSTLTSWYFATSSHFYSASATYGSASYSAYSCSGLPTCGDOVYSVRRO 598
QY 602 KPSDRADSRSMHEBSPFEKQPKRSCOMEFGEISIMSENRSEELGKVGSSSFGSGMEI 661
DB 599 KPSDRADSRSMHEBSPFEKQPKRSCOMERGESIMSENRSEELGKVGSSSFGSGMEI 658
QY 662 IEVS 665
|||
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Db 659 IEVS 662

RESULT 19

US-10-296-115-1259
; Sequence 1259, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc.
; TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ. ID NOS: 1478
; SEQ ID NO 1259
; LENGTH: 672
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(672)
; OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
US-10-296-115-1259

Query Match 38.8%; Score 258; DB 15; Length 672;
Best Local Similarity 100.0%; Pred. No. 5e-235;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIPESHFLRPVNDSECEKILPWLDSVDFIEKAKSNGCVLHCLAGISRSAT 253
Db 201 TCPKPDFIPESHFLRPVNDSECEKILPWLDSVDFIEKAKSNGCVLHCLAGISRSAT 260
QY 254 IAIAYIMKRMDSLDEAYRFVYKERTPTSPNPNFLGQLLDYKIKINQTAGSKPKL 313
Db 261 IAIAYIMKRMDSLDEAYRFVYKERTPTSPNPNFLGQLLDYKIKINQTAGSKPKL 320
QY 314 LHLKPNRPVPAVSEGGQKSETPISPPCADSATSSAAGRPVHPASVPSVQPSLLED 373
Db 321 LHLKPNRPVPAVSEGGQKSETPISPPCADSATSSAAGRPVHPASVPSVQPSLLED 380
QY 374 SPVVALSGHLHSARLSDSNLTKRSFSLDTSVSYSMAASLHGFSSSEBALTYKPS 433
Db 381 SPVVALSGHLHSARLSDSNLTKRSFSLDTSVSYSMAASLHGFSSSEBALTYKPS 440
QY 434 TTLDTNKLCOFSPVOEL 451
Db 441 TTLDTNKLCOFSPVOEL 458

RESULT 20

US-10-108-260A-4872
; Sequence 4872, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4872
; LENGTH: 253
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-108-260A-4872

Query Match 22.9%; Score 152; DB 15; Length 253;
Best Local Similarity 99.6%; Pred. No. 4.6e-135;

Matches 252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 MAASLHGFSSEDALEYKPPSTTLTGTKLCOFSPVOELSEOTPTSPDKESASIPKIQ 472
Db 1 MAASLHGFSSEDALEYKPPSTTLTGTKLCOFSPVOELSEOTPTSPDKESASIPKIQ 60
QY 473 TARPDSOSKRLHSAVRSSTSGTAQRSLSPHLRSGSVEDNYATSEFLGLSTSQHLTKSA 532
Db 61 TARPDSOSKRLHSAVRSSTSGTAQRSLSPHLRSGSVEDNYATSEFLGLSTSQHLTKSA 120
QY 533 GLGLKGMHSDILAPQSTSPSLTSSVYPATSSHPYSAAYGSAYSAYSCSQLPCTGD 592
Db 121 GLGLKGMHSDILAPQSTSPSLTSSVYPATSSHPYSAAYGSAYSAYSCSQLPCTGD 180
QY 593 QVYSVRRQKPSDRDPSRSMWHEEPFKQFRRSCQWEEFGSINSRREELKVGSG 652
Db 181 QVYSVRRQKPSDRDPSRSMWHEEPFKQFRRSCQWEEFGSINSRREELKVGSG 240
QY 653 SFFSGSMELIEVS 665
Db 241 SFFSGSMELIEVS 253

RESULT 21

US-09-964-277-7
; Sequence 7, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucite, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125, 434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 155
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-964-277-7

Query Match 16.2%; Score 108; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.3e-93;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIPESHFLRPVNDSECEKILPWLDSVDFIEKAKSNGCVLHCLAGISRSAT 253
Db 48 TCPKPDFIPESHFLRPVNDSECEKILPWLDSVDFIEKAKSNGCVLHCLAGISRSAT 107
QY 254 IAIAYIMKRMDSLDEAYRFVYKERTPTSPNPNFLGQLLDYKIKINQ 301
Db 108 IAIAYIMKRMDSLDEAYRFVYKERTPTSPNPNFLGQLLDYKIKINQ 155

RESULT 22

US-10-072-012-682
; Sequence 682, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernyev, Vellizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zetunuen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esna
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Raetelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.

APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Molenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 682
LENGTH: 660
TYPE: PRT
ORGANISM: Mus musculus
US-10-072-012-682

Query Match 10.1%; Score 67; DB 15; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.2e-54;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 15 LVALLSGTEKVLILDSRPFEYNTSHLEAININCSKIMKRRLOODKVLITELIOHSAK 74
QY 75 HKVDIDC 81
DB 75 HKVDIDC 81
RESULT 23
US-10-072-012-683
Sequence 683, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patcurajan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esna
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastecelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie

APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Molenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 683
LENGTH: 677
TYPE: PRT
ORGANISM: Mus musculus
US-10-072-012-683

Query Match 9.6%; Score 64; DB 15; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 114 SFNSVHLAAGFAEFRCFPGICEGKSTLVPICISOPCLPVANIGPTTILRNLYGCORD 173
QY 174 VLNK 177
DB 174 VLNK 177
RESULT 24
US-09-764-853-578
Sequence 578, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P1206
CURRENT APPLICATION NUMBER: US/09/764,853
PRIOR FILING DATE: 2001-01-17
Prior Application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 578
LENGTH: 88
TYPE: PRT

ORGANISM: Homo sapiens
US-09-764-853-578

Query Match 8.4%; Score 56; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.4e-44;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26 MAHEMIGTQIVTERLVALLSGSTERYLLIDSRPFVEYNTSHILEAININCSKLMKR 81

Search completed: February 9, 2005, 12:40:27
Job time : 138 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 14, 2005, 13:42:21 ; Search time 845 Seconds

(without alignments)
4643.557 Million cell updates/sec

Title: US-10-029-345a-109

Perfect score: 665
Sequence: 1 MAHEMIGQIVTERLVALDE.....LGKVGSGSFGSGSMIEIIVS 665

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Word size: 75

Total number of hits satisfying chosen parameters: 39

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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-ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAEXT=500 -MINLEN=0
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
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Database : Published Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472	71.0	1998	9	US-09-816-494-3
2	472	71.0	1998	17	US-10-377-072-27
3	472	71.0	1998	18	US-10-377-072-27
4	472	71.0	2102	17	US-10-094-749-673
5	472	71.0	2732	17	US-10-168-506-2
6	472	71.0	2966	17	US-10-296-115-520
7	472	71.0	3059	17	US-10-257-026-1
8	472	71.0	3332	9	US-09-964-277-20
9	472	71.0	3496	9	US-09-964-277-1
10	472	71.0	3521	18	US-10-370-715B-261
11	472	71.0	3544	9	US-09-816-494-1
12	472	71.0	3544	17	US-10-377-072-25
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14	472	71.0	3625	17	US-10-425-114-26234
15	472	71.0	3766	17	US-10-343-357-17
16	472	71.0	4790	18	US-10-648-593-115
17	472	71.0	5145	18	US-10-357-930-20824
18	472	71.0	5145	18	US-10-357-930-20869
19	472	71.0	5145	18	US-10-357-930-21071
20	472	71.0	5145	18	US-10-357-930-21083
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22	472	71.0	5145	18	US-10-357-930-21307
23	472	71.0	5145	18	US-10-357-930-22820
24	472	71.0	5145	18	US-10-357-930-26669
25	472	71.0	5145	18	US-10-357-930-26815
26	472	71.0	5145	18	US-10-357-930-26912
27	472	71.0	5145	18	US-10-357-930-26923
28	472	71.0	5145	18	US-10-357-930-27145
29	472	71.0	5145	18	US-10-357-930-27149
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33	178	26.8	1916	17	US-10-108-260A-2429
34	138	20.8	425	18	US-10-357-930-10717
35	137	20.6	467	18	US-10-357-930-131909
36	137	20.6	467	18	US-10-357-930-40868
37	137	20.6	467	18	US-10-357-930-41017
38	133	20.0	408	18	US-10-357-930-10898
39	132	19.8	438	18	US-10-357-930-32077

ALIGNMENTS

RESULT 1
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Length: 1998
Matches: 663
Conservative: 0
Mismatches: 2

Query Match: 70.98% Indels: 4
DB: 9 Gaps: 0

US-10-029-345A-109 (1-665) x US-09-816-494-3 (1-1998)

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QY 21 SerGIYThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 61 AGTGGAGCGGAAAAAGCTGGCTTAAATTGATAGCCGGCATTTGGATGCAATACATCC 120
QY 41 HisIleLeuGluValAlaIleAsnIleAsnGlySerLeuLeuLeuLeuLeuLeuLeu 60
DB 121 CACATTTTGGAAAGCATTAATATCATCTGCCAAGCTTATGAGAGCAAGGTTGCAACG 180
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaIleHisIleValAspIleAsp 80
DB 181 GACAAAGTGTAAATTACAGAGCTCATCAGCATTCAGGAAACATAAGTTGACATTGAT 240
QY 81 CysSerGlnIleValValIleValIleValIleValIleValIleValIleValIleVal 100
DB 241 TGCAAGTCAAGAGGTGTAGTTAGTTCAGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 300
QY 101 AspCysPheLeuThrValLeuLeuGlyIleValLeuGlyIleValLeuLeuLeuLeu 120
DB 301 GACTGTTTTCACCTGTAATCTTGGGTAACTGAGAAAGAGCTTCACCTGTTCACTG 360
QY 121 LeuAlaGlyIleGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyIle 140
DB 361 CTTCAGAGTGGTGTGCTGAGTCTCTGCTGTTTCTCCGCTGCTGCTGAGGAAATCC 420
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 421 ACTCTAGCTCTACCTGATTTCTCAGCTTGTACTTACCTGTGCAACATGGGCGCAACC 480
QY 161 ArgIleLeuProAsnLeuThrLeuGlyCysGlnArgPheValLeuAsnIleValIle 180
DB 481 CGAATTTCTCCCAATCTTATCTTGGCTGCGCAGAGATGTCCTCAACAGAGACTAT- 539
QY 181 -GlnGlnAsnGlyIleGlyIleValIleAsnAlaSerIleThrCysProIleAspProAsp 200
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DB 659 TGCGGTGGTGGCAAACTCAATGATTCATTGAGAAAGCAAAAGCTCCCATAGAGTGG 718
QY 240 AlLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIle 260
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QY 280 hrIleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspIleGluValIleVal 300
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QY 320 snGluProValProAlaValSerGluGlyIleValIleValSerGluThrProLeuSerPro 340
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DB 1019 CCTGTGCCACTCTGTACTTACAGAGCAGAGCAAGAGAGAGAGAGAGAGAGAGAGAG 1078
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DB 1259 TCTCCTCATCAGAAAGTCTTGGAAATACTACAAACCTTCCACTCTGTGATGGACCA 1318
QY 440 snIleValLeuGlyIlePheSerProValGlnGluLeuSerGluGlnThrProGluThr 460
DB 1319 ACAAGCTATGCAAGTCTCTCCCTGTGAGAACTATCGAGAGACTCCGAAACAGATC 1378
QY 460 roAspIleGluGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSer 480
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QY 560 LaThrGluSerSerHisPheIleValSerAlaIleIleValIleValIleValIleVal 580
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QY 640 snArgSerArgGluIleuGlyIleValAlaGlySerGlnSerSerPheSerGlySerMet 660
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QY 660 IuIleIleGluValSer 665
DB 1979 AAATCATTAAGTCTCC 1995

RESULT 2
US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Gluckmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Myoung
APPLICANT: Tsai, Fong-ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
FILE REFERENCE: MP103-0180NMIM
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
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PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
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SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27
Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Query Match: 70.98%
Length: 1998
Matches: 663
Conservative: 0
Mismatch: 2
Indels: 4
Gaps: 0
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DB 121 CACATTTTGGAACTTAAATCACTGCTCCAACTTAATGAAGCAAGTTGCAACG 180
QY 61 AspLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
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QY 101 AspCybPheLeuThValLeuLeuGlyLeuLeuGluValSerPheAsnSerValHsLeu 120
DB 301 GACTGTTTCTCAGCTGACTCTCGGTAACTGGAGAAAGCTTCAACTCTGTCACCG 360
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCybPheProGlyLeuCybGluGlyValSer 140
DB 361 CTTCAGAGGAGGTTGCTGTAATTCCTCTGTTTCTCGGCTCTGTAAAGAAATCC 420
QY 141 ThrLeuValProThrCybIleSerGlnProCybLeuProValAlaAsnIleGlyProThr 160
DB 421 ACTCTAGTCCCTACTGCTGCTTCTCAGCTTCTTCACTTGTGCAACCTGGCCAAAC 480
QY 161 ArgIleLeuProAsnLeuValLeuGlyCybGlnArgAspValLeuAsnLeuGluLeu 180
DB 481 CGAATTCCTCCAACTTTATCTGGCTGCCAGAGATGCTCTCAACAGAGCTGAT- 539
QY 181 -GlnGlnAnglyIleGlyThrValLeuAsnAlaSerThr-ThrCybProValProAsp 200
DB 540 GGAGCAGAAATGGATTTGTTATGTGTAAATGCCAGCA-TRCTGTCCAAAGCTGACT 598
QY 200 HsIleProGluSerHsPheLeuArgValProValAsnAspSerPheCybGluValIle 220
DB 599 TTAATCCGAGTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658
QY 220 euProTyrLeuAspLeuValAspPheIleGluValAlaValAsnAnglyCybVal 240
DB 659 TCCCGGTGGTGAACATCATGATGATTCATGAGAAAGCAAAAGCTCCATGATGAG 718
QY 240 AlLeuValHsCybLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIle 260
DB 719 TTCTAGTGCACGTTTATGCTGGAATCTCCGCTCCGCAACATGCTATGCTTCATCA 778
QY 260 eTLeuArgMetAspMetSerLeuAspGluAlaIleArgPheValValGluValArgPro 280
DB 779 TGAAGAGATGACATGCTTTTGAATGAACTTACAGATTTGTGAAGAAAGAAAGCTTA 838
QY 280 HsIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluValIleVal 300
DB 839 CTATATCTCCAAATCTTCAATTTCTGGGCCAATCTCTGCACTATGAGAAAGATTAAGA 898
QY 300 eGlnThrGlyAlaSerGlyProValSerLeuLeuLeuLeuLeuLeuLeuLeuLeu 320
DB 899 ACCAGACTGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTGGAGAAAGCCAA 958
QY 320 eGluProValProAlaValSerGluGlyGlyGlnLeuSerGlnThrProLeuSerPro 340
DB 959 ATGAACCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1018
QY 340 roCybAlaAspSerAlaThrSerGluAlaIleGlyGlnArgProValHsProAlaSerV 360
DB 1019 CCTGTGCCGACTCTGCTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1078
QY 360 AlProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 380
DB 1079 TCCCAAGCGTCCG 1138
QY 380 euSerGlyLeuHsIleAsnSerAlaAspArgLeuGluAspSerAsnLeuValAspSer 400
DB 1139 TCAATGGGCTGCACTGTCCGAGACAGGCTGGAAGACAGCAATAGCTCAAGCTTCT 1198
QY 400 HsSerLeuAspIleLeuSerValSerTyrSerAlaSerMetAlaIleSerLeuHsGlyP 420
DB 1199 TCTCTCGGATATCAATCAAGTTTCAATTCAGCAGATGGCAGCATCTTACATAGGCT 1258
QY 420 HsSerSerSerGluAspAlaLeuGluTyrTyrValProSerThrThrLeuAspGlyThr 440
DB 1259 TCTCTCTATCAAAATGTTTGAATCTCAAACTTCCACTCTGATGGAGGAGCA 1318
QY 440 eNlyLeuCybGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460

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Db 1319 ACAAGCTATGCCAGTTCCTCCCTCTTCAGGAACCTACGGAACCACTCCGGAACCACTGC 1378
QY 460 rGAspLySgLnGluLuuLaseRtLePoyLySLeuGlnThraLaarProSeRAspSec 480
Db 1379 CTGATTAAGGAGGAACCCAGCATCCCAAGGAAGCTGACAGCCGACGCTTCAGACAGCC 1438
QY 480 InSeRlyAsgLueuHIsSeRValArgThSeSeRSeRgLYThraLaagInaRSeRleuL 500
Db 1439 AGAGCAAGCCGATTCGCTCGATCGAAGACCAAGCAAGTGGACCCGCGCAAGGCTCCCTTT 1498
QY 500 euseRProLeuHIsArgSeRgLYSeRValGluApaPaNyThraLSeRSeRSeRleuPheg 520
Db 1499 TATCTCCAGCTGATCGAAGTGGAGCGCTGGAGGACATTAACAACACACTCTCTTTTCG 1558
QY 520 lyeuseRThSeRgLnGlnHIsleuThRlySeRSeRlaGlyLeuGlyLeuLySgLYTPH 540
Db 1559 GCCCTTCCACCAAGCCAGCAACCACTCAAGAGTCTGCGCTGGGCTTGAAGGCTGAGC 1618
QY 540 IsSeRAspLleLeuLaProGlnThSeRThProSeRleuThSeRSeRTPYrPhea 560
Db 1619 ACTCGATATCTTGGCCCCCAGACCTTAACCTTCCCTGACAGCAAGCTGGATTTTG 1678
QY 560 laThrguSeRSeRThIsPheTYrSeRSeRlaSeRlaLeTYrGlyLeuSeRlaSeRlyTS 580
Db 1679 CCAAGAGTCTCAACTTCTACTCTGCTCAAGCACTTAACGAGGCAAGTCCAGTTACT 1738
QY 580 exLaTySeRSeRSeRgLnLeuProThCYsGLYAspGlnValTYrSeRValArgArga 600
Db 1739 CTGCTTAAGCTGCAACCAAGCTGCACTGCGAGGAGCAAGTCTATTTCTGCGAGGC 1798
QY 600 rGGLuLYPProSeRAspArgLaApsSeRArgaRgSeRTPHIsGlnGluSeRProheg 620
Db 1799 GCGAGAGGCAAGTGAAGCTGAGCTGCGCGAGGAGTGGCAAGGAAGAGGCCCTTTTG 1858
QY 620 luLYeGlnPheLYaRgArSeRSeRgLnMeTgLnPheGlyGluSeRlEmeSeRgLn 640
Db 1859 AAAAGAGATTAAAGCAAGAGCTGCCAAATGAATTTGAGAGAGCATATGTCAGAGA 1918
QY 640 snArSeRArgGlnGluLeuGlyLYsValGlySeRgLnSeRSeRPhSeRgLYSeRMeTg 660
Db 1919 ACAAGTCAAGGGAAGAGCTGGGGAAGTGGCGAGTCAAGTCTTTTGGCGAGCATGG 1978
QY 660 luLeleGlnValSeR 665
Db 1979 AAATCATTAAGGCTCTCC 1995

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RESULT 3
 US-10-377-072-27
 / Sequence 27, Application US/10377072
 / Publication No. US20040157221A9
 / GENERAL INFORMATION:
 / APPLICANT: Millennium Pharmaceuticals Inc.
 / APPLICANT: Curtis, Roy A.J.
 / APPLICANT: Logan, Thomas Joseph
 / APPLICANT: Gluckemann, Maria A.
 / APPLICANT: Meyers, Rachel E.
 / APPLICANT: Williamson, Mark J.
 / APPLICANT: Rudolph-Owen, Laura A.
 / APPLICANT: Chun, Miyoung
 / APPLICANT: Tsai, Feng-Ying
 / TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
 / TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 / FILE REFERENCE: MP103-0180MNTM
 / CURRENT APPLICATION NUMBER: US/10/377.072
 / PRIOR FILING DATE: 2003-02-27
 / PRIOR APPLICATION NUMBER: US 09/895,860
 / PRIOR FILING DATE: 2001-06-29
 / PRIOR APPLICATION NUMBER: US 60/215,370
 / PRIOR FILING DATE: 2000-06-29
 / PRIOR APPLICATION NUMBER: US 09/723,806
 / PRIOR FILING DATE: 2000-11-28

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/ PRIOR APPLICATION NUMBER: US 60/187,455
/ PRIOR FILING DATE: 2000-03-07
/ PRIOR APPLICATION NUMBER: US 09/843,297
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: US 60/199,801
/ PRIOR FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: US 09/861,801
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: US 60/205,508
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 09/816,494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 09/815,419
/ PRIOR FILING DATE: 2001-03-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PaatSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 1998
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Query Match: 70.98%
DB: 18
Gaps: 0

US-10-029-345A-109 (1-665) x US-10-377-072-27 (1-1998)
QY 1 MetAlaHisGluMetLleGlyThRgLnLeuValThRgLnArgLeuValAlaLeuLeuGln 20
Db 1 ATGGCCATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
QY 21 SerGlyThRgLnLYsValLeuLeuLleApsSeRArgaRgSeRTPHIsGlnThraLSeR 40
Db 61 AGTGAACCGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 41 HisLleLeuGlnLleLeuLleLeuLleLeuLleLeuLleLeuLleLeuLleLeuLleLeu 60
Db 121 CACATTTTGAAGCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
QY 61 AspLYsValLeuLleThRgLnLeuLleGlnHIsSeRlaLYsHIsLYsValaAspLleAps 80
Db 181 GACAAAGTGTAAATTAACAGAGCTCATCCAGATTCAAGCAACATTAAGGTTGACATTGAT 240
QY 81 CYsSeRgLnLYsValaValaLYsAspGlnSeRSeRgLnAspValaLaseRleuSeRSeR 100
Db 241 TCGATCGAAGGTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
QY 101 AspCYsPheLeuThraLleuLeuGlyLYsLeuGlnLYsSeRSeRSeRSeRSeRSeRSeRSe 120
Db 301 GACTGTTTTCATCGATGATCTTCTGGTAACTGGAAGAGGCTTAACCTCTTCACTCG 360
QY 121 LeuLaGlyLYsPheLaGlnPheSeRArgYAspProGlyLeuCYsGlnGlyLYsSeR 140
Db 361 CTTCGAGGTGGTGTGCTGAGTCTCTCGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 141 ThRLeuValProThCYsLleSeRgLnProCYsLeuProValAlaAsnLleGlyProThR 160
Db 421 ACTTAATCTCTAAGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 161 ArgLYeLeuProAsnLeuTYrLeuGlyCYsGlnArgAspValLeuAsnLYsGlnLeuLle 180
Db 481 CGAATCTTCCCAATCTTAATCTTGTGCTGCAAGCAAGTCTCTCAACAAAGAGCTGAT- 539
QY 181 -GlnGlnAsnGlyLleGlyTYrValLeuAsnLaseRlyr-ThCYsProLYsProAsp 200

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Db      540 GCAGCAGAAATGGATGTATGTATGTTAATGCCACAA-TACCTGTCCAAAGCTGACT 598
Qy      200 helterProglusSerHisphenleuAArgValProValIshnapsSerPheCysGluValIle 220
Db      599 TTATCCCGAGTCTCATTTCTCGCTGTGTGTGAATGACACTTTTGTGAAAAATT 658
Qy      220 euProtrleuAapLySerValIaspPheIleGluValIalysAlasSerAenGlyCysV 240
Db      659 TGGCGGTGTGGACAAATGATGATTTCTTATGAAAGCAAAAGCTCCATGATGATG 718
Qy      240 alleuValHscYleuAlaGlyIleSerAysSerIalThrIleAlaIleAlaTyrIle 260
Db      719 TTCTAGTGCACGTGTAGCTGGGATCTCCGCTCCGCCACATCGCTATCGCTATCATCA 778
Qy      260 ellyAArgMetAapMetSerleuAapGluAlaTyrAArgPheValIyGluValAysPro 280
Db      779 TGAAGAGATGACAGTCTTATGATGAAAGCTTACGATTTGTGAAAAAAGACCTA 838
Qy      280 hrlIleSerProAenPheAenPheleuGlyGluIleuAapTyrGluValIleVal 300
Db      839 CTRATCTCCAACTTCAATTTTCTGGGCCACTCTGGACTRITGAAAGAAATTAAGA 898
Qy      300 enGlnThrGlyAlaSerGlyProLySerLySerLySerleuValIleuGluValPro 320
Db      899 ACCAGACTGAGATCAGAGGCCAAAGACAACTCAAGCTGTGACCTGAGAAAGCCAA 958
Qy      320 enGluProValProAlaValSerGluGlyGluIlySerGluThrProLeuSerPro 340
Db      959 ATGAACCTGTCTCTGTCTCAGAGGGTGACAGAAAGCCGAGAGCCCTCAGTCCAC 1018
Qy      340 rOCyAlaIaspSerIalThrSerGluAlaIleGlyGluIlyProValIshProIaSerV 360
Db      1019 CCTGTGCCACTGTGCTACTCAGAGGCAGCAGAAAGCCCGTGACTCCGCCAGCG 1078
Qy      360 alProSerValProSerValGlnProSerleuGluIlyAapSerProleuValGlnAl 380
Db      1079 TGGCCAGCGTCCGACAGCGTGCAGCGCTCCCTGTTAAGAGACGCCGCTGTACAGGCC 1138
Qy      380 euSerGlyLeuHisleuSerIalAapAArgleuGluAapSerAnlyIleuValAysSer 400
Db      1139 TCAGTGGCTGCACCTGTCTCGCAGACAGCGTGGAAACAGCAATAGCTCAAGCCTTCT 1198
Qy      400 heSerleuAapIleYserValSerTyrSerIalaserleuAlaIaserleuHisGlyP 420
Db      1199 TCTCTGTGATCAATCATCATGTTCAATTCAGCCAGCAATGGAGATCTTACATGAGCT 1258
Qy      420 heSerSerSerGluAapAlaIleuGluTyrTyrIlyAProSerThrThrleuAapGlyTh 440
Db      1259 TCTCCCATCAAGAAAGATGCTTGATGATCTACAAACCTTCCACTGCTGATGGACCA 1318
Qy      440 enlyleuCyeglInPheSerProValGlnGluIleuSerGluGlnThrProGluThrSer 460
Db      1319 ACAAGGTAGCCAGTCTCCCGCTGTCAAGAACTATCGAGAGAGACTCCGAAACAGATC 1378
Qy      460 rOaAapLyGluGluAlaSerIleProLyGlyIleuGlnThrIlaAArgProSerAapSer 480
Db      1379 CTGATTAAGAGAAAGCACATCTCCCAAGAACTGAGACCGCAGAGCTTACAGAGACC 1438
Qy      480 InSerIyAArgleuHisSerValAArgThrSerSerSerGlyThrIalInArgSerleu 500
Db      1439 AAGAGCAAGCATTTGCTTCGCTGACAAACAGCAGCGATGGACCGCCAGAGGTCCCTT 1498
Qy      500 euSerProleuHisAysSerGlySerValGluAapAnlyrHisThrSerPheleuPhe 520
Db      1499 TATCTCATCTGCATCGAAGTGGAGCGTGAAGAGCAATTAACAACCACTTCTCTTTCG 1558
Qy      520 IyIleuSerThrSerGlnGlnIleleuThrIlySerIalGlyIleuGlyIleuValGlyTh 540
Db      1559 GCTTTTCCACAGCCAGCAGCACTTACAGAAAGTCTGCTGCGGCTTAAAGGCTGAGC 1618
Qy      540 IaserAapIleleuAlaProGlnThrSerThrProSerleuThrSerSerTyrPheA 560

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Db      1619 ACTCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGATTTTG 1678
Qy      560 IalThrGluSerSerHisPheTyrSerIalaserAlaIleTyrGlyIySerIalaserTyr 580
Db      1679 CCACAGAGCTTCACACATTTACTCTGCTCAGCACTACAGAGCAGCTGCAAGTACT 1738
Qy      580 eAlaTyrSerCySerGlnleuProthrCyGlyAapGlnValTyrSerValAArgArg 600
Db      1739 CTGCTTACAGCTGCAGCAGCAGCTGCCACTTGGGAGACCAATCTTATTTGTGGCAGGC 1798
Qy      600 IyGlnLyAProSerAapArgAlaAapSerAysSerTyrHisGluIleuSerProPhe 620
Db      1799 GGCAGAACCAAGTACAGAGCTGACTCGCGCGAGCTGCATGAGAGAGACCCCTTGG 1858
Qy      620 IulYerGluPheYArgArgSerCyGlnMetGluPheGlyGluSerIleMetSerGlu 640
Db      1859 AAAAGCAGTTTAAAGCAGAACTCCCAATGAAATTTGAGAGAGCATCATGTCAGAA 1918
Qy      640 enAysSerAysGluIleuGlyIlyValIySerGlnSerSerPheSerGlySerMetG 660
Db      1919 ACAGGTCAAGGAGAAAGCTGGGGAAGTGGCAGTCAAGTCTAGCTTTTCCGACAGATG 1978
Qy      660 IulIleIleGluValSer 665
Db      1979 AAATCATGAGGTCTCC 1995

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RESULT 4

US-10-094-749-673
 / Sequence 673, Application US/10094749
 / Publication No. US20030219741A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO
 APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HIO, YUKI
 APPLICANT: OTSUKA, KAORI
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOJI
 APPLICANT: TAMECHIKA, ICHIRO
 APPLICANT: SEKI, NAOHITO
 APPLICANT: YOSHIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTOKU
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
 FILE REFERENCE: 08435/0160
 CURRENT APPLICATION NUMBER: US/10/094,749
 PRIOR FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: 60/350,435
 PRIOR FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: JP 2001-328381
 NUMBER OF SEQ ID NOS: 381
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 673
 LENGTH: 2102
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-094-749-673

Alignment Scores:

Pred. No.:	0	Length:	2102
Score:	472.00	Matches:	662
Percent Similarity:	99.10%	Conservative:	0
Best Local Similarity:	99.10%	Mismatches:	3
Query Match:	70.98%	Indels:	6
DB:	17	Gaps:	0

US-10-029-345A-109 (1-665) x US-10-094-749-673 (1-2102)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
 Db ATGGCCCATGAGATGATGGAACTCAATTTGTTACTAGAGAGGTGGTGGCTGCTGCGAA 115
 QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
 Db AGTGAACGGAAAGAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 116
 QY 41 HisIleLeuGluValAlaIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 175
 Db CACATTTTGAAGCATTAATATCACTGCTCCAACTTATGAGAGGAAAGGTTGCAACG 176
 QY 61 AspIleValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 235
 Db GACAAAGTGTAAATTAACAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATGAT 236
 QY 81 CysSerGlnIleValValValValValValValValValValValValValValValVal 295
 Db TGCAGTCAGAAAGGTGTAGTTTACATCAAGCTCCAAAGATGTTGCTCTCTCTTCA 296
 QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGlyValLeuGlyValLeuGlyVal 355
 Db GACTGTTTCTCATCTGATCTTCTGGGTAACTGGAGAAAGCTTCATCTGTTCACTG 356
 QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGlyGlyValSer 415
 Db CTTCGAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 416
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAlaGlyProThr 475
 Db ACTTATGCTCCATCTGATCTTCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGAG 476
 QY 161 Arg-IleLeuProAsnLeuIleLeuGlyCysGlnArgAspValLeuAsnIleGlyLeu 535
 Db CT-ATTCTTCCCATCTTATCTTGGCTGCGACGAGATGCTCTCAACAGAGCTGAT 536
 QY 180 e-GlnGlnAsnGlyIleGlyThrValLeuAsnIleSerThr-ThrCysProIleProAsp 594
 Db -GCAGCAGAAAGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 595
 QY 200 PheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIle 652
 Db TTTATCCCGCAGTCTCATTTCTGCGTGGCTGCTGATGACAGCTTTGTGAGAAAT 653
 QY 220 LeuProTrpLeuAspIleValLeuPheIleGlyValAlaValAlaValAlaValAla 712
 Db TTGCGGTGCTTGCACAAATCAATGATTCATTTGAGAAAGCAAGCCCTCCAAATGAT 713
 QY 240 ValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIle 772
 Db GTTCTAGTGCATGTTAGCTGGGATCTCCCGCTCCGCCACATGCTATGCTCATAC 773
 QY 260 MetIleArgMetSerPheSerLeuAspGluAlaIleThrPheValIleGlyValArgPro 832
 Db ATGAAGAGATGACATGCTTTAATGAAGCTTCAAGATTTGTAAGAAAGAAAGAAAGCT 833
 QY 280 ThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAspIleValIleValIleVal 892
 Db ACTAATCTCCAAACTTCAATTTTCTGGGCACTCTGAGCTTGAAGAGAAAGATTAG 893
 QY 300 AsnGlnThrGlyAlaSerGlyProIleSerIleValLeuLeuValLeuLeuValLeu 952
 Db AACGACATCGAGCATCGAGGCAAGCAAACTCAAGCTGCTGCACTGGAGAAAGCCA 953
 QY 320 AsnGluProValProAlaValSerGluIleGlyGlnIleSerGluThrProLeuSerPro 1012
 Db AATGAACCTGCTCCGCTGCTCAGAGGCTGAGCAAGAAAGCAAGAGCCCTCCAGTCCA 1013
 QY 340 ProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSer 1072
 Db CCTGTGCGCATCTGCTACTCAGAGGCAAGCAAGAGCCCGTGCATCCCGCCAGC 1073

QY 360 ValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 379
 Db GTGCGCAGCTGCGCCAGCGTGCAGCGCTGCTGTTAGAGACAGCCCGCTGATCAGGCG 1133
 QY 380 LeuSerGlyLeuHisIleLeuSerAlaAspArgLeuGluAspSerAsnIleValArgSer 399
 Db CTGATGGGCTGACCTGTGCGCAGACAGGCTGGAAAGACAGCAATTAAGCTCAAGGCTTC 1193
 QY 400 PheSerLeuAspIleValSerValSerIleSerAlaSerMetAlaIleSerLeuHisGly 419
 Db TTTCTCTCATCAAGAAAGCTTTGGAAATCAAAACCTTCATCTGAGATGCAATGATG 1253
 QY 420 PheSerSerSerGluAspAlaLeuGluIleValIleValIleValIleValIleVal 1312
 Db TTTCTCTCATCAAGAAAGCTTTGGAAATCAAAACCTTCATCTGAGATGCAATGATG 1313
 QY 440 AsnIleValCysGlnPheSerProValGlnIleLeuSerGluGlnThrProGluThrSer 1432
 Db AACAAAGTATGCAAGTTCTCCCTGTTCAAGAACTATCGAGCAAGCTCCGAAACCAAT 1373
 QY 460 ProAspIleValGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSer 1492
 Db CCGATTAAGAGAGAGCGAGCATCCCAAGAGCTGCAAGCTCCAGAGCTTCAGACAGC 1433
 QY 480 GlnSerIleValLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 1552
 Db CAGAGCAAGCGATTCATTCGCTCAGAACAGACAGAGTGGACCGCCAGAGGCTCCCTT 1493
 QY 500 LeuSerProLeuHisArgSerGlySerValGluAspAsnIleHisThrSerPheLeuPhe 1612
 Db TTTATCTCATCAAGAAAGCTTTGGAAATCAAAACCTTCATCTGAGATGCAATGATG 1553
 QY 520 GlyLeuSerThrSerGlnGlnHisLeuThrIleValSerAlaGlyLeuGlyValLeuGly 1672
 Db GGCCTTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1613
 QY 540 HisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerThrPhe 1732
 Db CACTGGATATCTTGGCCCCCAGACCTCTACCCCTCCCTGACAGCAGCGGTGATTTT 1673
 QY 560 AlaThrGlnSerSerHisPheThrSerAlaSerAlaIleValIleValIleValIleVal 1792
 Db GCCACAGAGTCCATCACTTACTGCTGCTGACATCAAGAGGAGGCGCAGTTAC 1733
 QY 580 SerAlaIleValSerCysSerGlnLeuProThrCysGlyAspGlnValIleValIleVal 1852
 Db TCGCTTACAGCTGACGACGAGCTGCCACTTGGCGAGACCAAGCTATTCGTGCGCAGG 1793
 QY 600 ArgGlnIleProSerAspArgAlaAspSerArgArgSerThrPheGluGluSerProPhe 1912
 Db CCGCAGAGCCAGAGTGAAGAGCTGATCTCGCGGAGGCTGGCATGGAAGAGAGCCCTTT 1853
 QY 620 GluIleGlnPheIleValArgSerCysGlnMetGluPheGlyGluSerIleMetSerGlu 1972
 Db GAAAGAGAGTGTAAACGCAAGAGCTGCCAAATGGAATTGAGAGAGCATCATGTCAAG 1913
 QY 640 AsnArgSerArgGluGluLeuGlyValValGlySerIleSerSerPheSerGlySerMet 1972
 Db AACAGGTCAACGGAAGAGCTGGGGAAGGTGGGAGTCACTAGCTATTCGCTTTCGCGCAG 1973
 QY 660 GluIleIleGluValSer 665
 Db GAAATCATTTGAGGTCTCC 2050

RESULT 5

US-10-168-506-2
 ; Sequence 2, Application US/10168506
 ; Publication No. US20040053229A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FLOMMAN, GREGORY D.
 ; APPLICANT: MARTINEZ, RICARDO
 ; APPLICANT: WHYTE, DAVID

[illegible]

Db 1446 GGCCTTCAAGCAGCAGCAGCAGCAGTTCGATTCGGTCAGAACCAAGAGAGGACCG 1505
QY 495 laaInArgSerLeuLeuSerProLeuHiAArgSerGlySerValGluAAspThrTyrHisT 515
Db 1506 CCCAGAGGCTCCCTTTATCTCCACTGCATCGAAGTGGAGCCGTGGAGGCAATTACCA 1565
QY 515 hysSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuG 535
Db 1566 CCAAGCTTCCTTTCCGCTTTCCACCAAGCAGCAGCAGCAGCAGTCTCAGCAAGTCTGCTG 1625
QY 535 lYLeuLysGlyTyrPheHisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrS 555
Db 1626 GCCTTAAGGCTGCGACCTCGATATCTTGGCCCCCAGACCTTACCCCTCCGACCA 1685
QY 555 eTserTrrPyrPheAlaThrGlySerSerHisPheTyrSerAlaSerAlaIleTyrGlyG 575
Db 1686 GCAAGCTGGATTTTGGCAGAGAGTCTCAGACTTCACTTGCCTCAGAGCCTACGAG 1745
QY 575 lYSerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAAspGlnValT 595
Db 1746 GCAATCCAGTTACTTGCCTACAGTGCAGCCAGCTGCCACTTGCAGAGACCAAGTCT 1805
QY 595 yTserValAArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTyrHisG 615
Db 1806 ATCTGTGGCAGAGCGGCGAGAACCAAGTACAGAGTCACTCGCGCGAGAGCTGGCATG 1865
QY 615 lUglUserProPheGlnLysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluS 635
Db 1866 AAGAGAGCCCTTTGAAAGCAGATTAAACGAGAAAGCTGCCAAATGGAATTTGGAGAGA 1925
QY 635 eTtleMetSerGluAAspArgSerArgGlnGluLeuGlnLysValGlySerGlnSerSerP 655
Db 1926 GCATCATGTCAAGAACAGGTCAAGGAAAGCTGGAGAAAGTGGCAGTCACTTACCT 1985
QY 655 hseSerGlySerMetGluIleLeuGluValSer 665
Db 1986 TTTCCGCGCAGCAGCAGGAATCATTTGAGTCTCC 2017

RESULT 7
US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDM5
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3059
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEPTIDE:
; NAME/KEY: CDS
; LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:
Pred. No.: 0 Length: 3059
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 17 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-257-026-1 (1-3059)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
Db 127 ATGGCCCATGAGATGATGGAACTCAAAATTTGTTACTGAGAGGTTGGTGGCTGCTGGAA 186

QY 21 SerGlyThrGluValLeuLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
Db 187 AGTGAACCGAAGAAAGTGGCTGCTAATTGATAGCCGGCCATTGTGGAAATACATACATCC 246
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerLeuMetLysArgArgLeuGlnGln 60
Db 247 CACATTTTGGAGCCATTAAATATCAATGCTCCCAAGCTTATGAGGAGGAAGTTGCAACG 306
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
Db 307 GACAAAGTGTATTAACAGAGCTCAATCCAGCTTACGCCAAACATTAAGTTGACATTGAT 366
QY 81 CysSerGlnLysValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 367 TCGATGACAGAGTTGTAATTCATCAATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 426
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGlnLysSerPheAsnSerValHisLeu 120
Db 427 GACTGTTTTCTACGTACTTCTGGGTAAACTGGAGAAAGCTTCAACTCTGTACCTG 486
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db 487 CTGGCAGGTGGGTTGCTGATGTTCTCTGTTGTTCCCTGGCCTGTGAGAGAAATCC 546
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 547 ACTCATGCTCCATCCAGCTGCAATTTCTAGCTTCTTACCTGTGGCCAACTTGGCCAAAC 606
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180
Db 607 CCAATTTCTCCAACTTTATTTATTTGGCTGCCAGCAGATGTCCTCAACAAGAGCTGAT- 665
QY 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProLysProAsp 200
Db 666 GCAGCAGAAATGGATGGATTATGTGTTAATCCAGCAA-TACCTGTCCAAAGCCGTGACT 724
QY 200 HeIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleL 220
Db 725 TTATCCCGAGTCTCATTTCTGCGGTGCTGTGATACAGCTTTGTGAAATAATTT 784
QY 220 eUpProTrrPheAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysAv 240
Db 785 TGCCTGTGTGACAAATCAGTATGATTTCAATTGAGAAAGCAAAAGCTCCATGATGAG 844
QY 240 AlLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleM 260
Db 845 TTCTAGTGCACTGTTAGCTGGATCTCCGCTCCGCCACATCGCTATCGCTACATCA 904
QY 260 eLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProT 280
Db 905 TGAAGAGATGGACATGCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTTA 964
QY 280 hrIleSerProAsnPheAsnPheLeuGlnLeuLeuAspTyrGlnLysLysIleLysA 300
Db 965 CTAATATCTCCAACTTCAATTTTCTGGGCCAACTCTGGACTTATGAGAAAGATTAA 1024
QY 300 sngIlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlnLysProA 320
Db 1025 ACCAGACTGAGCATCAGGGCGAAAGAGCAAACTCAAGCTGTGCACCTGGAGAGCCAA 1084
QY 320 sngIlnProValProAlaValSerGluGlyGlnLysSerGlnThrProLeuSerProp 340
Db 1085 ATGAACCTGTCTCTCTGTCTTGAAGGGTGAACAATAAGCAAGAGCCCTCACTCCAC 1144
QY 340 rOCysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaServ 360
Db 1145 CCTGTGCCAGCTCTCTACTTACAGGAGCAGAGCAAAAGCCCTGTGATCCCGCAGCG 1204
QY 360 aLProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaL 380
Db 1205 TCCCCAGGTGCGCAGCGTGAAGCGCTGTGTTAGAGGACAGCCGCGGTGTAAGGCGC 1264

QY	380	eUsErGjLyEuHi;slEuSeRi;aaPaRgLeuGl;uAsPSe;ASuLyLeuLyAigSeR	400
Db	1265	TCAGTGGGCTGCACCTGTCCGACAGCAGGCTGGAAAGACAGCAATAACTCAACGTTCT	132
QY	400	heSeRLeuApRl;eLySeRValSeRrYrSeRi;laSeRMeRl;aaLaseRLeuHi;GlyP	420
Db	1325	TCCTCTGGATATCAAAATCAGTTTCATATTCAGCAGAGATGGACGACTCTTTCATAGGCT	138
QY	420	heSeRSeSeRGu;uApRl;alEuGl;uLyTyTyLyP;ProSeRThrThrLeuApGlyThRa	440
Db	1385	TCCTCCATCAGAAAGATGCTTGGAAATCTCAAAACCTTCACACTCTGGATGGACCA	144
QY	440	suLy;leuCyGlnPheSeRProV;lgInGlu;eUsErGj;uGlInThRProGluThRSeR	460
Db	1445	ACAGAGTATCCAGATTCTCCCTGTTCAGGAACATATGAGAGCACTCCGAAACCAAGTC	150

QY	46	roAspIySgIuJlulaseRlleProlysluSleuGlnTrlAaGpProSerAaspSerg	480
Db	1505	CTGATMAGGAGAACCCAGCATCCCCAGAAAGCTGACAGACGGCAGGCGCTTCAAGACACC	1564
QY	480	lInSerlyAArgLeuHlIservAlArgThrserserserglyThralaGlnIargserLeuL	500
Db	1565	AAGAGCAGGAGATGGATTCGGTCCGAACACAGCAGCAGTGGCACCGCCAGAGTCCCTTT	1624
QY	500	eusSerProLeuHlIsargserGlySeraGluSapasnTrpHsnTrsSerPheLeuPheG	520
Db	1625	TATCTCCACTGCATCGAAGTGGAGCGCTGGAGAGCAATTACACACACACTCTCTTTCG	1684
QY	520	lyLeuSerThsSerGlnGlnHlIsleuThrllysSeraIaglyLeuGlyLeuYpGlyTrpH	540
Db	1665	GCCTTTCACACAGCAGAGAGACCTCCAGAAgCTGCTGGCGCTTGAAGGGCTGGC	1744
QY	540	laserAspIleLeuAlaProGlnThrserThrpProSerLeuThrsSerTrpYrPhea	560
Db	1745	ACTGGATATCTTGGCCCCCAGACCTCTAACCCCTTCCTCCAGACAGCAGCTGGATTTTG	1804
QY	560	lathnGusSerSeriHsPheTyrsSerAlaSerAlaIetyrGlyGlySeraIaserTyrs	580
Db	1805	CCACAGAGTCTCTACACTTCTACTCTGCTCCAGCACCATTCACGAGGCGAGTCCAGTTACT	1864
QY	580	exAlaTyrsSerCySserGlnLeuProThrCySglYAspGlnValTyrsSerValArgArgA	600
Db	1865	CTGCGTCACTGACCTGACGCAGCTGCCACTTGGCGAGAACCAAGTCAATTCTGTGGCAGGC	1924
QY	600	rgGlnLysProSerAPArgAlaaspSerArgArgSerTrpHlIsGluGluSerProPheG	620
Db	1925	GCGAAGAGCCAAAGTACAGAGCTGACTCGCGCGGAGGTGGCAATGAAGAGAGCCCTTTG	1984
QY	620	lulysGlnPheLySArgArgSerCySglmMetGluPheGlyGluSerIlawMetSerGlnA	640
Db	1985	AAAAGCAGTTAAACCCAGAACCTGCCAAATGAAATTGGAGAGAGCATCATGTCAAGAA	2044
QY	640	snArgSerArgGluGluLeuGlyLySValGlySerglnSerSerPheSerGlySerMetG	660
Db	2045	ACAGGTCACGGAGAGAGCTGGGGAAAGTGGGAGTCAAGTCAAGCTTTTTCGGGAGCATGG	2104
QY	660	lulalIleGlnValSer	665
Db	2105	AAATCAATTAGAGGTCTCC	2121

RESULT 8
 JS-09-964-277-20
 Sequence 20. Application US/09964277
 Patent No. US20020137170A1
 GENERAL INFORMATION:
 APPLICANT: Lucche, Ralf M.
 APPLICANT: Wei, Bo
 TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125 434
 CURRENT APPLICATION NUMBER: US/09/964,277
 CURRENT FILING DATE: 2001-09-25
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 20
; LENGTH: 3332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-20

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Alignment Scores

Pred. No.:	0	Length:	3332
Score:	472.00	Matches:	472
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	70.98%	Indels:	0
DB:	9	Gaps:	0

US-10-029-345A-109 (1-665) x US-09-964-277-20 (1-3332)

QY 194 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgAlaProValAsnasp 213
Ddb 977 ACCTGTCCAAAGCCGACTTATATCCCGAGTTCATTTCTGCGTGTGCTGTGAATGAC 1033

214 SerPheCysGluIuylleLeuProTrieuAspLysSerValAspPheIleGluLysAla 233

Db 1037 AGCTTTGTGAGAAATTTTTCGCCGTGCTTGACCAATCAGTAGATTTCATTGAGAAAGCA 1096

Db 253 1097 AAGCCTCCATGATGTGTTCTAGTGCATGTTAGCTGGATCTCCGGTCCGGTACC 1156
LysAlaAspIAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 253

QY 254 IleAlaIleAlaTyrIleMetIysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 273

Db
1157 ATCGTATCGCCTACATCATGAGAGATGGACATGCTTTAGATGAAGCTTACAGATTT 1216

274 ValLYGILuLyarGProThrIIeSePProAsnPhaasnPhelGcJgInLeuLeuAsp 293

294 Tyrgtulybvi1elvsanglInthrgIvataSergIvProIvSertvslentIvIen 313

Db 1277 TATGAGAGGATTAAACCAAGCTGAGCATCAGGCGCAAGACCAACTCAAGCTG 1336

QY 314 LeuHISLeuGLYSPROANGluPRoVALPRoAlaValSERGLUGLYGlnLYSSer 333

1337 CTGACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGACAGAAAAGC 1396

1397 GAGTGGCCCTCAGTCCACCCCTGGCCGACTCTGTACTCTCAGAGGTAGTACGACCAAAATG 1456

QY	354	373	1738
	ProValHiProAlaSerValProSerValGlnProSerLeuGluLysP		

Db 1457 CCGTGCATCCGCGCAGCGTGCCAGCGTGCCAGCGTGCCAGCGTGCGCTGTTAGAGAC 1516

374 SerProLeuValGlnIleLeuSerGlyLeuHisIleLeuSerAlaAspArgLeuGlnIleAspSer 393

394 AsnLysLeuLysArgSerPheSerLeuAspIleValSerValSerTyrSeraIAsnMet 413
1027 AACCCGACGGAGCGCCTCAAGTGGCTGCACCCTGTTCGCCAGGACGGCTGGAAAGACAGC 1576

1577 AATAGCTCAAGCGTCTCTCTGATATCAATACAGTTTCATATTACGCCAGATG 1636

414 AlaAspSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrTyrLysProSer 433

1637 GCAGCATCTTACATGGCTTCTCTCATCAGAAAGATGCTTGGAAATACTAACAACTTCC 1696

1697 ACTACTGTGATGGACCAACAGCTATGCGAGTTCTCCCTGTTGAGGAACTATGGGAA 1766

454 GlnThrProGluThrSerProAspIyGluGluAsaSerIleProIyAspLeuGlnThr 473

1757 CAGACTCCGGAACCACTCTGATTAAGAGGAAGCCAGCATCTCCCAAGAGCTGCAGACC 1816

474 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrIleSerSerGly 493

DB 1817 GCCAGGCTTCACAGACGCCAGAACGATTCGATTCGGTCAGAACGACGACGCTGCG 1876
QY 494 ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGlnAspArgTyr 513
DB 1877 ACCGCCCAAGAGGTCCTTTATCTCCATCGCATCGAAGTGGAGCGCTGGAGGACAAATTAC 1936
QY 514 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerValGly 533
DB 1937 CACACACAGCTTCCTTTTCGGCTTCACACAGCCAGCAGACCTTCACAGAACTGCTGGC 1996
QY 534 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 553
DB 1997 CTGGGCTTAAAGGCTGGGACCTCGGATATCTGGCCCCCAGACCTACCCCTTCCTCG 2056
QY 554 ThrSerSerTyrPheAlaThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyr 573
DB 2057 ACCAGACAGCTGGTATTTTGGCAGACAGTCTCTCACACTTCTACTCTGCTCAGCATCTAC 2116
QY 574 GlnGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 593
DB 2117 GAGGAGAGTCCGCTTACTCTGCTTACAGCTGCAAGCTGCTGCTGCTGCTGCTGCTG 2176
QY 594 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTyr 613
DB 2177 GTCTATCTGTGGCGAGCGCGGAGAGCCAGATGACAGAGCTGACTCGGCGGAGCTGG 2236
QY 614 HisGlnGlnSerProPheGlnLysGlnPheLysArgArgSerCysGlnMetGlnPheGly 633
DB 2237 CAGGAAGAGAGCCCTTTGAAAGCAGTTTAAAGCAGAGCTGCCAAATGGAAATTTGGA 2296
QY 634 GluSerIleMetSerGlnAsnArgSerArgGlnGlnLeuGlyLysValGlnSerGlnSer 653
DB 2297 GACAGCATCTGTCAGAGAACAGCTCACGGAAGAGCTGGGGAAGTGGGAGCTGACT 2356
QY 654 SerPheSerGlySerMetGlnIleIleGlnValSer 665
DB 2357 AGCTTTTCGGGAGCATGGAATCATTTGAGGTCTCC 2392

RESULT 9
US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Alignment Scores:
Pred. No.: 0 Length: 3496
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 9 Gaps: 0

US-10-029-345a-109 (1-665) x US-09-964-277-1 (1-3496)

QY 1 MetAlaHisGlnMetIleGlyThrGlnIleValThrGlnArgLeuValAlaLeuLeuGlu 20
DB 562 ATGGCCCATGAGATGATTTGAACTCAAAATTGTACTAGAGATGTGGTGGCTGTGCTGGAA 621
QY 21 SerGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGlnTyrAsnThrSer 40

DB 622 AGTGGAAACGGAAGAAAGTGTCTTAATTGATACCCGGCCATTGTGGAAATACATATACCC 681
QY 41 HisIleLeuGlnAlaIleAsnIleAsnLysSerLysLeuMetLysArgArgLeuGlnGln 60
DB 682 CACATTTTGGAAAGCCATTAATATCAATGCTCCAAAGCTTATAGAAGGAGGTGGCAACAG 741
QY 61 AspLysValLeuIleThrGlnLeuLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
DB 742 GACAAAGTTTATTTACAGAGCTCATCGCATTCAGCCAAACATTAAGTTGACATTGAT 801
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 802 TCGAGTCAGAGAGTTGATGATTTACGATCAAGACTCCAAAGATGTTGCTCTCTCTTCA 861
QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGlnLysSerPheAsnSerValHisLeu 120
DB 862 GACTGTTTCTCATCTGATCTTCTGGGTAAACGAGAGAGAGCTTCAACTCTGTCACTG 921
QY 121 LeuAlaGlyGlyPheAlaGlnPheSerArgCysPheProGlyLeuCysGlnGlyLysSer 140
DB 922 CTTCAGAGTGGGTTTGCTGAGTTCCTCTGTTTCCCTGCTCTGTGAAGGAATATC 981
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 982 ACTCTAGTCCCTACCGCATTTCTCAGCCTTGCTTAACGTGGCAACATTGGGCCAAC 1041
QY 161 ArgIleLeuProAsnLeuTyrIleuGlyCysGlnArgAspValLeuAsnLysGlnLeuIle 180
DB 1042 CCAATTTCTCCAAATCTTTATCTGTGCTGCCAGCGAGAGTCTCTCAACAGAGCTGAG- 1100
QY 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProLysProAsp 200
DB 1101 GAGAGCAATGGGATTTGTTATGTATTATATCCAGCAA-THCCTGTCCAAAGCTTGACT 1159
QY 200 HisIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnLysIle 220
DB 1160 TTATCCCGAGCTCATTTCCGCGTGGCTGATGATGACAGCTTTGTGAAGAAATTT 1219
QY 220 LeuProTyrLeuAspLysSerValAspPheIleGlnLysAlaLysAsnGlyCysVal 240
DB 1220 TCCCGTGGTGGACAAATCAGTATGATTTCAATGAGAAAGCAAGCTCAATGAGATGG 1279
QY 240 AlLeuValHisCysValLeuIleGlyIleSerArgSerAlaThrIleAlaIleTyrIle 260
DB 1280 TTCTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCAACATCGCTATCGCTATACATCA 1339
QY 260 LeuValArgMetAspMetSerLeuAspGlnAlaTyrArgPheValLysGlnLysArgPro 280
DB 1340 TGAAGAGATGACATGCTCTTTAGATGAAAGCTTACAGATTTGTGAAGAAAGAAAGACCT 1399
QY 280 HisIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnLysValIleLys 300
DB 1400 CTATATCTCCAAATCTCAATTTTCTGGGCCAATCTCTGGAATATGAGAAAGATTAA 1459
QY 300 SerGlnThrGlyAlaSerGlyLysProLysSerLysLeuLeuLeuLeuLeuLeuLeuLeu 320
DB 1460 ACCAGACTGAGACATCAGGCGCAAGAGCAAACTCAAGTGTGCACTCGAGAGAGCCAA 1519
QY 320 SerGlnProValProAlaValSerGlnGlyGlyGlnLysSerGlnThrProLeuSerPro 340
DB 1520 ATGAACCTGTCCCTGCTGTCTCAGAGGAGTGAACAAGAGAGAGAGAGAGAGAGAGAG 1579
QY 340 LeuValAspSerAlaThrSerGlnAlaIleGlyGlnArgProValHisProAlaSerV 360
DB 1580 CCTGTGCCCACTCTGCTACTCAGAGGAGAGAGCAAGAGGCGCGTGCATCCCGCAGAG 1639
QY 360 AspProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAla 380
DB 1640 TCCCAAGCTGGCCAGCGGAGCGGTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1699
QY 380 LeuSerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnLysLeuLysArgSerP 400

QY 260 etlyarqmetarpeMetSerleuaspGluAlaTyraRphValIyrgIuYsarProT 280
 DB 1342 TGAAGAGATGACATGCTTTTATGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTA 1401
 QY 280 hrtIleSerProaenPheanPheleuGIyGluLeuaspTyrgIuYblyIleYsa 300
 DB 1402 CTATATCTCCAAACCTTCATTTTCTGGGGCAACTCTCGACTATGAGAAAGAAATTAAGA 1461
 QY 300 angIthrGluYAlaSerGIyProlySerIyIleuYleuHIsleuGIuYsaPro 320
 DB 1462 ACCAGACTGAGATGACGGGCAAGAGCAAACTCAAGCTGTGACCTGGAGAAAGCCAA 1521
 QY 320 angIuProValProAlaValSerGIuGIyGIuYlySerGIuThrProLeuSerPro 340
 DB 1522 ATGAACTGTCTCTGCTGTCTCAGAGGGTGAACAGAAAGCGAGAGCCCTCACTCAC 1581
 QY 340 rGcYaaIaapSerAlaThrSerGIuAlaAlaGIyIuYnarProValHIsproAlaSer 360
 DB 1582 CCTGTCCGCACTGTCTGCTCACTCAGAGGAGCAAGAAAGCCGCTGCACTCCGCAAG 1641
 QY 360 aIProSerValIProSerValGIuProSerIleuGIuYblySerProLeuValGlnAla 380
 DB 1642 TGCACAGCCGTGACAGGTGACACCCGTCTGTAGAAGACAGCCGCTGTGACAGCCG 1701
 QY 380 euserGIyLeuHIsleuSerAlaaspArgleuGIuYblySerAenlyblyeYsaRseP 400
 DB 1702 TCGTGGGCTGCACTGTCTCGCAGACAGGCTGGAAGACAGCAATTAAGCTTCAGCCGTTCT 1761
 QY 400 heseleuapIleYlySerValSerTyserIleuSerAlaIleuSerIleuGIyP 420
 DB 1762 TCTCTCTGATATCAATCATGTTTCAATTCAGCAGCAATGAGCATCTTACATGGCT 1821
 QY 420 heseleuSerGIuYblySerAlaIleuGIuTyTyIyIyProSerThrtIleuaspGIyThra 440
 DB 1822 TCTCTCATCAGAAAGATGCTTGTGAATACTAACAACCTTCACTCTGGAAGGAGCA 1881
 QY 440 enlyleuCyegIuPheSerProValGIuGIuYblySerGIuThrProGIuThSerP 460
 DB 1882 ACAAGCTATGCCAGCTTCTCCCTGTTCAGGAATATTCAGAGCAAGATCCCGAAACAGATC 1941
 QY 460 roaApIyGluGIuAlaSerIleProlyblyleuGIuThraIaargProSerAapSerG 480
 DB 1942 CTGATTAAGAGGAAAGCAGACATCCCAAGAAAGCTGACAGACCCGCAAGGCTTCAGACAGCC 2001
 QY 480 InserIyargIeuhIservAlaIyrgThSerSerGIyThraIaGlnaYserIleu 500
 DB 2002 AGAGCAAGGATTCATTCGTGTGAGAAACAGCAGAGTGGCACCCGCCAGAGGTCTCCCTT 2061
 QY 500 euserProleuHIsaYserGIySerValGIuYblySerAenlyblyeYsaRsePheLeuPheG 520
 DB 2062 TATCTCATCTGATCAAGTGGAGGCTGGAGGACAAATTCACACACAGCTTCTTTTGG 2121
 QY 520 IyLeuSerThSerGIuGIuHIsleuThIySerIleuGIyLeuGIyLeuYblyIyTPH 540
 DB 2122 GCTTTTCAACAGCAGCAGACACTCAGCAAGTCTGTGGCCGTGGCCCTTTAAGGGCTGGG 2181
 QY 540 IIservapIleuAlaProGIuThSerThPProSerIleuThrSerSerTyrgIyPheA 560
 DB 2182 ACTCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACACAGAGTGTATTTTGG 2241
 QY 560 IathrGIuSerSerHIsPheTySerAlaSerAlaIleTyrgIyGIySerAlaSerTyS 580
 DB 2242 CACAGAGTCTTACCTTCTACTCTGCTCAGCCATCTACGAGGAGGAGGAGGAGGAGTACT 2301
 QY 580 exrIaTySerCySerGIuLeuProThCyegIyAapGIuAlaIyYserValaYsaRga 600
 DB 2302 CTGCTACAGCTGACAGCAGCTGCCCACTTGGGAGACCAAGTCTATTCGTGTGCGAGGCG 2361
 QY 600 rGcIuYlyPProSerAapArgAlaapSerAryaRseGTTPHIsGIuGIuYblyPProPheG 620
 DB 2362 GGGAGAGGCCAAATGTACAGAGCTGACTCGGGGAGGAGTGGCATGAAGAGAGGCCCTTTGG 2421
 QY 620 IuYblyGIuPheYblyAryaRseCyegIuMetGIuPheGIuYblyIleuMetSerGIu 640

DB 2422 AAAAGAGTTTAAAGCAAGACCTGCCAAATGGAATTTTGAAGAGACATCATGTACAGAGA 2481
 QY 640 snarSerArgIuGIuLeuGIyYlyValGIySerGIuSerPheSerGIySerMetG 660
 DB 2482 ACAAGTCAAGGAGAAAGCTGGGGGAAAGTGGGAGTCAAGTCACTTTTGGGGCAGATGA 2541
 QY 660 IuIleGIyValSer 665
 DB 2542 AAATCATTAAGGTCTCC 2558
 RESULT 11
 US-09-816-494-1
 ; Sequence 1, Application US/09816494
 ; Patent No. US20020034807A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel A.
 ; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
 ; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: 10448-030002
 ; CURRENT APPLICATION NUMBER: US/09/816,494
 ; PRIOR FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 60/191,858
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3544
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (589) ... (2583)
 ; US-09-816-494-1
 Alignment Scores:
 Pred. No.: 0 Length: 3544
 Score: 472.00 Matches: 663
 Percent Similarity: 99.40% Conservative: 0
 Best Local Similarity: 99.40% Mismatches: 2
 Query Match: 70.98% Indels: 4
 Gaps: 0
 US-10-029-345A-109 (1-665) x US-09-816-494-1 (1-3544)
 QY 1 MetAlaHIsGluMetIleGIyThrGlnIleValIThrGIuYblyValAlaLeuLeuGIu 20
 DB 589 ATGGCCCATGAGATGATTGGAATCAATTTTACTGAGAGGTGTGCTGTGCTGGGAA 648
 QY 21 SerGIyThrGIuYblyValLeuLeuIleApsSerAryaRseProPheValGIuTyraenThrSer 40
 DB 649 AGTGAACCGAAAGAGTGTGCTAAATGTATGATACCCGCAATTTGTGAATTAACAATACATCC 708
 QY 41 HIsIleuGIuAlaIleAenIleAenCySerIyIleuMetIyAryaRseGIuGIu 60
 DB 709 CACATTTTGAAGCATTATATCAATCTCTCAAGCTTATGAAGGAGTTTGAACAG 768
 QY 61 AapIyValIleuIleThrGIuLeuIleGIuHIservAlaYblyIleYblyValIleap 80
 DB 769 GACAAAGTGTATTAACAGAGCTCATCCAGATTGAGCGAAACATTAAGGTTGATCATTTGAT 828
 QY 81 CySerGIuYblyValValIyTyraPginserSerGIuAapValAlaSerLeuSer 100
 DB 829 TGCAGTCAAGAGGTGTGATTAACATCAATCAAACTCCCAAGATGTGCTCTCTCTTCA 888
 QY 101 AapCyPheLeuThrValIleuLeuGIyYblySerPheApsSerValHIsleu 120
 DB 889 GACTGTTTCTACCTGACTTCTGGGTAACTGAGGAGAGCTTCACTCTTACCTG 948
 QY 121 IeuaIleGIyIlePheAlaGIuPheSerArgCyPheProGIyLeuCyegIuGIyYblySer 140
 DB 949 CTTGAGAGGTGTGCTGATGATTTCTCTGTTTCCCTGGGCTGTGTGAAGAAATTC 1008

Db	2087	TATCTCACTGATCGAATGTGGAGCCGTGGAGGACAAATTACCAACGAGCTTCTTTCCG	2146
QY	520	lyDeuSerThSerGInGInHIsLeuThrylSerAlaGlyLeuGlyLeuLysGlyTyrPh	540
Db	2147	GCCTTCCACACGACGACGACGACCTCACGAACTCTGCTGGCTGGCTTAAAGGAGCTGGC	2206
QY	540	IseSerApIleLeuAlaProGInThSerThrProSerLeuThrSerSerTyrTyrPheA	560
Db	2207	ACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTTGACACGAGCTGGATTTTG	2266
QY	560	IaThrGlySerSerIapherTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrS	580
Db	2267	CCACGAGAGCTCCACACTTCTACTCTGCTTCAGCACTTACGAGGAGGAGGACCAATTACT	2326
QY	580	eAlaTyrSerCysSerGInLeuProThrCysGlyAspGlnValTyrSerValArgA	600
Db	2327	CTGCTTACAGCTGCGACGACCTGCCACTTGGCGAGCCAAAGTCATTTCTGTGCGGAGGC	2386
QY	600	IGInLysProSerAspArgAlaIseSerIArgIserSerTyrPheGlyGlyGlySerProPheG	620
Db	2387	GGCAGAAACCCAGATGACAGAGCTGATCTGGGGGAGCTGGCACTTGAAGAGAGAGCCCTTGG	2446
QY	620	IuLyGlnPheLysArgArgSerCysGlnMetGluPheGlyGlyGlySerIleMetSerGluA	640
Db	2447	AAAGACAGATTAAACGACGAAGCTGCCAAATGGAATTTGGAGAGGACATCATGTCAAGAC	2506
QY	640	sNArgSerArgGlnGluLeuGlyLysValGlySerGlnSerSerPheSerArgLysMetG	660
Db	2507	ACAAGTACCGGAAAGAGCTGGGAAAGTGGGACATGATGATGCTTTCGGGACGACATGG	2566
QY	660	IuIleIleGluValSer	665
Db	2567	AAATCATTTGAGTCTCC	2583
RESULT 12			
US-10-377-072-25			
; Sequence 25, Application US/10377072			
; Publication No. US2004009501A1			
GENERAL INFORMATION:			
APPLICANT: Millennium Pharmaceuticals Inc.			
APPLICANT: Curtis, Rory A.J.			
APPLICANT: Logan, Thomas Joseph			
APPLICANT: Glucksmann, Maria A.			
APPLICANT: Meyers, Rachel E.			
APPLICANT: Williamson, Mark J.			
APPLICANT: Rudolph-Owen, Laura A.			
APPLICANT: Chun, Miyoung			
APPLICANT: Tsai, Fong-Ying			
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,			
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES			
FILE REFERENCE: MP103-0180NMTM			
CURRENT APPLICATION NUMBER: US/10/377, 072			
CURRENT FILING DATE: 2003-02-27			
PRIOR APPLICATION NUMBER: US 09/895, 860			
PRIOR FILING DATE: 2001-06-29			
PRIOR APPLICATION NUMBER: US 60/215, 370			
PRIOR FILING DATE: 2000-06-29			
PRIOR APPLICATION NUMBER: US 09/723, 806			
PRIOR FILING DATE: 2000-11-28			
PRIOR APPLICATION NUMBER: US 60/187, 455			
PRIOR FILING DATE: 2000-03-07			
PRIOR APPLICATION NUMBER: US 09/843, 297			
PRIOR FILING DATE: 2001-04-25			
PRIOR APPLICATION NUMBER: US 60/199, 801			
PRIOR FILING DATE: 2000-04-26			
PRIOR APPLICATION NUMBER: US 09/861, 801			
PRIOR FILING DATE: 2001-05-21			
PRIOR APPLICATION NUMBER: US 60/205, 508			
PRIOR FILING DATE: 2000-05-19			
PRIOR APPLICATION NUMBER: US 09/816, 494			
PRIOR FILING DATE: 2001-03-23			

; PRIOR APPLICATION NUMBER: US 09/815,419
 ; PRIOR FILING DATE: 2001-03-22
 ; Remaining Prior Application data removed - See File Wrapper or PAM.
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: PaSeq for Windows Version 4.0
 ; SEQ ID NO 25
 ; LENGTH: 3544
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (589) ... (2586)
 ; US-10-377-072-25

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1	472.00	3544	663	0	2	4	0
Percent Similarity:	99.40%						
Best Local Similarity:	99.40%						
Query Match:	70.98%						

US-10-029-345a-109 (1-665) x US-10-377-072-25 (1-3544)

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QY 1 MetAlAhIeGIuMeTlIeGIYThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 589 ATGGCCCATGAGTATGATGTAATCTCAAAATTGTTACTGAGAGTGGTGGCTGCTGGA 648
QY 21 SerGIYThrGluYValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 649 AGTGAACGGAAAGAGTGTCTATGATGATGAGCCGCGCATTTGTGAAATACATATACCC 708
QY 41 HsIIleuGluAlaIleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
Db 709 CACATTTTGGACCCATTAATATCACTGCTCAAGCTTATGAAAGGAGTTGCAACAG 768
QY 61 AspLyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 769 GACAAAGTGTATTAACAGAGCTCATCCAGCATTCAGCCAAACATTAAGTTGACATTGAT 828
QY 81 CysSerGlnYValValValValYrAapGlnSerSerGlnAapValAlaSerLeuSerSer 100
Db 829 TGCAGTCAGAGGTTGATGATTAAGATCAAGCAAGCTCCCAAGATGTTGCTCTCTCTCA 888
QY 101 AspCyPheLeuThrValLeuLeuGluYrLeuGluYrLeuGluYrLeuGluYrLeuGlu 120
Db 889 GACTGTTTCTCACTGATCTTCTGGGTAACTGAGAGAGCTTCAACTCTGTTCACTG 948
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGluYrLeuSer 140
Db 949 CTTCAGAGTGGGTTGCTGAGTCTCTCTGTTGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAanIleGlyProThr 160
Db 1009 ACTCTAGTCCCTACCTGATTTCTCAGCCTTGTCTTCACTGTTGCCAAACATGGGCCAAC 1068
QY 161 ArgIleLeuProAanLeuYrLeuGluYrGlnAargPheValLeuAanLeuYrLeuLeu 180
Db 1069 CGAATTTCTCCCAATCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
QY 181 -GlnGlnAanGlyIleGlyTyrValLeuAanAlaSerTyr-ThrCysProYrProAap 200
Db 1128 GCGCAGAGATGGATGGTATGTTATGTTAAATGCCAGCA-TACCTGTCCAAAGCTGACT 1186
QY 200 HeIIeProGlnSerThsPheLeuArgValProValAanPheSerPheCysGluYrIle 220
Db 1187 TTAATCCCGAGTCTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246
QY 220 eueProTrpLeuAapYrSerValAapPheIleGluYrAlaYrAlaSerAanGlyCys 240
Db 1247 TGCCGTGGTGGTGAACAATCAGTGAATTTCAATTGAGAAAGCAAGCCCTCCAAAGGATGG 1306
QY 240 alLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
  
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Db 1307 TTCTAGTGACATGTTAGTGGGATCTCCGCTCGCCACCATCTGATCGCTCATCATCA 1366
QY 260 eLYyArgMeLaspMetSerLeuAapGluAlaTyrArgPheValYrGluYrAapPro 280
Db 1367 TGAAGAGATGAGATGCTTTTATGATGAAGCTTACAGATTTGTGAAAGAAAAAGCTTA 1426
QY 280 hrIleSerProAanPheAanPheLeuGlyGlnLeuLeuAapYrGluYrIleYr 300
Db 1427 CTATATCTCCAACTTCAATTTTCTGGGCCCACTCTGAGCTATGAGAAAGATTTACA 1486
QY 300 HsGlnThrGlyAlaSerGlyProYrSerYrLeuYrLeuLeuLeuLeuLeuLeuLeuLeu 320
Db 1487 ACCAGCTGAGCATCAGGCGCCAAAGAGCAACTCAAGCTGCTGCACTGAGAGAGCCAA 1546
QY 320 HsGlnProValProAlaValSerGluGlyGlnYrLeuYrLeuYrLeuYrLeuYrLeuYr 340
Db 1547 ATGAACCTGTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1606
QY 340 roCysAlaAapSerAlaThrSerGlnAlaIleGlyGlnArgProValHisProAlaSerY 360
Db 1607 CCTGTGCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1666
QY 360 alProSerValProSerValGlnProSerLeuLeuGlnAapSerProLeuValGlnAla 380
Db 1667 TGCCAGAGGTCGCCAGCGCGTGCAGCGCGTGTGAGAGACAGCCGCTGTACAGCGCC 1726
QY 380 eusSerGlyLeuHisLeuSerAlaAapArgLeuGluAapSerAanYrLeuYrAapSer 400
Db 1727 TCAGTGGCTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1786
QY 400 HeSerLeuAapIleYrSerValSerYrSerAlaSerMeAlaAlaSerLeuHisGlyP 420
Db 1787 TCTCTGATATCAATATCATGTTTCAATTTCAAGCAGATGCGAGATCTTACATGCT 1846
QY 420 HeSerSerSerGlnAapAlaLeuGluYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYr 440
Db 1847 TCTCCATCAAGAGATGCTTTGGAATCTAACAACCTTCACTGATGAGGAGCA 1906
QY 440 HsYrLeuYrCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSer 460
Db 1907 ACAAGCTAGGACAGATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1966
QY 460 roAapLyGlnGluAlaSerIleProYrValLeuGlnThrAlaArgProSerAapSerG 480
Db 1967 CTGATTAAGAGAGAGCAGATCCCAAGAGCTGAGACCCAGGCTTCAAGACGCC 2026
QY 480 InSerYrArgLeuHisSerValArgThrSerSerSerGlyYrAlaGlnArgSerLeu 500
Db 2027 AAGAGCAGAGATGATGATTCGTCAGAACAGCAGAGTGGCACCGCCAGAGTCCCTT 2086
QY 500 eusSerProLeuHisArgSerGlySerValGluAapAanYrHisThrSerPheLeuPhe 520
Db 2087 TATCTTCACTGATGAGAGTGGAGAGCTGAGAGCAATTAACAACAAGCTTCTTTTGG 2146
QY 520 YrLeuSerThsSerGlnGlnIleuThrIleuThrIleuThrIleuThrIleuThrIleu 540
Db 2147 GCTTTTCAACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2206
QY 540 IeSerAapIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPhe 560
Db 2207 ACTCGGATATCTTGGCCCCCAGACCTTACCTTCCCTGACAGAGCTGATTTTGG 2266
QY 560 IeThrGlnSerSerHisPheYrSerAlaSerAlaIleYrGlyYrLeuSerAlaSerYrS 580
Db 2267 CCACAGAGTCCCAACATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2326
QY 580 ePAlaTyrSerCysSerGlnLeuProThrCysGlyAapGlnValYrSerValAargA 600
Db 2327 CTGCTTACAGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2386
QY 600 rGlnYrSerProSerAapArgAlaAapSerArgSerTyrHisGluGluSerProPhe 620
  
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Db 2387 GGCAGAGCAAGTACAGACTGACCTCCGCGAGACTGTCATGAAGAGCCCTTTG 2446
Qy 620 LulvGlnPheIyehArqArqSerCyqgInwctGluPheGlyGluSerIleMetSerGlu 640
Db 2447 AAAGCAGTTTAAACGCGAAGCTGCGCAATGCAATTGGAGAGAGCATCATTCAGACA 2506
Qy 640 snArqSerArqGluGluLnuGlyLysValGlySerGlnSerSerPheSerGlySerMetG 660
Db ACAGGTACCGGAGAGAGCTGGGAAAGTGGGACAGTCACTTCTTTCGGGAGCATGG 2566
Qy 660 LulleIleGluValSer 665
Db 2567 AAATCATTGAGGTCTCC 2583

RESULT 13
US-10-377-072-25

/ Sequence 25, Application US/10377072
/ Publication No. US20040157221A9
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals Inc.
/ APPLICANT: Curtis, Kory A.J.
/ APPLICANT: Logan, Thomas Joseph
/ APPLICANT: Glucksmann, Maria A.
/ APPLICANT: Meyers, Rachel E.
/ APPLICANT: Williamson, Mark J.
/ APPLICANT: Rudolph-Owen, Laura A.
/ APPLICANT: Chun, Miyoung
/ APPLICANT: Tsai, Feng-Ying
/ TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
/ TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
/ FILE REFERENCE: MP103-0180NM1M
/ CURRENT APPLICATION NUMBER: US/10/377,072
/ PRIOR APPLICATION NUMBER: US 2003-02-27
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215,370
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: US 09/723,806
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/187,455
/ PRIOR FILING DATE: 2000-03-07
/ PRIOR APPLICATION NUMBER: US 09/843,297
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: US 60/199,801
/ PRIOR FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: US 09/861,801
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: US 60/205,508
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 09/816,494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 09/815,419
/ PRIOR FILING DATE: 2001-03-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PasterSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 3544
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (589)...(2586)
US-10-377-072-25

Alignment Scores:

Pred. No.: 0 Length: 3544
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-377-072-25 (1-3544)

Qy 1 MetAlaHsGluMetIleGlyThrGlnIleValAlaThrGluValAlaLeuGlu 20
Db 589 ATGGCCATAGATGATTTGGAGCTCAAAATTTGACTGAGAGGTTGGTCTCTCGGAA 648
Qy 21 SerGlyThrGluLysValLeuLeuIleApsSerArqProPheValGluTyArAsnThSer 40
Db 649 AGTGAACCGGAAAGAGTGTCTAAATGATATAGCCGGCATTTGGAGATACAAATCATCC 708
Qy 41 HsIleLeuGluAlaIleAsnIleAsnGlySerIleValMetIleValArgLeuGln 60
Db 709 CACATTTTGGAGCCATTATATCACTGCTCCAGCTTAAGAGCGAAGGTTGCAACAG 768
Qy 61 AspLysValLeuIleThrGluLeuIleGlnHsSerAlaLysHsLysValAspIleAsp 80
Db 769 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 828
Qy 81 CySerGlnLysValValValTyArqGlnSerSerGlnApsValAlaSerLeuSerSer 100
Db 829 TCCAGTCAAGAGCTTGTATGATCAATCAAGCTCCCAAGATGTGCTCTCTCTTCA 888
Qy 101 AspCyPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHsLeu 120
Db 889 GACTGTTTTCTCAGTACTTCTGGTAACTGGAAAGCTTCACTGTTCACTG 948
Qy 121 LeuAlaGlyLysPheAlaGluPheSerArqPheProGlyLeuCyGluGlyLysSer 140
Db 949 CTTCAGAGTGGGTTTGGCTGAGTTCTCGTGTTCCTCGCTCGTGAAGGAAATCC 1008
Qy 141 ThrLeuValProThrCyLysSerGlnProCyLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGCTCCACCTGATCTTCAGCCCTGCTTACTCTGTCACAACTGGGCCAACCC 1068
Qy 161 ArgIleLeuProAsnLeuTyLeuGlyCyqgInwctGluPheValLeuAsnLysGluLeu 180
Db 1069 CGAATTTCTCCCAATCTTATCTTGGCTCCAGCGAGATGCTCAACAGAGAGCTGAT- 1127
Qy 181 -GlnGlnAsnGlyIleGlyTyLeValLeuAsnAlaSerTyThrCyPheProLysProAsp 200
Db 1128 GCAGCAGAAATGGATGTTATGTGTAAATCCAGCA-THCTGTCCAAAGCTGACT 1186
Qy 200 HsIleProGlnSerHsPheLeuArgValProValAsnApsSerPheCyGluLysIleL 220
Db 1187 TTATCTCCCAAGCTCTATCTCTGCGTGCCTGTAAGACAGCTTGTGCAAAAATTT 1246
Qy 220 eubProIleuApsLysSerValApsPheIleGluLysAlaLysSerAsnGlyCySV 240
Db 1247 TGCCTGTTGGACAAATCAATCAATGATTTCAATTGAGAAAGCCCTCCAAATGATGTG 1306
Qy 240 allLeuValHsCyLeuLeuAlaGlyLysSerArqSerAlaThrIleAlaIleAlaTyIleW 260
Db 1307 TTTCTAGTGAAGCTTTTACTGCGATCTCCCGCTCCGCAACATGCTATGCGCTACATCA 1366
Qy 260 eLyArqMetApsPheSerLeuApsGluAlaTyArqPheValLysGluLysArgProT 280
Db 1367 TGAAGAGATGAGACATGCTTTAGATGAAGCTTACAAATTTGGAAGAAAGAAAGACTTA 1426
Qy 280 HsIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuApsTyTyGluLysIleLeuA 300
Db 1427 CTATATCTCCAAATTTCAATTTCTGGGCCAACCTCGACTATGAGAAAGATTTAA 1486
Qy 300 snGlnThrGlyAlaSerGlyProLysSerTyLeuLysLeuHsLsLeuGluLysProA 320
Db 1487 ACCAGACTGAGAGCATCAGGGCCAAAGCAAACTCAAGCTGCTGCACTCGAGAAAGCCAA 1546
Qy 320 snGluProValProAlaValSerGluGlyGlyGlnLysSerGluThrProLysSerProp 340
Db 1547 ATGAACCTGTCCTGCTGCTCAGAGGGTGAAGCAAGAAAGCAAGACGCCCTCAATCCAC 1606
Qy 340 roCyAlaApsSerAlaThrSerGluAlaGlyGlnArgProValHsProAlaSerV 360

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Db      1607 CCTGCTCCGACCTGCTGCTACCTAGAGGACAGAGCAAAAGCCCGTGCATCCCGCCAGCG 1666
QY      360 A|P|roSerValP|roSerValG|n|P|roSer|leu|en|G|u|a|b|p|er|P|ro|leu|Val|G|n|A|L 380
Db      1667 TGCCCGACGGCCGACGCGACGACCCCTGCTGTTAAGGACACCCGCTGGTACAGACGCC 1726
QY      380 e|u|s|e|r|l|e|u|H|s|e|u|s|e|r|A|A|p|A|g|l|e|u|H|u|b|p|e|r|A|e|n|l|y|b|l|e|u|Y|A|g|S|e|r|P 400
Db      1727 TCGTGGGCTGCACCTCTCCGACAGACGCTGGAAAGACGATTAAGCTTACAGCTTCTCT 1786
QY      400 h|e|s|e|r|e|u|b|l|e|u|S|e|r|V|a|l|S|e|r|T|y|s|e|r|A|a|s|e|r|e|u|A|a|l|a|s|e|r|e|u|H|g|l|y|P 420
Db      1787 TCTCTCGAGATCAATCATGTTTCAATTCATTCAGCCAGCATGGACATCCTTACATAGGCT 1846
QY      420 h|e|s|e|r|e|u|S|e|r|G|l|u|a|p|A|l|e|u|G|l|u|T|y|T|y|P|ro|S|e|r|T|H|T|H|l|e|u|A|g|l|y|T|H|A 440
Db      1847 TCTCTCATCAGAAAGATGCTTTGGAAATCACTAACAACCTTCCACTACTCTGGATGGAGACCA 1906
QY      440 s|u|l|y|a|u|C|y|S|G|n|P|H|e|s|e|r|P|ro|V|a|l|G|n|l|u|e|u|S|e|r|G|l|u|H|T|H|P|ro|G|l|u|T|H|S|e|r|P 460
Db      1907 ACAAGCTATGCCAGTTCTCCCTGTTCAAGAACTATCGAGAGCACTCCGAAACCAAGTC 1966
QY      460 r|o|A|p|l|y|S|G|u|a|l|a|s|e|r|l|e|P|ro|l|y|b|l|e|u|G|n|T|H|A|A|T|g|P|ro|S|e|r|A|p|S|e|r|G 480
Db      1967 CTGATTAAGGAGGAAGCCAGCATCCCAAGAAAGCTGGACAGCCGCGACAGGCTTTCAGACAGCC 2026
QY      480 l|n|s|e|r|l|y|b|a|g|l|e|u|H|s|e|r|V|a|l|g|T|H|S|e|r|S|e|r|G|l|y|T|H|A|l|a|G|n|A|g|S|e|r|e|u| 500
Db      2027 AGAGCAAGCATTTGCAATTCGGTTCAGAAACGACGACGCTGGACACCGCCAGAGGTCTCCCTTT 2086
QY      500 e|u|s|e|r|P|ro|leu|H|A|g|S|e|r|G|l|y|S|e|r|V|a|l|G|u|a|b|p|a|n|T|H|S|e|r|P|H|e|u|P|H|e|G 520
Db      2087 TATCTCACTGCTCATCGAGTGGAGGTGGAGGACATTAACCAACCAAGCTTCTTTTGG 2146
QY      520 l|y|e|u|S|e|r|T|H|S|e|r|G|n|H|s|e|u|T|H|y|S|e|r|A|a|g|l|y|e|u|G|l|y|T|H|P 540
Db      2147 GCCTTCCACCAACGACGACGACCTCAAGAAAGCTGGCTGGCTGGCTTTAAGGCTGGC 2206
QY      540 l|e|s|e|r|l|e|u|A|P|ro|G|n|T|H|S|e|r|T|H|P|ro|S|e|r|e|u|H|T|H|S|e|r|T|T|y|P|H|e|A 560
Db      2207 ACTCGATATCTTGGCCCCCAGACCTTACCCCTTCCGACACAGCAGCTGATATTTTG 2266
QY      560 l|a|T|H|G|l|u|S|e|r|H|s|e|T|H|S|e|r|A|s|e|r|A|l|e|T|y|G|l|y|S|e|r|A|s|e|r|T|H|S 580
Db      2267 CCAAGATCTTCACTTACTTCTGCTTCAAGCATTAAGAGGAGGACAGTTACT 2326
QY      580 e|r|A|T|y|S|e|r|C|y|S|e|r|G|n|l|e|u|P|ro|T|H|C|y|S|l|y|A|p|G|n|V|a|l|T|y|S|e|r|V|a|l|A|g|A|T|g|A 600
Db      2327 CTGCTTACAGCTCAGCGACGCTCCCACTTGGGAGACCAAGCTATTTCTGTCGCAAGC 2386
QY      600 r|G|l|u|y|P|ro|S|e|r|A|p|A|g|A|A|p|S|e|r|A|g|A|T|g|S|e|r|T|H|S|G|l|u|S|e|r|P|ro|P|H|e|G 620
Db      2387 GGCAGAGCCAGCAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGGAAGAGAGCCCTTTTG 2446
QY      620 l|u|y|e|u|G|n|P|H|e|y|A|g|A|T|g|S|e|r|C|y|S|G|l|u|e|r|G|l|u|P|H|e|G|l|y|S|e|r|I|e|T|S|e|r|G|l|u|A 640
Db      2447 AAAAGCATTTAAACGAGAAAGCTGCCAAATGGAATGGAAGAGCATATCTCAGAGA 2506
QY      640 s|u|A|T|g|S|e|r|A|g|l|u|e|u|G|l|y|V|a|l|G|y|S|e|r|G|n|S|e|r|P|H|e|S|e|r|G|l|y|S|e|r|e|u|C 660
Db      2507 ACAAGTCAACGGAAGAGCTGGGGAAGTGGGCACTACGTTACTTTTGGGCAAGATGG 2566
QY      660 l|u|l|e|l|e|g|u|A|S|e|r 665
Db      2567 AAATCATTTGAGTCTCC 2583

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RESULT 14

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US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua

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; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Query Match: 70.98%
DB: 17
Gaps: 0

US-10-029-345a-109 (1-665) x US-10-425-114-26234 (1-3625)

QY      1 MetAlAH|e|G|u|e|l|e|G|l|y|T|H|G|l|u|e|V|a|l|T|H|G|u|a|g|l|e|u|V|a|l|A|e|u|e|u|G|u 20
Db      692 ATGGCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
QY      21 S|e|r|G|l|y|T|H|G|l|u|e|V|a|l|e|u|e|u|l|e|A|p|S|e|r|A|g|P|ro|P|H|e|V|a|l|G|l|u|T|H|S|e|r| 40
Db      752 AATGGAACGGAAGAAAGTGTGCTAATGTATGATCCGCGCATTTGTGAAATACATATCATCC 811
QY      41 H|s|l|e|e|u|G|A|l|l|e|a|n|l|e|a|n|l|e|a|n|C|y|S|e|r|l|y|S|e|r|e|u|e|y|A|g|A|T|g|l|u|G|n| 60
Db      812 CACATTTTGGAGCCATTAATATCAATGCTTCAAGCTTATTAAGGAAAGTTGGCAACG 871
QY      61 A|A|p|l|y|V|a|l|e|u|l|e|T|H|G|l|u|e|l|e|G|n|H|s|e|r|A|l|y|H|s|l|y|V|a|l|P|l|e|A|P 80
Db      872 GACAAAGTGTATTATTAAGAGCTCATCCAGCATTCAGCAAAACATTAAGTTGACATTTGAT 931
QY      81 C|y|S|e|r|G|n|l|y|V|a|l|V|a|l|y|T|H|P|H|e|G|n|S|e|r|G|n|A|p|V|a|l|A|s|e|r|e|u|S|e|r| 100
Db      932 TCACGTCAAGAAAGTGTATGATTCATCAAACTCCCAAGATGTGCTCTCTCTTCA 991
QY      101 A|A|P|C|y|P|H|e|u|T|H|V|a|l|e|u|e|u|G|l|y|S|e|r|G|l|u|y|S|e|r|P|H|e|A|n|S|e|r|V|a|l|H|s|l|e|u 120
Db      992 GACTGTTTCTCACTGATCTTCTGGGTAACTGGAGAAAGCTTCAACTCTGTTCACTG 1051
QY      121 l|e|u|A|g|l|y|l|P|H|e|A|g|l|u|P|H|e|S|e|r|A|g|C|y|P|H|e|P|ro|G|l|y|e|u|C|y|S|G|l|u|y|S|e|r 140
Db      1052 CTTGACAGGTGGGTTTGTCTAGTCTCTGTTGTTTCCCTGGCTGCTGTAAGGAAATATCC 1111
QY      141 T|H|l|e|u|V|a|l|P|ro|T|H|C|y|S|l|e|S|e|r|G|n|P|ro|C|y|l|e|u|P|ro|V|a|l|A|A|e|n|l|e|G|l|y|P|ro|T|H 160
Db      1112 ACTCTAGTCCCTTACCTGCACTTCTCAAGCTTCTTCACTTCTTGGCCCAACTTGGGCCCAACC 1171
QY      161 A|g|l|l|e|u|P|ro|A|n|l|e|u|T|H|y|T|H|G|l|u|e|u|G|l|y|S|e|r|G|l|u|A|g|A|T|g|V|a|l|e|u|A|n|l|e|u|l|e 180
Db      1172 CCAATTCCTCCCAATCTTATCTTGGCTCCAGCGAGATGCTTCAACAAGAGCTGAT- 1230
QY      181 -G|l|n|l|a|e|n|G|l|y|l|e|G|l|y|T|H|V|a|l|e|u|A|n|l|a|S|e|r|T|H|C|y|P|ro|l|y|P|ro|A|P|P 200
Db      1231 GCAGCAGATGGGATTTGTTATGTGTAAATCCAGCAA-TACCTGTCCAAAGCTGACT 1289
QY      200 h|e|l|P|ro|G|l|u|S|e|r|H|s|e|l|e|u|A|g|V|a|l|P|ro|V|a|l|A|n|A|p|S|e|r|P|H|e|C|y|S|G|l|u|y|S|e|r|l|e|u 220
Db      1290 TTATCCCGCAGCTCATTTCTCGCGTGTGCTGTGATACAGCTTTTGTGAAATATTT 1349
QY      220 e|u|P|ro|T|H|P|H|e|u|b|l|y|S|e|r|V|a|l|A|p|P|H|e|l|G|l|u|y|A|l|y|V|a|l|A|S|e|r|A|e|n|G|l|y|C|y|A|V 240

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QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuGlu 20
 DB 538 ATGGCCATAGATGATGTAAGTCAATTTGTAAGAGCTTGGTGGCTCTGCTGGAA 597
 QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyrAenThrSer 40
 DB 598 AGTGAACCGGAAAGAGCTGCTAATTGATAGCCGGCATTGTGGAAATCAATATCACTCC 657
 QY 41 HisIleLeuGlnAlaIleAenIleAenCysSerIleLeuMetIleValArgLeuGlnGln 60
 DB 658 CAAATTTTGGAAACCAATTAATATCACTGCTCCAGGCTTAAGAGGAAAGTGGCAACG 717
 QY 61 AspGlyValLeuIleThrGluLeuIleGlnHisSerAlaIleHisIleValAspIleAsp 80
 DB 718 GACAAAGCTGTAATTAACAGCTCATCCAGCATTTCCAGCGAAACATAAGGTGGCATTTGAT 777
 QY 81 CysSerGlnIleValValValTyrAspGlnSerSerGlnAspValAlaSerIleAspSer 100
 DB 778 TGCAGTCAGAAAGGTTGATTAAGATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA 837
 QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGlnIleValSerPheAenSerValIleLeu 120
 DB 838 GACTGTTTCTCACTGACTTCTGGGTAACTGGAGAAAGACTTCAACTGTGTCACTG 897
 QY 121 LeuAlaGlyValPheAlaGluPheSerArgCysPheProGlyLeuGlyGluGlyValSer 140
 DB 898 CTTCGACGAGGTTTGTGAGTTCTCTCGTTGTTTCCCTGGCTCTGTGAAGAAATTC 957
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAenIleGlyProThr 160
 DB 958 ACTCTAGTCCCTCAACGCAATTTCTCAGCCTTGCTTACCTGTGCAACATGGGCCAAC 1017
 QY 161 ArgIleLeuProAenIleLeuTyrLeuGlyCysGlnArgAspValLeuAenIleGluLeu 180
 DB 1018 CGAATCTTCCCAATCTTAATCTGTGCTGACGAGATGCTCTCAACAGAGCTGAT- 1076
 QY 181 -GlnGlnAenGlyIleGlyTyrValIleAenAlaSerTyr-ThrCysProValProAsp 200
 DB 1077 GCGCAGATGGATGGATTGTTATGTGTAATGCCAGCA-TACCTGTCCAAAGCCCTGACT 1135
 QY 200 HeIleProGlnSerHisPheLeuArgValProValAenAspSerPheCysGluIleIle 220
 DB 1136 TATATCCCGAGTCTCAATTTCTCGTGTGCTGTGATGACACTTTTGGAAATTT 1195
 QY 220 EupProTleuAspIleValSerValAspPheIleGluValAlaIleAspAenGlyCys 240
 DB 1196 TGCCTGCTGGTGGCAATCAATGATTTCAATGAGAAAGCAAAAGCTCCAAATGATGTC 1255
 QY 240 AlLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
 DB 1256 TTCTAGTGCATGTTAGCTGGGATCTCCGCTCCGACACATGCTATGCTTACATCA 1315
 QY 260 eLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleValIleValArgPro 280
 DB 1316 TGAAGAGATGAGCATGCTTTAGATGAAGCTTACAGATTGTGGAAAGAAAGAAAGCTTA 1375
 QY 280 hrlIleSerProAenPheAenPheLeuGlyIleLeuAenIleValIleValIleVal 300
 DB 1376 CTATATCTCCAAATCTCAATTTCTGGGCAACTCTCGACTATGAGAAAGATTAAG 1435
 QY 300 sngIthrGlnAlaSerGlyProValSerIleLeuValLeuHisIleGluValPro 320
 DB 1436 ACCAGACTGAGATCAAGGCGCAAAAGCAAACTCAAGCTGCACTGGAGAAACCA 1495
 QY 320 sngIleuProValProAlaValSerGluGlyValIleValSerGluThrProLeuSerPro 340
 DB 1496 ATAACTGCTGCTGCTGCTGAGAGGTGAGCAAGAAAGCGAGAGCCCTCACTCAGTCAC 1555
 QY 340 rocCysAlaAspSerAlaThrSerGlnAlaAlaGlyIleValProValHisIleProIleSer 360
 DB 1556 CCTGTGCTGAGCTGCTGCTGCTGAGAGGCAAGCAAAAGGCGCGTGCATCCGCGCAAG 1615
 QY 360 alProSerValProSerValGlnProSerIleLeuGluAspSerProLeuValGlnAla 380

DB 1616 TGGCCAGCTGCGCCAGCGTGCAGCGCTGCTGTTAAGAGACAGCCGCTGTACAGGCG 1675
 QY 380 eusSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAenIleValIleValArgSer 400
 DB 1676 TCAGTGGCTGCACTGCTGCGGAGAGCGCTGGAAAGCAATTAAGCTCAAGCTTCTCC 1735
 QY 400 heSerLeuAspIleValSerValSerTyrSerAlaSerValAlaIleSerHisGlyP 420
 DB 1736 TCTCTGATATCAATATGATTTCAATTCAGCCAGCATGGAGCATCTTACATGAGCT 1795
 QY 420 heSerSerSerGlnAspAlaLeuGluTyrTyrLeuProSerThrThrLeuAspGlyThr 440
 DB 1796 TCTCTCATCAAGAAAGTCTTTGAAATATACAAACCTTCCACTGATGAGAGGAGCA 1855
 QY 440 smlValLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
 DB 1856 ACAAGCTATGCAAGTTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACCAATC 1915
 QY 460 roAspIleGluGlnAlaSerIleProValIleLeuGlnThrAlaArgProSerArgSerG 480
 DB 1916 CTGATTAAGAGAGAGCCAGCATTCCTCAAGAGCTGCAAGCCGCAAGCTTCAAGACGC 1975
 QY 480 InsSerIleArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
 DB 1976 AAGAGCAAGGATTTGATTTGCTGCTCAAGACAGCAAGCTGACCCGCGCAAGAGCTCTT 2035
 QY 500 eusSerProLeuHisArgSerGlySerValGluAspAenTyrHisSerPheLeuPheG 520
 DB 2036 TATCTTCATGTCATCAAGATGGAGGCTGAGAGCAATTAACCAACCACTTCTTTCG 2095
 QY 520 IlyLeuSerThrSerGlnGlnIleLeuThrIleValSerAlaGlyLeuGlyValIleVal 540
 DB 2096 GCTTTTCCACAGCCAGCGACCTCAAGAGCTGCTGCGCTTAAAGGCTGAG 2155
 QY 540 IeSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheA 560
 DB 2156 ACTCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCACTGATTTTG 2215
 QY 560 IatThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIleSerAlaSerTyrS 580
 DB 2216 CCACAGAGCTTCACACTTCTACTGCTGCTGACCATTAACGAGGCAAGTGCAGATTACT 2275
 QY 580 eLysIleTyrSerCysSerGlnLeuProThrCysGlyAspGlnAlaTyrSerValArgArg 600
 DB 2276 CTGCTTACAGCTGCAAGCCAGCTGCGCACTTGGAGAACCAAGCTATTTGTGCGCAG 2335
 QY 600 rGlnIleProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPheG 620
 DB 2336 GGCAGAGCCAGATGACAGAGCTGACTCGCGCGAGCTGGCATTAAGAGAGCCCTTTG 2395
 QY 620 IlyLeuGlnPheIleValArgArgSerCysGlnMetGluPheGlyIleSerIleMetSerGln 640
 DB 2396 AAAAGAGATTAAAGCAAGCAAGCTGCAATGGAATTTGAGAGAGCATCATGTCAAG 2455
 QY 640 smlArgSerArgGluGluLeuGlyValGlyValSerGlnSerIleSerPheSerGlySerMetG 660
 DB 2456 ACAAGCTACAGGAGAGAGCTGGGAGAAAGTGGAGTCAAGTCACTTTTGGGCAAGCATG 2515
 QY 660 IuIleIleGlyValSer 665
 DB 2516 AAATCATTAAGGCTTCC 2532

RESULT 16 US-10-648-593-115

; Sequence 115, Application US/10648593
 ; Publication No. US20040106132A1

; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
 ; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
 ; FILE REFERENCE: D0273 NP

```
/ CURRENT APPLICATION NUMBER: US/10/648,593
/ CURRENT FILING DATE: 2003-08-26
/ PRIOR APPLICATION NUMBER: 60/406,385
/ PRIOR FILING DATE: 2002-08-27
/ NUMBER OF SEQ ID NOS: 557
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 115
/ LENGTH: 4790
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-648-593-115

Alignment Scores:
Pred. No.: 0          Length: 4790
Score: 472.00        Matches: 663
Percent Similarity: 99.40%      Conservative: 0
Best Local Similarity: 99.40%    Mismatches: 2
Query Match: 70.98%             Indels: 4
DB: 18                         Gaps: 0

US-10-029-345A-109 (1-665) x US-10-648-593-115 (1-4790)

QY      1 MetAlHisgluMetIleGlyThrGlnIleValThrGluValAlaLeuLeuGlu 20
Db      184 ATGGCCCATGAGATGATGGAATCTAAATTGTTACTGAGAGGTGGTCTCTCGGAA 243
QY      21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyraThrSer 40
Db      244 AGTGAAGCGAAAGAAAGTGTCTGAATTGATAGCCGGCATTTGGTGAATCAATATCC 303
QY      41 HisIleLeuGluAlaIleAsnIleAsnCyseSerIleuMetIleValGluLeuGln 60
Db      304 CACATTTTGGAGCCATTATATCACTGCTCCAAAGCTTATGAAGCCAAAGTTGCAACG 363
QY      61 AspIleValIleIleThrGluLeuIleGlnHisSerAlaIleValIleAspIleAsp 80
Db      364 GACAAAGGTATATTAACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 423
QY      81 CyseSerGlnValValValIleValIleAspIleSerGlnIleAspValIleSerIleAsp 100
Db      424 TGCAGTCAGAAAGTTGATGATTACGATCAAGCTCCCAAGATTTGCTCTCTCTCTCA 483
QY      101 AspCysePheLeuThrValLeuLeuGluValLeuGluValLeuSerPheAsnSerValHisIleu 120
Db      484 GACGTGTTCTCACTGATCTTCTGGGTAACTCGAAGAGAGCTTCACTCTGTTCACTG 543
QY      121 LeuAlaGlyGlyPheAlaGluPheSerArgCysePheProGlyLeuCyseGluGlyIleSer 140
Db      544 CTTCAGAGTGGGTTGCTGAGTTCTCTCGTTGTTCTCTGGCCTCTGTGAAAGAAATCC 603
QY      141 ThrIleuValProThrCyseIleSerGlnProCyseLeuProValAlaAsnIleGlyProThr 160
Db      604 ACTCTAGTCTCCCTACCTGCAATTTCTCAGCCCTTGCTTACCTGTTGCCCACTTGGGCAACC 663
QY      161 ArgIleLeuProAsnLeuTyreLeuGlyCyseGlnArgAspValLeuAsnIleGluLeuIle 180
Db      664 CGAATTCCTCCCAATCTTATCTTGGCTCCGACGAGAGTCTCTCAACAAAGAGCTGAT- 722
QY      181 -GlnGlnAsnGlyIleGlyTyraValLeuAsnAlaSerTyra-ThrCyseProIleProAsp 200
Db      723 GCGACGAAATGGGATGGTTATGTGTAAATGCCAGCAA-TACCTGTTCCAAAGCTTAACT 781
QY      200 IleIleProIleSerHisPheLeuArgValProValAsnAspSerPheCyseGluIleIle 220
Db      782 TTAATCCCGAGTCTCAATTCCTGCTGAGCTGTGAATGACAGAGCTTTGTGAGAAATTT 841
QY      220 euProIlePheAspIleSerValIleAspPheIleGluTyraValLeuValIleSerAsnGlyCyse 240
Db      842 TCCCGTGTGGACAATCAAGATTTCACTTGAAGAAAGCAAAAGCTTCAATAGGAGTGG 901
QY      240 alleuValHisCyseLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyraIle 260
Db      902 TTCTAGTCACTGTTAGCTGGAGTCTCCGCTCCGACCAATCGCTATCGCTTAATCA 961
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QY      260 eLlyBaGMetAspMetSerIleuAspGluAlaTyraPheValIleGlyIleArgProT 280
Db      962 TGAAGAGATGGAATGATCTTTAGATGAGCTTACAGATTGTGAAAGAAAGAAAGCTTA 1021
QY      280 hrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrcyluIleIleVal 300
Db      1022 CTATATCTCCAACTTCAATTTCTGGGGCAACTCTGTGACTATGAGAAAGATTAAGA 1081
QY      300 enGlnThrGlyAlaSerGlyProIleSerIleLeuIleLeuIleAsnIleuIleuIleu 320
Db      1082 ACCAGACTGGAGCATCAGGGCCAAAGAGAACTCAACTGCTGCACTTGAGAAAGCCAA 1141
QY      320 snGluProValProAlaValSerGluGlyGlyGlnIleuSerGluThrProLeuSerPro 340
Db      1142 ATGAACCTTCTCTGCTGTCTGAGAGGGTGAAGAAAGCGAACCGCCCTCAGTCCAC 1201
QY      340 roCyAlaAspSerAlaThrSerGluAlaIleGlyGlnArgProValHisProAlaSerV 360
Db      1202 CCTGTGCCGACTCTGTACTCAAGAGGAGAGCAAGAGCCCTGTGATCCGCGACGC 1261
QY      360 alProSerValProSerValGlnProSerLeuLeuGluIleuAspSerProLeuValGlnAla 380
Db      1262 TCCCAAGGAGTCCAGCGGTGAGCCGTCTGTATAGAGACAGCCCGCTGTACAGGCGC 1321
QY      380 euSerGlyLeuHisIleuSerAlaAspArgLeuGluAspSerAsnIleuIleuArgSer 400
Db      1322 TCAGTGGGCTCAGCTGTGCGCAAGAGCTGAGAACACAAATTAAGCTTAAGCTTCT 1381
QY      400 heSerLeuAspIleIleuSerValSerTyraSerAlaSerMetAlaIleAsnIleuIle 420
Db      1382 TCTCTGGATATCAATCAAGTTTCATATTCACCGAGATGCGAGCATCTTAACATGGCT 1441
QY      420 heSerSerSerGluAspAlaLeuGluIleTyraTyraProSerThrThrIleuAspGlyThr 440
Db      1442 TCTCTCATCAGAAAGATGCTTGGATATCTTAACAACTTCCACTCTGATGAGGAGCA 1501
QY      440 snIleuIleuCyseGlnPheSerProValGlnGluLeuSerGluIleThrProGluThrSer 460
Db      1502 ACAAGCTATCCAGATTCCTCCCTGTTCAAGAACTATCGGAGAGACTCCGAAACCAATC 1561
QY      460 roAspIleuGluGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSer 480
Db      1562 CTGATAGAGAGAGAGCAACATTCACAGAACCTGACAGCCGAGGCTTCAACAGCC 1621
QY      480 InsSerValArgLeuHisIleSerValArgThrSerSerGlyThrAlaGlnArgSerIleu 500
Db      1622 AGAGCAAGCGATTGATTCGTGACAAACAGCAGCAGTGGACACCGCCAGAGGTCCCTT 1681
QY      500 euSerProLeuHisIleArgSerGlySerValGluAspAsnTyraHisThrSerPheLeuPhe 520
Db      1682 TATCTCACTGATGAGATGGAGAGCTGAGAGACAAATTAACACACAGCTTCTCTTTCG 1741
QY      520 ILeuSerThrSerGlnGlnHisIleuThrIleuSerAlaGlyLeuGlyIleuIleGly 540
Db      1742 GCTTTTCAACCAAGCAGACGACCTCAAGAACTCTGCTGGCTGGGCTTAAGGCTGGC 1801
QY      540 IAspAspIleuAlaProGlnThrSerThrProSerIleuThrSerSerTyraPheAla 560
Db      1802 ACTGGATATCTTGGCCCCCAAGACTCTACCCCTTCCGACCAAGAGCTGATATTTTG 1861
QY      560 IatThrGluSerSerHisPheTyraSerAlaIleTyraGlyGlySerAlaSerTyra 580
Db      1862 CCACAGATCTTCACTCACTTCACTGCTCAGCANTTAAGAGGCAATGCAATTAAT 1921
QY      580 eAlaTyraSerCyseSerGlnLeuProThrCyseGlyAspGlnValTyraSerValArgArg 600
Db      1922 CTGCTACAGCTGAGGCAAGCTGCTCACTTGGAGAACCAAGGTATTTCTGAGCGCAGGC 1981
QY      600 rGlnIleuProSerAspArgAlaAspSerArgArgSerThrHisGluGluIleuSerProPhe 620
Db      1982 GGCAGAAAGCAAGTGAACAGAGTGACTCGGGGGAGAGCTGCAATGAAGAGAGCCCTTTG 2041
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QY	61	AspSerValLeuLeuLeuThrGluLeuLeuLGIshIserLAlayshIleValAspLIleap	80
DB	769	GACAAAGTGTtATtACAGAGCTCATtCCAGATTCCAGCAAACTAAAGTTGACATTGAT	828
QY	81	CysSerGlnuYValValtYrAspGlnSerSerGlnuYValAlaSerLeuSerSer	100
DB	829	TGCAGTCAGAAAGTGTtAGTTtACGATCAAAAGCTCCCAAGATGTtGCTCTCTCTTCA	888
QY	101	AspCyPheLeuThrValLeuLeuGlyIlyleuGlnuYysSerPheAsnSerValHileu	120
DB	889	GACGTTTtTCCACGTACGTACTtGGGtTAACTGAGAAAGACTTCACTGTtTCACTG	948
QY	121	LeuAlaGlyIlyPheAlaGluPheSerArgCyPheProGlyLeuCySGluGlySer	140
DB	949	CTTCCAGGTGGGTtTGCtGAGTtCTCTGtTGTtTCCtGGCTCTGTGAAAGAAATtCC	1008
QY	141	ThrLeuValProThrCyAlleSerGlnProCyLeuProValAlaAsnIleGlyProThr	160
DB	1009	ACTCTAGtCCCTtACCTGCAATTtCCAGCTGTtACCTGTtGtCCAACTtGGGtCAAC	1068
QY	161	ArgIleLeuProAsnLeuTyrtLeuGlyCyGlnArgAspValLeuAsnIlyGlnLeuIle	180
DB	1069	CGAATTCTtCCCAATCTtTATCTtGGtGtCCAGAGAAATGtCTtCAACAGAGCTGAT-	1127
QY	181	-GlnGlnAsnGlyIleGlyIlyValLeuAsnAlaSerTyrt-ThrCyProIlyProAsp	200
DB	1128	GCAGCAAAATGGATtGGTtATtGtGTTAAATCCAGCA-ThCTGTtCCAAAGCTGACT	1186
QY	200	heIleProGlnuSerHIsPheLeuArgValProValaAsnAspSerPheCyGlnuYsIleL	220
DB	1187	TTATtCCCGAGtCTCATtTCTCGtGTGtCGCTGAAATGACAGCTTtGTtAGAAATtTT	1246
QY	220	eupProTtPleuAspIlySerValaAspHeIleGluYsValaIlyAlaSerAsnGlyCySv	240
DB	1247	TGCGGTGGtTGGCAAAATCAGTAAATTtCATtTGAGAAAGCAAAAGCTtCCATAGATGtG	1306
QY	240	alleuValHIsCyLeuAlaGlyIlyleSerArgSerAlaThrIleAlaIleAlaTyrtIleM	260
DB	1307	TTCTAGtGCATGtTtTAGtGGATtCTCCGCTtCGGCACATGtGtATtGtCCtTACATCA	1366
QY	260	etIlyAsArgMetAspMetSerleuAspGlnAlaTyrtArgPheValIleGlnuYsArgProt	280
DB	1367	TGAAGAGAGtGGAATGtCTtTAAATAGAGCTTtCAATtTGTGAAGAAAGAAAGCACTA	1428
QY	280	hrlIleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrtGlnuYsIlyValIleYsA	300
DB	1427	CTAATATCTtCCAACTtCAATtTtTGTGGtCCAACTtCCGAGCTAAGAGAAAGATtTAAGA	1486
QY	300	asnGlnThrGlyAlaSerGlyProIlySerIlySleuIlySleuHIsleuGlnuYsProCA	320
DB	1487	ACCAAGACTGAGACTtACAGGtCCAAAGCAAACTCAAGCTtGtGCACTGGAGAGACCA	1546
QY	320	engIuProValProAlaValSerGlnuYgIlyGlnuYsSerGlnuYsProLeuSerProp	340
DB	1547	ATGAACCTGTtCCCTGtGTCTtCAGAGGtTGAAGAAAGGAAAGCCCTtCACTGCTCAC	1606
QY	340	roCyValaAspSerAlaThrSerGlnuYAlaGlyGlnArgProValHIsProAlaSerV	360
DB	1607	CTGTGTGGtCCACTGCTtCACTCAAGAGGACAGAGCAAAAGCCGtGtATtCCtCCAGCG	1666
QY	360	alProSerValProSerValGlnProSerLeuLeuGlnuYAspSerProLeuValGlnAlaL	380
DB	1667	TGCCACAGtGCCCGAGGtGtGACGCCtGtGCTtTtAGAGACAGCCCGCTtGTACAGGCGC	1726
QY	380	eusSerGlyLeuHIsleuSerAlaAspArgLeuGlnuYAspSerAsnIlyeIlyAsArgSerP	400
DB	1727	TCAATGTGGtGCACCTtGtCGGACAGAGCTGGAAGACACCAATtAACTCAAGCGTtCT	1786
QY	400	heserLeuAspIlyleYserValSerTyrtSerAlaSerMetAlaIleSerleuHIsGlyP	420
DB	1787	TCTCTGTGAGATCAAAATCAAGTtTTCATtTtCCAGCAAGCAAGAGCAATtCCtTtACATGCT	1846

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QY 420 heserSergluAspAlaLeuGluTyrTyrTyrPserThrThrLeuAspGlyThra 440
Db 1847 TCTCTCATCGAAGAGTCTTGGAAATACCAACCTTCACCTACCTGAGTGGAGCA 1906
QY 440 snlyLeuCyGlnPheSerProValGlnGluLeuSergluGlnThrProGlnThrSerp 460
Db 1907 ACAAGCTATGCAAGTCTCCCTCTTTCAGGAACATACGAGAGCACTCCGAAACCACTC 1966
QY 460 roApLySGluGluAlaSerIleProLyLeuGlnThrAlaArgProSerAspSerg 480
Db 1967 CTGATTAAGAGAGAACGACGATCCCAAGAACCTGACAGCCGACAGCTTCAGACAGCC 2026
QY 480 lnseryAsArgLeuHisSerValArgThrSerserSergIlyhrIaGlnAspSergLeu 500
Db 2027 AGAGCAAGCATTTGATTCGTGATGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2086
QY 500 euserProLeuHisArgSergIlySerValGluAspAsnTyrHisThrSerpheLeuPheg 520
Db 2087 TATCTCATGCAATTCAGAGTGGAGAGCTGAGAGACAAATACCAACAGCTTCCTTTTGG 2146
QY 520 lyleuSerrThrSergGlnGlnHisLeuThrLySeraGlyLeuGlyLeuLySgIlyTrpH 540
Db 2147 GCCTTCCACCAAGCAGAGACACCTACAGAAAGTGTGCTGCTGCTGCTTAAAGGCTGGC 2206
QY 540 lserAspIleLeuAlaProGlnThrSerrThrProSerLeuThrSerrTrpYrPhea 560
Db 2207 ACTCGAATATCTTGGCCCCCAGACCTGACCTCCCTTCCCTGACAGAGCTGATTTTGG 2266
QY 560 lathrGluSerrSerHisPheTyrSeraIleSeraIleTyrGlyGlySeraIleSerrTyrS 580
Db 2267 CCACAGAGTCCCTACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2326
QY 580 eRAlaTyrSerrCySergGlnLeuProThrCySgIlyAspGlnValTyrSerrValArgAsp 600
Db 2327 CTGCTCAAGCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2386
QY 600 rGlnLyPserSeraAspArgAlaAspSeraArgAspSerrTrpHisGluGlnSerrProPheg 620
Db 2387 GCGAAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2446
QY 620 lulyGlnPheLyArgArgSerrCySgInmetGluPheGlyGlnSerrIleMetSergIua 640
Db 2447 AAAAGAGATTAAACGAGAAAGCTGCAAAATGGAAATTGGAGAGACATCATCTCAGAA 2506
QY 640 snAsSeraArgGluGlnLeuGlyLySvalGlySergInserSerrPheSergIlySermErg 660
Db 2507 ACAAGTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2566
QY 660 lullellegluvalser 665
Db 2567 AAATCATTTGAGTCTCC 2583

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RESULT 18

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US-10-357-930-20969
; Sequence 20969, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: HUMAN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454

```

```

; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20969
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20969

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Alignment Scores:

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Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Beet Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
Db: 18 Gaps: 0

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US-10-029-345A-109 (1-665) x US-10-357-930-20969 (1-5145)

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QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 589 ATGGCCATGAGAGAGATTTGAACTCAAAATTTACTAGAGAGGTTGGCTGCTGCTGAGAA 648
QY 21 SerGlyThrGluLySValLeuLeuLeuIleAspSeraArgProPheValGluTyrThrSerp 40
Db 649 AGTGGAGGAGAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCySerrLyLeuMetLyArgArgLeuGln 60
Db 709 CACATTTTGGAAACCATTAATATCACTGCTCAAGCTTATAGAGAGAGAGAGAGAGAGAG 768
QY 61 AspLyValLeuIleThrGluLeuIleGlnHisSerAlaLyHisLyValAspIleAsp 80
Db 769 GACAAAGTGTATTAACAAGCTCATCAGACATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
QY 81 CySerrGlnLySValValValTyrAspGlnSerrSergIleAspValAlaSerLeuSerr 100
Db 829 TGCAGTCAGAGAGGTGTAGTTCAGATCAAGCTCCCAAGATTTGCTCTCTCTCTCA 888
QY 101 AspCySerpheLeuThrValLeuLeuGlyLySValLeuLySerrPheAsnSerrValHisLeu 120
Db 889 GACTGTTTCTCACTGACACTTCTGGGTAAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 948
QY 121 LeuAlaGlyGlyPheAlaGluPheSeraArgCySerpProGlyLeuCyGlnGlyLySerr 140
Db 949 CTTCAGAGGTGGGTGTGCTGAGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1008
QY 141 ThrLeuValProThrCySerrIleSerrGlnProCySLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGTCCCTCACTGACATTTCTCAGCCTTGTCACTGTTGCAACATTTGGGCCAAC 1068
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCyGlnArgAspValLeuLeuLySgIleuIle 180
Db 1069 CGAATTTCTCCCAATCTTTATCTTGCTGCTGACAGAGAGATTTCTCAACAGAGAGAGAT- 1127
QY 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCySProLySProAsp 200
Db 1128 GAGAGAGATGAGATTTGTATGTGTTAAATGCAGAA-TACTGTCCAAAGCTGAGAT 1186
QY 200 heileProGluSerrHisPheLeuArgValProValAsnAspSerrPheCySgIlyLySleu 220
Db 1187 TTATCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246

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QY 220 euProTIPLeuAspLysSerValAspPheIleGluValAlaLysSerAsnGlyCysV 240
 Db 1247 TGCGGTGGTTGGACAAATTCAGTATTCATTGATGAAAGCAAAAGCCTCCAAATGAGATG 1306
 QY 240 alleuValHisCysLeuAlaGlyLysSerArgSerAlaThrIleAlaIleAlaTyrIleM 260
 Db 1307 TTCTAAGTGCATGCTTTAGCTGGGATCTCCGCTCCGACCATGCTATGCGCTACATCA 1366
 QY 260 eluValAspMetAspMetSerLeuAsnArgIleValTyrArgPheValLysGluLysArgPro 280
 Db 1367 TGAAGAGATGAGATGCTTTAGATGATGATTCACATTTGTGAAAGAAAAGAAAGACCTA 1426
 QY 280 hrIleSerProAsnPheAsnPheLeuGlyLysLeuLeuAspTyrGlyLysLeuIleLysA 300
 Db 1427 CTAAATCTCCAAATTCATATTTTCTGGGCCAACTCCCTGGAATGAGAAAGATTAGA 1486
 QY 300 engInThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGluLysProA 320
 Db 1487 ACCAGACTGGAGCATCGAGGCAAAAGACAAACTCAAGCTGCTGCACCTGGAGAGCCAA 1546
 QY 320 engIUProValProAlaValSerGluGlyGlyLysSerGluThrProLeuSerPro 340
 Db 1547 ATGAACCTGTCCTCGCTGCTCAGAGGAGTGAACGAAAGAGAGACGCCCCCTCAGTCCAC 1606
 QY 340 roCyAlaAspSerAlaThrSerGluAlaAlaGlyLysArgProValHisProAlaSerV 360
 Db 1607 CTTGTGCGACTCTGCTACTCAGAGGACAGACGAAAGGCGCTGATCCCGCCACGCG 1666
 QY 360 alProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaL 380
 Db 1667 TGCCCAACGTCGCCAGAGTGCAGCGCTGCTTGAAGAGACAGCCCGCTGATCAGGCGC 1726
 QY 380 euseRgLyLeuHisLeuSerAlaAspArgLeuGluAspSerAlaLysLeuLysLeuLysArg 400
 Db 1727 TCAGTGGCTGACCTCTCGCAGACAGCGCTGGAAGACAGCAATTAACCTCAAGCGTCTCT 1786
 QY 400 heserLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyP 420
 Db 1787 TCTCTCGGATATCAATTCAGTTTCATATTCAGCCAGCATGCGACATCTCTTACATGGCT 1846
 QY 420 heserSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThra 440
 Db 1847 TCTCCTCATCAGAAAGATGCTTTGGAAATACAAACCTTCACATCTGATGGAGCA 1906
 QY 440 enlyLysLeuCyGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
 Db 1907 ACAAGCTATGCGCAATTCCTCCCTGTTTCAAGAACTATGAGAGACATCCCGAAACCGCTC 1966
 QY 460 roAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerG 480
 Db 1967 CTGATTAAGAGAGAGAGCAAGCATCCCAAGAAAGCTGCAAGCCGCGCATTCAGACAGCC 2026
 QY 480 inserLyAspGluHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuL 500
 Db 2027 AGAGCAAGCGCATTCGATTCGATGAGAACGAGCAAGCATGAGCAAGGCCCAAGGCTCTTT 2086
 QY 500 euseRProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520
 Db 2087 TATCTCCATGCAATCGAAGTGGAGCTGAGAGCAATTCACACACAGCTTCCTTTTCG 2146
 QY 520 lylLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLysGluLysLeuGlyTyrP 540
 Db 2147 GCGTTTCCACAGGACGACAGCACTTCAGAAAGTCTGCTGGCTGGAGCTTAAAGGCTGGC 2206
 QY 540 lAspAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheA 560
 Db 2207 ACTCGAATATCTGGCCCCCAGACCTTAACCTTCCTCGACAGACAGCTGGATATTTG 2266
 QY 560 lathRgIysSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrS 580
 Db 2267 CCAAGAGTCTCTCAGACTTCTACTCTGCTCAGCCACTCAGGAGGAGGAGGAGGAGGAGTACT 2326
 QY 580 exAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgA 600

Db 2327 CTGCTACAGCTGACAGCCAGCTGCGCCACTTGGCGAGACCAAGCTATTCTGTGCGAGCG 2386
 QY 600 rglInlyProSerAspAlaAlaAspSerArgArgSerThrPHisGluGluSerProPheG 620
 Db 2387 GGCAGAGCGCAAGTGAACAAGCTGACTCGCGGAGCTGGCAATGAAAGAGAGGCCCTTTG 2446
 QY 620 lylLysGlnPheLysArgSerCysGlnMetGluPheGlyLysSerIleMetSerGluA 640
 Db 2447 AAAAGCATTTTAAACCAAGCTGCGCAATGAAATTTGGAGAGACATCATGTCAGAGA 2506
 QY 640 snArgSerArgGluGluLeuGlyLysValGlySerGlnSerPheSerGlySerMetG 660
 Db 2507 ACAGGTCAAGGAGAGAGCTGGGAGAAAGTGGAGAGTCAAGTCACTTTTGGCGACGATG 2566
 QY 660 lylleIleGluValSer 665
 Db 2567 AAATCATTTGAGGTCTCC 2583

RESULT 19

US-10-357-930-21071
 ; Sequence 21071, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; FILE REFERENCE: MRI-0078CN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21071
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A, T, C or G
 ; US-10-357-930-21071

Alignment Scores:

Pred. No.: 0 Length: 5145
 Score: 472.00 Matches: 663
 Percent Similarity: 99.408 Conservative: 0
 Best Local Similarity: 99.408 Mismatches: 2
 Query Match: 70.984 Indels: 4
 DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-21071 (1-5145)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
 Db 589 ATGGCCCATGAGATGATGTAATTCGAACTCAAAATTTGTAATGAGAGGTGCTGCTGAGAA 648

QY 21 SerGIYThrGIuLysValLeuLeuIleIleAspSerArgProPheValGIuTYrAsnThrSer 40
Db 649 AGTGAACGGAAAAAGTCTCTTAATGATGACGGCCATTGTGGAAATCAATACATCC 708
QY 41 HisIleLeuGIuLAlIleAsnIleAsnCYSerIlyLeuNecIlySAAGIleuGIuIn 60
Db 709 CACATTGTGGAAGCCATTAAATATCACTGCCAAGCTTATGAAGCGAAGTTTGCAACAG 768
QY 61 AspLysValIleuIleThrGIuLeuIleGIuNHISerLAluYSHIstLysValIleAsp 80
Db 769 GACAAAGTGAATTATACAGAGCTCATCCAGATTACCGCAAAACATAGGTGACATGAT 828
QY 81 CysSerGIuLysValIValIValIYrAspGIuSerSerGIuAspValIleSerIleuSerSer 100
Db 829 TGCAGTCAGAGGTGTGATGTTTACATCAAAAGCTCCCAAGATTTCCCTCTCTCTCA 888
QY 101 AspCysPheLeuThrValIleuLeuGIuLysLeuGIuLysSerPheAsnSerValIleu 120
Db 889 GACTGTTTCTCACTGACTTCTGGGGTAACTGGAGAGAGCTTCAACTCTGTCACCTG 948
QY 121 LeuAlaGIuLysPheAlaGIuPheSerArgCysPheProGIuLysGIuGIuLysSer 140
Db 949 CTTCAGAGTGGGTTTCTGAGTTCTCTGCTGTTCCCTGAGCTCTGTGAAGAAATCC 1008
QY 141 ThrLeuValProThrCysIleSerGIuProCysLeuProValIleAsnIleGIuProThr 160
Db 1009 ACTCTAGTCCCTACCTGACATTTCTCAGCCTTCTTACCTGTGCAACATTTGGGCAACC 1068
QY 161 ArgIleLeuProAsnLeuTYrLeuGIuCYSGIuAGAspValIleAsnIlyGIuLeuIle 180
Db 1069 CGAATTCTTCCCAATCTTATCTTGGCTGCCAGCGAAGTGTCTCAACAGAGACTAT- 1127
QY 181 -GIuGIuAsnGIuIleGIuTYrValIleuAsnAlaSerTYr-ThrCysProIlyAspAsp 200
Db 1128 GAGCAGAGATGGAGATGTGATGTTAAATGCCAGCA--TACCTGTCCAAGCTGAC 1186
QY 200 HeIleProGIuSerHisPheLeuArgValIProValIleAspSerPheCysGIuLysIle 220
Db 1187 TTATCCCCGAGCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGTGAAGAAATTT 1246
QY 220 euProThLeuAspLysSerValIleAspHeIleGIuLysAlaIlyAsnSerGIuCYsV 240
Db 1247 TGCCTGTGTGACAAATCAGTACATTTCAATTGGAAGCAAAAGCTCCCAATGATGTG 1306
QY 240 AlLeuValHisCysLeuAlaGIuIleSerArgSerLAluThrIleAlaIleAlaTYrIle 260
Db 1307 TTCTAGTGCATGTTTATGCTGGATCTCCGCTCCGACACATCGCTATCGCTCATCA 1366
QY 260 etLysArgMeAspMetSerLeuAspGIuAlaTYrArgPheValIlySGIuLysArgPro 280
Db 1367 TGAAGAGATGACATGCTTTAGATGAGCTTACAGATTTGTGAAGAAAAAGAAACCTA 1426
QY 280 hrIleSerProAsnPheAsnPheLeuGIuGIuLeuLeuAspTYrGIuLysIlyIleYSA 300
Db 1427 CTAAATCTCCAACTCAATTTCTTGGGCCAACTCTGTGACTATGAGAAAGATTAGA 1486
QY 300 snGIuThrGIuAlaSerGIuProLysSerLysLeuLysLeuLeuHisIleuGIuLysPro 320
Db 1487 ACCAGACTGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGTGACCTTGAGAAACCA 1546
QY 320 snGIuProValIProAlaValIleGIuGIuLysSerGIuThrProLeuSerPro 340
Db 1547 ATGAACTGTCTCTGCTGTCTCAAGAGGTGACAAAGAGAGAGCGCTTCAGTCCAC 1606
QY 340 roCYAlaAspSerLAluThrSerGIuAlaAlaGIuLysArgProValIleAspIleAsp 360
Db 1607 CCTGTGCCACTCTGTCTCTCAGAGGACAGAGCAAAAGCCCTGTGATCCCGCCAGCG 1666
QY 360 alProSerValIProSerValGIuProSerIleuLeuGIuAspSerProLeuValGIuAla 380
Db 1667 TCCCAAGGTGCCAGCTGTGACCGCTGTGTGAAGAGACGCCCTGTGTGACAGCGC 1726
QY 380 euSerGIuLeuHisLeuSerLAlaAspArgLeuGIuAspSerAsnLysLeuLysArgSer 400

Db 1727 TCAATGGAGCTGACCTGTCCGAGAGAGGCTGGAAAGACATAGCTCAAGCTTCT 1786
QY 400 heSerLeuAspIleLysSerValSerTYrSerLAspSerLAlaAspIleuHisGIuY 420
Db 1787 TCTCTGTGATTCATCAATCATCGTTTCTATATTCAGCCAGCAATGGACATCTTACATGCT 1846
QY 420 heSerSerSerGIuAspAlaLeuGIuTYrTYrLysProSerThrThrLeuAspGIuThra 440
Db 1847 TCTTCATCAGAAAGATGGCTGTGAATACATCAAACTTCCACTCTGATGGAGACA 1906
QY 440 snLysLeuCYSGIuPheSerProValGIuGIuLysSerGIuThrProGIuThrSerP 460
Db 1907 ACAAGCTAAGCCAGTTCTCCCTCTGTTCAGAACTATCCAGAGACTCCCAAAACAGATC 1966
QY 460 roAspLysGIuLysAlaSerIleProLysLysLeuGIuThrAlaArgProSerAspSer 480
Db 1967 CTGATTAAGAGAGAACCCAGCATCCCAAGAGCTGACAGCCGCAAGGCTTCAAGACGCC 2026
QY 480 InSerLysArgLeuHisSerValArgThrSerSerSerGIuThrAlaGIuArgSerLeu 500
Db 2027 AGAGCAGAGATGTCATTCGCTCAGAACAGCAGCAGATGGACCGCCAGAGGCTTCT 2086
QY 500 euSerProLeuHisArgSerGIuSerValGIuAspAsnTYrHisThrSerPheLeuPhe 520
Db 2087 TATCTCCACTGCATCGAAGTGGAGCGTGGAGGACATTCACACACAGCTTCTTTTG 2146
QY 520 IlyLeuSerThrSerGIuNHISerThrLysSerAlaGIuLeuGIuLysGIuTYrPH 540
Db 2147 GCTTTCCACAGCAGCAGACGACCTTCAGAACTGTGTGCGCTGTGAGGCTTAAAGGCTG 2206
QY 540 IeSerAspIleLeuAlaProGIuThrSerThrProSerLeuThrSerSerTYrPhe 560
Db 2207 ACTGGATATCTTGGCCCCCAGACCTCTACCTTCCCTGACACAGACTGTATTTG 2266
QY 560 IatThrGIuSerSerHisPheTYrSerLAspSerLAlaIleTYrGIuLysSerLAspTYrS 580
Db 2267 CCACAGAGCTCTACACTTCTACTCTGCTCAGCCATTCACGAGAGCAGTGCACATACT 2326
QY 580 erAlaTYrSerCysSerGIuLeuProThrCysGIuAspGIuAlaTYrSerValaArga 600
Db 2327 CTGCTACAGCTCAGACAGCTGCCCATTTGGAGAGACCAATCTTATTTGTGGCAGGC 2386
QY 600 rGIuLysProSerAspArgAlaAspSerArgArgSerTYrHisGIuLysSerProPhe 620
Db 2387 GCGAAGAGCAATGACAGAGCTGACTCGCGCGAGCTGGCATGAGAGAGCCCTTTG 2446
QY 620 IuLysGIuPheLysArgArgSerCysGIuMetGIuPheGIuGIuSerIleMetSerGIu 640
Db 2447 AAAAGCAGTTTAAACGACAGACTGCCAAATGGAAITTTGAGAGAGCATGTTCAGAGA 2506
QY 640 snArgSerArgGIuGIuLeuGIuLysValGIuLysSerInSerPheSerGIuSerMetG 660
Db 2507 ACGATCACGGGAAAGCTGGGGAAGTGGCAGTCACTTTCGGGAGCAGATGG 2566
QY 660 IuIleIleGIuValSer 665
Db 2567 AAATCATTTGAGGTCTCC 2583

RESULT 20
US-10-357-930-21083
Sequence 21083, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endesge, William
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FIDE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785,276
 PRIOR FILING DATE: 2003-02-16
 PRIOR APPLICATION NUMBER: 60/183,119
 PRIOR FILING DATE: 2000-02-17
 PRIOR APPLICATION NUMBER: 60/189,862
 PRIOR FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/207,454
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/211,114
 PRIOR FILING DATE: 2000-06-09
 PRIOR APPLICATION NUMBER: 60/219,007
 PRIOR FILING DATE: 2000-07-18
 PRIOR APPLICATION NUMBER: 60/255,281
 PRIOR FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 62232
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 21083
 LENGTH: 5145
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1, 5144, 5145
 OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-21083

Alignment Scores:
 Pred. No.: 0 Length: 5145
 Score: 472.00 Matches: 663
 Percent Similarity: 99.40% Conservative: 0
 Best Local Similarity: 99.40% Mismatches: 2
 Query Match: 70.98% Indels: 4
 DB: 18 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-21083 (1-5145)

1 MetAlhIeGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuGlu 20
 589 ATGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
 649 AGTGAACGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 708
 41 HleIleGluGluAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAla 60
 709 CACATTTTGGACCCATTAATCACTGCTCCAGGCTTGAAGGAGGATGCAACAG 768
 61 AspGlyValLeuIleThrGluLeuIleGlnIleSerAlaIleValIleValIle 80
 769 GACAAAGTGTAAATACAGAGCTCAATCCAGCAATCCAGCAATCCAGCAATCC 828
 81 CysSerGlnIleValValValValValValValValValValValValValVal 100
 829 TGCAGTCAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 888
 101 AspCysPheLeuThrValIleLeuLeuGlyValLeuGluValSerPheAlaIle 120
 889 GACTGTTTCTCACTGACTTCTGGGTAACTGAGAGAGAGCTTCAACTGTTCACT 948
 121 LeuAlaGlyValPheAlaGluPheSerArgCysPheProGlyLeuGlyGlySer 140
 949 CTTCAGAGTGGGTTGCTGAGTCTCTGTTGTTCTGCTGCTGCTGCTGCTGCTG 1008
 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAlaIleGly 160
 1009 ACTCTAGTCCCTACCTGCACTTCTCAAGCTTGTGCTTGTGCTTGTGCTTGTG 1068
 161 ArgIleLeuProAlaLeuLeuLeuGlyCysGlnArgPheValIleAlaIleGly 180
 1069 CGAATCTTCCCAATCTTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1127
 181 -GlnGlnAlaGlyIleGlyTyrValIleAlaIleSerTyr-ThrCysProGlyPheAsp 200

1128 GGAGCAAGATGGGATGTTGTTATGTTAATGCAACA- TACTGTCACAAAGCTGACT 1186
 200 heIleProGluSerIlePheLeuValProValAlaIleAspSerPheCysGluValIle 220
 1187 TTAATCCCAAGTCTCAATTCCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246
 220 euProTrpLeuAspIleSerValAspPheIleGluValAlaValIleAspAsnGly 240
 1247 TGCCGTGTTGACAAATCAATGATTTCTGAGCACTTGAAGAAAGCAAGCTTCAAT 1306
 240 alLeuValIleCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleValIle 260
 1307 TTCTAGTCACTGTTAAGTGGGATCTCCGCTCGGCAACCACTGCTATGCTTACAT 1366
 260 eLlybArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluValArg 280
 1367 TGAAAGAGATGACATGCTTTAGATGAAGCTTCAATTTGTGAAGAAAGAAAGCT 1426
 280 hrIleSerProAlaPheAlaPheLeuGlyGluLeuAlaIleValIleValIleVal 300
 1427 CTATATCTCAAACTTCAATTTCTGAGCACTTGAAGCTTGAAGAAAGATTTAAG 1486
 300 enGlnThrGlyAlaSerGlyProGlySerIleValLeuLeuIleValLeuGlyPro 320
 1487 ACCAGACTGAGATCAGGCGCAAGAGCAAACTCAAGCTGCTGCACTGAGAGCA 1546
 320 enGluProValProAlaValSerGlyGlyGluValSerGlyThrProLeuSerPro 340
 1547 ATGAACTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1606
 340 roCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValIleProAlaSer 360
 1607 CCTGTCACACTCTGTACTCTCAGAGCAGCAGAGCAAGCCCGTGCATCCGCAAG 1666
 360 alProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAl 380
 1667 TGCCAGCTGCGCCAGCGAGCGAGCCGCTGTTAAGAGACAGCCGCTGTTAAG 1726
 380 euSerGlyLeuIleLeuSerAlaAspArgLeuGluAspSerAlaValLeuValArg 400
 1727 TAGTGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1786
 400 heSerLeuAspIleLeuSerValSerTyrSerAlaSerMetAlaIleSerLeuIle 420
 1787 TCTCTGATTAACAATGATGTTCTATATTCAGCCAGCAATGGAGATCTTACATG 1846
 420 heSerSerSerGluAspAlaLeuGluTyrTyrIleAspSerThrThrLeuAspGly 440
 1847 TCTCTCAACAAAGATGCTTTGGAATACTCAAACTTCCACTGCTGAGTGGAGCA 1906
 440 snIleLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThr 460
 1907 ACAAGCTAGCCAGTCTCCCTGTTCAAGAACTATCGAGAGAGATCCCGAAACAG 1966
 460 roAspIleGluGluAlaSerIleProGlyValLeuGlnThrAlaArgProSerAsp 480
 1967 CTGATTAAGAGAGAGCAGCACTCCCAAGAACTGAGAGCCGCAAGCTTCAAGAG 2026
 480 IleSerIleArgLeuIleSerValArgThrSerSerSerGlyThrAlaGlnArgSer 500
 2027 AGAGCAAGCATTTGATTCGCTCAGAACCAAGCAGTGGACCGCCAGAGTCCCT 2086
 500 euSerProLeuIleArgSerGlySerValGluAspAsnTyrIleThrSerPheLeu 520
 2087 TATCTCACTGATGAGATGAGAGGAGTGAAGAGCAATTAACAACCACTTCTTT 2146
 520 ILeuSerThrSerGlnGlnIleLeuThrIleValSerAlaGlyLeuValArgIle 540
 2147 GCTTTTCCACCAAGCAGCACTTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTG 2206
 540 IeSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPhe 560

Db 2207 ACTCGATATCTTG9CCCCGAGACTCTACCCCTTCTGACGACGAGCTGTATTTTG 2266
 QY 560 lATHrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrS 580
 Db 2267 CCAAGAGTCTCTCACTTCTACTCTCTCTGACGACATCTACGAGGACAGTGCAGTTACT 2326
 QY 580 eAlaIYrSerCySerGlnLeuProThrCysGlyIleAspGlnValIYrSerValArgAla 600
 Db 2327 CTGCTTACAGCTGACGACCACTGCTCCCACTTGCAGAGCCAAAGTCTATTCTGTGCGCAGGC 2386
 QY 600 rGgInUlyPProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPhe 620
 Db 2387 GGCAGAACCAAGGAGAGAGAGTGAAGTCTGCGGCGAGCTCGGAGATGAGAGACCCCTTTG 2446
 QY 620 lUlyGlnPheUlyArgArgSerCysGlnMetGlnUheGlyGluSerIleMetSerGlu 640
 Db 2447 AAAAGCAGTTTAAACGCAAGACTGCGCAATGGAATTGTGAGAGAGCATGATGTACAGAG 2506
 QY 640 snArgSerArgGluGluLeuGlyUlyValGlySerGlnSerSerPheSerGlySerMetG 660
 Db 2507 ACAGGTCACGGGAGAGCTGGGGAAAGTGGGAGTCAAGTCAAGTCTTTTGGGCGAGTGG 2566
 QY 660 lUleIleGluValSer 665
 Db 2567 AATCATTTAGGCTCTCC 2583

RESULT 21

US-10-357-930-21303
 / Sequence 21303, Application US/10357930
 / Publication No. US20040259086A1
 / GENERAL INFORMATION:
 / APPLICANT: Schlegel, Robert
 / APPLICANT: Monahan, John
 / TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 / TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 / FILE REFERENCE: MRI-007BCN
 / CURRENT APPLICATION NUMBER: US/10/357,930
 / PRIOR FILING DATE: 2003-02-04
 / PRIOR APPLICATION NUMBER: 09/785,276
 / PRIOR FILING DATE: 2003-02-16
 / PRIOR APPLICATION NUMBER: 60/183,319
 / PRIOR FILING DATE: 2000-02-17
 / PRIOR APPLICATION NUMBER: 60/189,862
 / PRIOR FILING DATE: 2000-03-16
 / PRIOR APPLICATION NUMBER: 60/207,454
 / PRIOR FILING DATE: 2000-05-25
 / PRIOR APPLICATION NUMBER: 60/211,314
 / PRIOR FILING DATE: 2000-06-09
 / PRIOR APPLICATION NUMBER: 60/219,007
 / PRIOR FILING DATE: 2000-07-18
 / PRIOR APPLICATION NUMBER: 60/255,281
 / NUMBER OF SEQ ID NOS: 62232
 / SOFTWARE: PaSeq for Windows Version 4.0
 / SEQ ID NO 21303
 / LENGTH: 5145
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / LOCATION: 1, 5144, 5145
 / OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-21303

Alignment Scores:

Pred. No.: 0
 Score: 472.00
 Percent Similarity: 99.40%
 Best Local Similarity: 99.40%
 Query Match: 70.98%
 DB: 18

Length: 5145
 Matches: 663
 Conservative: 0
 Mismatches: 2
 Indels: 4
 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-21303 (1-5145)
 QY 1 MetAlaHisGluMetIleGlyThrGlnIleValIleThrGlnArgLeuValAlaLeuLeuGlu 20
 Db 589 ATGGCCCATGAGATGATGTTGAACTCAAAATTGTTACTGAGAGGTGTGGCTGCTGGAA 648
 QY 21 SerGlyThrGlnUlyValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
 Db 649 AGTGAACCGGAAAGAGTGTCTTAATTGATACCGGCATTTGTGAATACATTCATCC 708
 QY 41 HisIleLeuGlnAlaIleAsnIleAsnCySerSerIleMetIleArgArgLeuGlnGln 60
 Db 709 CACATTTTGGAGCCATTATATTCATAGCTCTCAAGCTTATGAGACGAAAGGTTCACACG 768
 QY 61 AspIleValLeuIleThrGlnLeuIleGlnHisSerAlaIleValHisIleValAspIleAsp 80
 Db 769 GACAAAGTGTATTATACAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 828
 QY 81 CysSerGlnUlyValValIleValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSer 100
 Db 829 TGCAGTCAGAGAGTGTGTATGTTACGATCAAGCTCCAAAGTGTGCTCTCTCTCTTCA 888
 QY 101 AspCysPheLeuThrValLeuLeuGlyUlySerGlnUlySerPheAsnSerValHisLeu 120
 Db 889 GACTGTTTCTCAGTGTACTTCTGGGTAACCTGGAGAAAGCTTCATCTGTTCACCTG 948
 QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyIleSer 140
 Db 949 CTTCAGAGTGTGTTTCTGAGAGTCTCGGTTGTTTCCCTGGCTCTGTGAAGGAAATCC 1008
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
 Db 1009 ACTTAGTCCCTACCTCACTTCTCAGCTTGTCTTACCTTCCCAATGGGCCCAACC 1068
 QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnUlyGluLeuIle 180
 Db 1069 CGAATTTCTCCCAATCTTATCTTGCTGCGCAGCGAGATGCTCTCAACAAGAGCTGAT- 1127
 QY 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProCysProAsp 200
 Db 1128 GCAGCAAGATGGGATGTTATGTGTATATGCGAGCA-TCCTGTCCAAAGCCGTGACT 1186
 QY 200 helLeuProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIleIle 220
 Db 1187 TTATCCCGAGTCTCATTTCTGCGGTGCTCGTGAATGACGCTTTGTGAGAAATTT 1246
 QY 220 euProTrpLeuAspUlySerValAspPheIleGlnUlyAlaIleValAsnGlnCys 240
 Db 1247 TGCCTGTGTTGGCAAAATCAGTATGATTCATTGATGAAAGCAAAAGCCCTCAATGATGTG 1306
 QY 240 alleuValHisCysIleuValagIlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
 Db 1307 TTCTAGTGAAGTGTGTTAGCTGGAGATCTCCGCTCGGCAACCATGCTATGCTCATAC 1366
 QY 260 euIleArgMetAspMetSerIleuAspGluAlaTyrArgPheValIleGlnUlyAspPro 280
 Db 1367 TGAAGAGATGACATGTCTTATGATGAAGCTTACAGATTGTGTAAGAAAGAAAGACCTA 1426
 QY 280 hrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnUlyIleVal 300
 Db 1427 CTATATCTCCAAACTCAATTTTCTGGGCCAACTCTGGACTATGAGAAAGATTGAGA 1486
 QY 300 enGlnThrGlyAlaSerGlyProCysSerIleUlyIleUlyHisLeuGlnUlySerPro 320
 Db 1487 ACCAGACTGAGACATCAGGCGCCAAAGAGCAAACTCAAGCTGTGCACTTGAAGAACCA 1546
 QY 320 enGluProValProAlaValSerGluGlyGlnUlySerGlnUlyTrpProLeuSerPro 340
 Db 1547 ATGAACCTGTCTCGTGTCTCAAGGCTGAGCAAGAAACGAGAGCCCTTCAAGTCCAC 1606
 QY 340 roCysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSerV 360

Alignment Scores:

Pred. No.: 0
 Score: 472.00
 Percent Similarity: 99.408
 Best Local Similarity: 99.408
 Query Match: 70.988
 DB: 18
 Length: 5145
 Matches: 663
 Conservative: 0
 Mismatches: 2
 Indels: 4
 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-22820 (1-5145)

QY 1 MetAlaHIGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
 DB ATGGCCCATGAGATGATGGAACTCAAAATTGTAAGAGAGGTGGTGGCTCGCTGAA 648
 QY 21 SerGlyThrGlnIleuValLeuLeuIleAspSerArgProPheValGlnIleThrSer 40
 DB AGTGAACCGAAGAAAGTGTGCTAATGATGAGCCGCCAATTGTGGAATACATACATCC 708
 QY 41 HisIleLeuGlnIleAlaIleAsnIleAsnGlySerLeuMetLeuArgArgLeuGlnGln 60
 DB CACATTTTGGAGGCACTTAATATCACTGCTCCAGCTTATGAGCGAAGTTGGCAACG 768
 QY 61 AspLeuValLeuIleThrGluLeuIleGlnHisSerAlaLeuHisAlaValAspIleAsp 80
 DB GACAAAGTGTATATACAGAGCTCATCCAGCATTCAGCGAAACATAGAGTGAATGAT 828
 QY 81 CysSerGlnIleValValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
 DB TGGAGTCAGAAAGGTTGATGATTCAGATCAAGTCCCAAGATGTTCCCTCTCTTCA 888
 QY 101 AspCysPheLeuThrValLeuLeuGlyLeuGlnIleuValLeuSerPheAsnSerValHisLeu 120
 DB GACTGTTTCTCAGCTGATCTTCTGGGTAACAGAAAGAGCTTCAACTCTGTCACCTG 948
 QY 121 LeuAlaGlyLeuPheAlaGlnPheSerArgCysPheProGlyLeuGlyGlySer 140
 DB CTGGCAGGTGGGTTTCTGAGTTCTCTCGTTGTTTCCCTGGCCTGTGAAAGGAAATCC 1008
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
 DB ACTCTGATCCCTACCTGCAATTCCTGCTGCGACGAGATGCTTCAACAGAGCTGAT 1068
 QY 161 ArgIleLeuProAsnLeuThrLeuGlyCysGlnArgAspValLeuAsnIleGlyLeu 180
 DB CGAATCTTCCCAATCTTATCTTGGCTGCGACGAGATGCTTCAACAGAGCTGAT 1127
 QY 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProLysProAsp 200
 DB GAGAGAGATGGGATGGTTATGTTATGTTAATGCCAGCA-TACCTGTCCAAAGCCGACT 1186
 QY 200 IleIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnIleLeu 220
 DB TTATCCCGCAGTCTCAATTCCTGCGTGTGCTGTGATGACAGCTTTTGTGAAATTT 1246
 QY 220 AspProThrLeuAspIleSerValAspPheIleGlnIleValAlaValAlaSerAsnGlyCys 240
 DB TGGCGGTGGTGGCAATCATGATGATTCATGAGAAAGCAAAAGCTCCCAATGAGTGG 1306
 QY 240 AlLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
 DB TTTCTATGACCTGTTTACGTGGGATCTCCGCTCCGCAACATCGTATCGCTTACATA 1366
 QY 260 eLysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValIleGlnIleValArgPro 280
 DB TGAAGGAGATGACATGCTCTTATGATGAGCTTACAGATTTGTGAAAGAAAGAAAGCTCA 1426
 QY 280 hrlIleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrGlnIleValIleVal 300
 DB CTATATCTCCAAATCTCAATTTCTGGGCCAATCTCTGAGCTATGAGAAAGATTAAGA 1486
 QY 300 snGlnThrGlyAlaSerGlyProLysSerLeuValLeuValLeuGlnIleValPro 320
 DB ACCAGCTGGAGATCAGGGGCCAAAGAGCAAACTCAAGCTGTGACCTGGAGAGCA 1546

QY 320 snGlnProValProAlaValSerGlnGlyGlyGlnIleuSerGlnThrProLeuSerPro 340
 DB ATGAACCTCTCTCTGCTGTCTCAGAGGGTGGACAAAGAACAGAGCCCTCAGTCCAG 1606
 QY 340 roCysAlaAspSerAlaThrSerGlnIleAlaGlyValArgProValHisProAlaSer 360
 DB CCTGTGGCACTCTGCTACCTCAGAGGCGAGCAAAAGGCCCGGTGATCCCGCAGCG 1666
 QY 360 AlProSerValProSerValGlnProSerLeuLeuGlnIleAspSerProLeuValGlnAla 380
 DB TCCCCAGCCTGCCAGCGCGCGCTGCTTTAGAGACAGCCCGCTGGATACAGGCC 1726
 QY 380 SerSerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnIleuValArgSer 400
 DB TTAGTGGCTGACCTGTCCGAGAGAGCTGGAAGACAGAAATAGCTCAAGCTTCT 1786
 QY 400 hSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGly 420
 DB TCTCTGTGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGATCATAGGCT 1846
 QY 420 hSerSerSerGlnAspAlaLeuGlnIleTyrTyrLysProSerThrThrLeuAspGlyThr 440
 DB TCTCTCATCAGAAAGATGCTTGGAAATCTACAAACCTTCCACTCTGATGGAGCA 1906
 QY 440 snIleLeuCysGlnIlePheSerProValGlnIleuSerGlnIleThrProGlnThrSer 460
 DB ACAGCTATGCCAGATCTCCCTGTTCAGAACTATCGAGAGACATCCGAAACAGATC 1966
 QY 460 roAspLeuGlnIleAlaSerIleProLysLeuGlnThrAlaArgProSerAspSer 480
 DB CTGATTAAGAGGAGAACCCAGCATCCCAAGACCTGCAAGCCGCGCTTACAGAGCC 2026
 QY 480 IAsnIleArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
 DB TATCTCATCTGATGAGATGGAGCGTGGAGAGCAATTAACACACACCTTCTTTTG 2086
 QY 500 SerProLeuHisArgSerGlySerValGlnAspAsnThrHisPheSerPheLeuPhe 520
 DB TATCTCATCTGATGAGATGGAGCGTGGAGAGCAATTAACACACACCTTCTTTTG 2146
 QY 520 ILeuSerThrSerGlnGlnHisLeuThrIleuValSerAlaGlyLeuGlyLeuValGlyTyr 540
 DB GCCTTCCACAGCCAGACAGACCTCAGAACTCTGCTGGCCCTTAAGGCTGGC 2206
 QY 540 IAspAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPhe 560
 DB ACTCGAATATCTGGCCCCCAGACCTCAACCTTCCCTGACAGAGCTGTATTTTG 2266
 QY 560 IAThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIleSerAlaSerTyr 580
 DB CCACAGAGCTCCACACATTCATCTGCTCAGCAATTCAGAGGAGATGCAAGTACT 2326
 QY 580 eAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArg 600
 DB CTGCTTACAGCTGACGACGCTGCCCATTTGGGAGACCAATCTATTTCTGCGCAGGC 2386
 QY 600 IArgIleAspProSerAspArgAlaAspSerArgArgSerTyrHisGlnIleuSerProPhe 620
 DB GGCAGAGGCAAGTACAGAGCTGACTCGCGCGAGCTGGCATGAGAGAGACCCCTTG 2446
 QY 620 IuIleGlnPheLysArgArgSerCysGlnMetGlnPheGlyGlnSerIleMetSerGln 640
 DB AAAACAGATTAAAGCAGAAAGCTCCAAATGGAATTTGAGAGAGCATCATGTACAGA 2506
 QY 640 snArgSerArgGlnIleuGlyLysValGlySerGlnSerSerPheSerGlySerMet 660
 DB ACGATCAGCGGAAGAGCTGGGGAAGTGGAGATCACTTACCTTTTCGGCAGCATGG 2566
 QY 660 IuIleIleGlnValSer 665
 DB AAATCATGAGGCTCC 2583

RESULT 24
US-10-357-930-26669
Sequence 26669, Application US/10357930
Publication No. US2004025908A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: WI-0078CN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26669
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26669

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-26669 (1-5145)

QY 1 MetAlaHISGLuMeTlleglYThrGlnlIeValThrGluArgLeuValAlaIleuLeuGlu 20
Db 589 ATGGCCATGAGATGATGTGAATCTCAATTTGTTACTGAGAGGTGGTGGCTTCTGTGAA 648
QY 21 SerGlyYThrGlnLysValIleuLeuLysSerArgProPheValGluTyrAsnThrSer 40
Db 649 AGTGAACCGAATAATGTCTGTAATGTATACCGGCAATTTGTGAATACATACATCC 708
QY 41 HisIleLeuGluAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 60
Db 709 CACATTTTGGAGCCATTAAATATCACTGCTCAAGCTTAAGAGCGAAGGTTCCAAACAG 768
QY 61 AspIysValIleuLysThrGlnLeuLysGlnHisSerAlaLysHisLysValAspIleAsp 80
Db 769 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGGAAACATTAAGCTTTGACATGAT 828
QY 81 CysSerGlnLysValValValLysProGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCATTCAGAGAGCTTGTAGTTTACATCAAGCTCCCAAGATGTTCCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValIleuLeuGlyLysLeuGlnLysSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTTCACATGACTTCTGGGTAACTGAGAGAGCTTCACTGTTCACCTG 948

QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCyseGluLysSer 140
Db 949 CTTCAGAGGTGGATTTCTGATGTTCTCTGTTTCCCTGGCCCTGTGAGAGAAATCC 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysIleProValAlaAsnIleGlyProThr 160
Db 1009 ACTCATGTCCCTACCTGATCTTCTCAAGCTTGTCTTACCTGTTCACAACTGGGCAACC 1068
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgPheValLeuAsnLysGlnLeuIle 180
Db 1069 CGAATTCCTCCAACTTATCTTGTGGCCAGGAGATGCTTCAACAAGACTGAT- 1127
QY 181 -GlnGlnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProLysProAsp 200
Db 1128 GGAGAGAGATGGGATTTGTTATGTGTAAAGCCAGCAA-TACCTGTCCAAAGCTGACT 1186
QY 200 helLeProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleL 220
Db 1187 TTATCCCGAGCTCATTTCTGCGGTGCGGTGAGATGACAGCTTTGTGAGAAATTT 1246
QY 220 euProTrpLeuAspLysSerValAspPheIleGlyValAlaLysAsnGlyCysV 240
Db 1247 TCCCTGTGTGGCAAAATCAATCAATTTCAATTGAGAAAGCAAAAGCTCCAAATGATGTG 1306
QY 240 alLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleW 260
Db 1307 TTCTAGTGCATGTTTGTAGCTGGATCTCCGCTCCGACCACTGCTATCTCATCATCA 1366
QY 260 elLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProT 280
Db 1367 TGAAGAGATGAGATCTTGTAGTAACTTACAGATTGGAAGAAAGAAAGAAAGCTTA 1426
QY 280 hrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysA 300
Db 1427 CTATATCTCCAAACTTCAATTTCTGGGCCAACTCTGGACATAGAGAAAGATTAGA 1486
QY 300 snGlnThrArgLysAlaSerGlyProLysSerLysLeuLysIleuGlnLysProA 320
Db 1487 ACCAGACTGGAGATCAGGGCCCAAGAGCAAACTCAAGCTGTGACCTGGAGAAAGCCAA 1546
QY 320 snGluProValProAlaValSerGluGlyGlyGlnLysSerGlnThrProLysSerProP 340
Db 1547 ATGAACCTGTCCCTGTGTCTCAGAGAGGTGAGCAAGAAAGCCAGCGCTCAGTCCAC 1606
QY 340 rocYsaIAspSerAlaThrSerGluAlaIleGlyGlnArgProValHisProAlaSerV 360
Db 1607 CCTGTCCCACTCTGTACTCTCAGAGGAGCAGAGCAAAAGCCGTGATCCGCCACGC 1666
QY 360 alProSerValProSerValGlnProSerIleuLeuGluAspSerProLeuValGlnAlaL 380
Db 1667 TGGCCAGCTGTCCAGCGTGCAGCGCGGTGTGTAGAGAGCAAGCCCGTGTGTAACGCGC 1726
QY 380 euSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerP 400
Db 1727 TAGAGGGGTGACCTGTCTCCGACAGAGCTGGAAGACAGCAATTAAGCTTAAGCTTCT 1786
QY 400 heSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaLysSerIleuHisGlyP 420
Db 1787 TCTCTCTGATATCAAAATCAATTTCAATTCAGACACATGCGACATGCGATCTTCAATGCT 1846
QY 420 heSerSerSerGluAspAlaLeuGlnLysTyrLysProSerThrThrLeuAspGlyThra 440
Db 1847 TCTCTCATCAGAGAGATCTTGTGAATATCAAACTTCACTTCTGATGAGAGCA 1906
QY 440 snLysLeuCyseGlnPheSerProValGlnGluLeuSerGlnGlnThrProGluThrSerP 460
Db 1907 ACAAGCTATGCAATTTCTCCCTGTTCAGAGAACTATGAGAGAGATCCCGAAACAGTC 1966
QY 460 roAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerG 480
Db 1967 CTGATTAAGAGAGAGAGATCCCAAGAGCTGAGAGAGCTGCAAGGCTTTCAGACAGCC 2026

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QY 480 InSerlySArGLeuHISerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
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|
|
Db 2027 AGAGCAAGCATTCATTCGCTGAGAAACGACGACGAGTGCACCGCCAGAGTCCCTTT 2086
|
|
|
QY 500 euSerProLeuHISarSerGlySerValGlnuAphAntYrHISerSerPheLeuPheG 520
|
|
|
Db 2087 TATCTCCACATGCATCAAGTGGAGCGTGGAGGACATATTCACACACAGCTTCTTTTCG 2146
|
|
|
QY 520 lyLeuSerThrSerGlnGlnHISerThrlySerSerAlaGlyLeuGlyLeuGlyTTPH 540
|
|
|
Db 2147 GCGTTTTCACACACCGACGACACCTTCAGAAAGTCTGCGCTGGGCTTTAAGGCTGCG 2206
|
|
|
QY 540 ISerAphleuAlaProGlnThrSerThrProSerLeuThrSerSerSerTryptPhea 560
|
|
|
Db 2207 ACTCGATATCTTGCGCCCGCCACACCTTACCTTCCCTGACACGACGCTGTATTTTG 2266
|
|
|
QY 560 lathrGluSerSerHISerThrSerSerAlaSerAlaIleYrGlyGlySerAlaSerTyrS 580
|
|
|
Db 2267 CCAAGAGTCTCCTCACTTCTTCTGCTGCTGACGACCTTACGAGGACAGTGCAGTTACT 2326
|
|
|
QY 580 exrAlaYrSerCySerSerGlnLeuProThrCyaglYapGlnValYrSerSerValArgArg 600
|
|
|
Db 2327 CTGCCCTACAGCTGCAGCAGCTGCCCACTTGCAGAACCAAGTCTATTTCTGTCGAGAGC 2386
|
|
|
QY 600 rglInlySProSerAapArgAlaAspSerArgArgSerTrpHISGluGluSerProPheG 620
|
|
|
Db 2387 GGCAGAGCCCAATGACAGAGCTGACTCGCGGAGAGCTGGCATGAGAGAGCCCTTTG 2446
|
|
|
QY 620 lylySglnPheLySArGArgSerCySglnMetGlnPheGlyGluSerIleMetSerGlnu 640
|
|
|
Db 2447 AAAAGCAGTTTAAACGAGAGAGCTGCCAATGTGAATTGGAGAGACATCATTCAGAGA 2506
|
|
|
QY 640 snArSerArgGluGluLeuGlyLyValGlySerGlnSerSerPheSerGlySerMetG 660
|
|
|
Db 2507 ACAGGTCACCGGAAAGCTGGGGAAGTGGGCAATGTCAGTCTAGCTTTTGGGCGCAGATG 2566
|
|
|
QY 660 lyIleIleGluValSer 665
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Db 2567 AAATCATTTAGGTCTCC 2583
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RESULT 25
US-10-357-930-26815
; Sequence 26815, Application US/10357930
; Publication No. US20040259086A1
;
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-0078CN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62332
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26815
; LENGTH: 5145
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26815

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-26815 (1-5145)

QY 1 MetAlaHISGluMetIleGlyThrGlnIleValIrnGluArgLeuValAlaLeuGln 20
|
|
|
Db 589 ATGGCCCATGAGATGATTGGAATCAAAATTGTACTGAGAGGTTGGTGGCTGCTGGAA 648
|
|
|
QY 21 SerGlyThrGlnLyValIleuLeuIleAapSerArgProPheValGluTyrAnThrSer 40
|
|
|
Db 649 AGTGGAAACGAAAAAGTGTCTTAATTGATACCGGCACTTGTGGAAATACATATCATCC 708
|
|
|
QY 41 HISIleGluAlaIleAsnIleAsnCySerlySleuMetLySArGArgLeuGln 60
|
|
|
Db 709 CACATTTTGAAGCATTATATATCACTGCTCCAGCTTATAGGAAAGTTGCAACAG 768
|
|
|
QY 61 AapLyValIleuIleThrGluLeuIleGlnHISerAlaValHISlyValAapIleAap 80
|
|
|
Db 769 GACAAAGTCTTAATTCAGAGCTCATCCAGCATTCAGCAAAACATTAAGTTACATGAT 828
|
|
|
QY 81 CySerGlnLyValIleValIleValIleValIleValIleValIleValIleValIle 100
|
|
|
Db 829 TCGAGTCAGAAAGTTGATTTACATCAAACTCCCAAGATGTTGCTCTCTCTTCA 888
|
|
|
QY 101 AapCyPheLeuThrValIleuLeuGlyLyValIleGlnLySArGArgLeuValHISleu 120
|
|
|
Db 889 GACTGTTTCTCAGCTGACTTCTGGGTAACTGGAGAAAGCTTCAACTCTTCACTCG 948
|
|
|
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCyPheProGlyLeuCySglnGlyLySer 140
|
|
|
Db 949 CTTCGAGGTGGSTTTGCTGAGTCTCTGCTTTTCCCTGGGCTCTGTGAAGAAATTC 1008
|
|
|
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
|
|
|
Db 1009 ACTTAGTCCCTACCTGACCTTCTCAGCTTCTTACCTGTCGCAACATTTGGGCCAAC 1068
|
|
|
QY 161 ArgIleuProAsnLeuTyrIleuGlyCySglnArgAapValIleuAsnlySglnLeuIle 180
|
|
|
Db 1069 CGAATTTCTCCAAATCTTATCTTGGCGCAGCAGAGAGTCTTCAACAAAGAGCTGAT- 1127
|
|
|
QY 181 -GlnGlnAsnGlyIleGlyTyrValIleuAsnAlaSerTyr-ThrCySProLySProAap 200
|
|
|
Db 1128 GAGCAGAAATGGATGGTATGTGTTAATCCAGCAA-TACCTGTCCAAAGCTGACT 1186
|
|
|
QY 200 IleIleProGluSerHISerPheLeuArgValProValAsnAapSerPheCySglnlyIle 220
|
|
|
Db 1187 TTATCCCGAGTCTCATTTCCGCGTGCGCTGTAATCAAGCTTTTGTGAGAAATTT 1246
|
|
|
QY 220 euProTyrPheuAapLySerValAapPheIleGluValAlaValAlaSerArgNlyCyGv 240
|
|
|
Db 1247 TCCCGTGTGTGACAAATCAATGATTTTCATTGAGAAAGCAAAAGCTTCATGAGATGG 1306
|
|
|
QY 240 alleuValHISCySeruAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
|
|
|
Db 1307 TTCTAGTGCATGCTTTAGCTGGATCTCCGCTCCGCAACATCCCTATCCGCTACATCA 1366
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|
|
QY 260 eLySArMetAapMetSerLeuAapGluAlaTyrArgPheValIleGlyLySArGProt 280
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Db 1367 TGAAGAGATGAGCAATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTTA 1426
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QY 280 htlleSerProAsnpheAsnpheleuglygluLeuLeuaprryrgluLylyleIlelya 300
 Db 1427 CTATATCTCCAAACTTCAATTTTCTGGCCCACTCCCTGAGACTGTGAGAAATAATTAAGA 1486
 QY 300 anGlnThnGlyAlaSerGlyProLySerLySleuLySleuLhSleuGluLyProA 320
 Db 1487 ACCAGACTGGAGCATCGAGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAGCCAA 1546
 QY 320 anGluProValProAlValSerGluLygluGluLySerGluLyThrProLeuSerProp 340
 Db 1547 ATGAACCTGCTCCCTGCTCTCAAGGGGTGAGCAAAAAGCGAGCGCCCTCACTGCAC 1606
 QY 340 roCyValaAspSerAlaThrSerGluAlaAlaGlyGluInaGProValHISproAlaSerV 360
 Db 1607 CCGTGGCCGACTCTGCTACTCTCAGAGGACGAGCAAAAGGCCCTGCACTCCGCGACGG 1666
 QY 360 alProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaL 380
 Db 1667 TGCCGAGCGTGGCCAGGCTGAGCCGCTGCTGTAGAGGACAGCCCGCTGGTACAGCGCC 1726
 QY 380 euSerGlyLeuHISleuSerAlaAspArgLeuGluAspSerAnlyleuLyAspSerP 400
 Db 1727 TCGATGGGCTGACCTGCTCGAGACAGGCTGGAAGACCAATTAAGCTCAAGGGTCTT 1786
 QY 400 heserLeuAspIleLySerSerValSerLySerAlaSerMetAlaAlaSerLeuHISglYp 420
 Db 1787 TCTCTTGGAAATCAATCAATGATTTCATTTTCAGCCAGCATGAGCATCTTCAATGGCT 1846
 QY 420 heserSerSerGluAspAlaLeuGluLyryrLyLyPProSerThThleuAspGlyThra 440
 Db 1847 TCTCTTCATCAAGATAGTCTTGGAAATCTHCAAACTTCCACTACTCTGGATGGAGCA 1906
 QY 440 snLyLeuCyngInheSerProValGlnGluLeuSerGluGlnInThProGluThSerP 460
 Db 1907 ACAACTATGCCAGTTCCTCCCTGTTCAGAACTATGAGAGAGACTCCGCAACCAAGTC 1966
 QY 460 roAspLyGluGluAlaSerIleProLybLySleuGlnThraAlaArgProSerAspSerG 480
 Db 1967 CTGATTAAGAGAGAGCCAGCATCCCAAGAGCTGACAGACGGCCAGGCTTTCAGAGACGC 2026
 QY 480 InSerLyArgLeuHISerValArgThrSerSerSerGlyThraAlaInArgSerLeuL 500
 Db 2027 AGAGCAAGCATTCATTCGGTCCAGAACCAAGAGCTGAGCAGCGCCAGAGAGTCCCTTT 2086
 QY 500 euSerProLeuHISargSerGlySerValGluAspAsnLyryHISThrSerPheLeuPheG 520
 Db 2087 TATCTCCAGTCGATCGAAGTGGAGCGTGGAGAGCAATTAACAACACACTTCTTTTCG 2146
 QY 520 LyLeuSerThnSerGlnGlnHISleuThrySerSerAlaGlyLeuGlyLeuLybGlyTPH 540
 Db 2147 GCTTTCACACAGCCAGACACACACCTCAAGAGCTGCGGCTTAAAGGCTGGC 2206
 QY 540 IsSerAspIleLeuAlaProGlnThnSerThProSerLeuThnSerSerTPryrPhea 560
 Db 2207 ACTCGGATATCTGGCCCCCAACCTCTAACCCTTCCCTGACAGAGCTGGTATTTTG 2266
 QY 560 laThrGluSerSerHISpheTySerAlaSerAlaIleTyryGlyYleSerAlaSerTyS 580
 Db 2267 CCAACAAGTCTCACTCTACTCTGCTCAGCCATCTTAACAGAGCGATGCCAGTTACT 2326
 QY 580 ezAlaTySerCySerSerGluLeuProThnCyGlyAspGlnValTySerValArgArg 600
 Db 2327 CTGCCCTACAGCTGACGCCAGCTGCCACTTGGGAGACCAAGTCAATCTCTGGCAGGC 2386
 QY 600 rGlnLybProSerAspArgAlaAspSerArgArgSerTPHISGluGluSerProPheG 620
 Db 2387 GGCAGAGCCAAAGTACAGAGCTGACTCGCGCGAGCTGGCAAGAAAGAGCCCTTTG 2446
 QY 620 llyLeuGluPheLyArgArgSerCyngInMetGluPheGlyGluSerIleMetSerGlu 640
 Db 2447 AAAAGCACTTTAAAGCAAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGCAAGA 2506
 QY 640 snArgSerArgGluGluLeuGlyLyValGlySerGlnSerSerPheSerGlySerMetG 660

Db 2507 ACAAGTACAGGAAAGAGCTGGGAGAGGAGGAGTCAAGTCACTTTTGGGACAGATCG 2566
 QY 660 lulleleGluValSer 665
 Db 2567 AAATCATTTGAGGTCTCC 2583
 RESULT 26
 US-10-357-930-26912
 ; Sequence 26912, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; PRIOR FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26912
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-26912
 Alignment Scores:
 Pred. No.: 0
 Score: 472.00
 Percent Similarity: 99.40%
 Best Local Similarity: 99.40%
 Query Match: 70.98%
 DB: 18
 Gaps: 0
 Length: 5145
 Matches: 663
 Conservative: 0
 Mismatches: 2
 Indels: 4
 Gaps: 0
 US-10-029-345A-109 (1-665) x US-10-357-930-26912 (1-5145)
 QY 1 metaLanISglumeIleGlyThnGlnIleValThnGluArgLeuValAlaLeuLeuGlu 20
 Db 589 ATGGCCCATGAGATGATTTGAACTCAATGTTTACTAGAGGTTGGCTGCTGCTGAA 648
 QY 21 SerGlyThnGluLyValLeuLeuIleAspSerArgProPheValGluTyraentThSer 40
 Db 649 AGTGAAAGGAAAAAGTCTGCTTAATGATAGCCGCGCATTTTGGAAATCAATACATCC 708
 QY 41 HIsIleuGluAlaIleAnIleAsnCySerLySleuMetLyAspArgLeuGlnGln 60
 Db 709 CACATTTTGAAGCATTAATCAACTGCTCAAGCTTATGAAGCAAGTTGCAAG 768
 QY 61 AspLyValLeuIleThnGluLeuIleGlnHISerAlaTybHISlyValAspIleAsp 80
 Db 769 GACAAAGTGAATTAATTAACAGAGCTCATCCAGCATTCAGCCAAACATTAAGGTGATGAT 828

/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ. ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 26923
/ LENGTH: 5145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1, 5144, 5145
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26923

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-26923 (1-5145)

QY 1 MetAlaHieGluMerIlegIyThrgInIleValThrgIuaGrLeuValAlaleuLeuGlu 20
DB 589 ATGGCCCATGAGATGATGATGGAATCAAAATGTTACTGAGAGCTTGCGCTGCTGGA 648
QY 21 SerGIyThrgIuLyEvAlleuLeuIleApsSerArgProPheValIGluYrAsnThrSer 40
DB 649 AGTGAACGGAABAAAGTCTGCTAATTAATGCGGCAATTTGGAAATCAATATCAATCC 708
QY 41 HseIleuGluAlaIleAsnIleAsnCySerIySeuWeIySaTgLeuGIn 60
DB 709 CACATTTGGAGCCATTAATATCACTGCTCAAGCTTATGAGCGAAGCTTGCAACG 768
QY 61 ApsIyValIleuIleThrgIuLeuIlegIhIseSerIalysHsIlyValAapIleAp 80
DB 769 GACAAAGGTTAATTAACAGAGCTCAATCAAGATTCAGCGAAACATTAAGTTGACATGAT 828
QY 81 CySerGIuLyValIleValIyAspGIuSerSerGIuAspValAlaserIeSer 100
DB 829 TGCAGTCAAGAGTGTGCTGATGTTACGATCAAAAGCTCCCAAGATGTTCCCTCTCTTCA 888
QY 101 ApsCyPheLeuThrValIleuLeuGIyVleuGIuLySerPheAsnSerValHsIleu 120
DB 889 GAGCTTTCTCACTGACTTCTGGGTAACGGAAGAGAGCTTCAACTGTTCACCTG 948
QY 121 LeuAlaGIyGIyPheAlaGIuPheSerArgCyPheProGIyLeuCySeGIuGIyIySer 140
DB 949 CTGCGAGTGGGTGTGCTGAGTCTCTCGTGTGTTCCCTGAGCTCTGTGAGGAAATCC 1008
QY 141 ThrIleuValProThrCySIIeSerGIuProCySleuProValAlaAsnIlegIyProThr 160
DB 1009 ACTCTAGTCCCTACCTGCAATTTCTTCAAGCTTCTTAACCTGTGCAAACTGGGCAACC 1068
QY 161 ArgIleuProAsnLeuThyIleuGIyCySIIuAspValIleuAsnIyGIuLeuIle 180
DB 1069 CGAATTCCTCCAAATCTTATCTTGCTGCGCCAGCAAGTCTCTCAAGAGAGACTGAT- 1127
QY 181 -GIuGIuAsnGIyIlegIyYrValIleuAsnAlaserIy- ThrCySProLyProAsp 200
DB 1128 GAGCGAATGGAGATGTTATGTTAAATGCCAGCA- TACCTGTCCAAAGCTGACT 1186
QY 200 HeIleProGIuSerHsIlePheLeuArgValProValAsnApsSerPhCySeGIuLyIle 220
DB 1187 TTATCCCGAGTCTCATTTCTCGCGCTGTGCTGTGAATGACAGCTTTTGGAGAAATTT 1246
QY 220 euProTIleuAspIySerValAapPheIlegIuLySaIyAlaSerAsnGIyCyAr 240
DB 1247 TGCCTGTGTGACAAATCAATGATTTCAATGGAAGCAAAAGCTCCAAATGAGATG 1306
QY 240 alIleuValHsIeCySeLeuAlaGIyIleSerArgSerAlaThrIleAlaIleAlaYrIleu 260

DB 1307 TTCTAGTCACTGTTAAGCTGGGATCTCCCGCTCCGCAACATCGCTACATCA 1366
QY 260 eCIySaRMeIaPMeSerIeAspGIuAlaIyThrAphValIySeGIuLySaGrProT 280
DB 1367 TGAAGAGATGACAGTCTCTTATGATGAAGCTTACGATTTGTGAAGAAAAAAGACCTTA 1426
QY 280 hrtIleSerProAsnPheAsnPheLeuGIyGInIleuAspTYrGIuLySlySIIeIySA 300
DB 1427 CTATATCTCAACTTCATTTTCTGGGCAACTCCTGCACTATGAGAAAGATTTAAGA 1486
QY 300 smGIuThrGIyAlaserGIyProLySerIyVleuLyLeuIleHsIleuGIuLyProA 320
DB 1487 ACCAGCTGAGACATCAAGGCCAAGAGCAACTCAAGCTGCTCACCCTGAGAGCA 1546
QY 320 smGIuProValProAlaValSerGIyGIyGInIySserGIuThrProIeSerPro 340
DB 1547 ATGAACCTGTCCCTGCTGTCTCAGAGGGTGAAGAAAGAGCAAGCCCTCAGTCCAC 1606
QY 340 roCyAlaApsSerAlaThrSerGIuAlaIlegIyGInAgrProValHsIleProAlaser 360
DB 1607 CCTGTGCCGACTGTCTACTCAAGAGCGAGCAAGCAAGCCCGTGCATCCGCGCAGCG 1666
QY 360 alProSerValProSerValGIuProSerIeLeuGIuAspSerProIeValGIuAla 380
DB 1667 TGCACAGCTGCCAGCGTGCAGCGCTGCTGTTAAGAGACACCCGCTGTGTACAGGCG 1726
QY 380 euSerGIyLeuHsIeSerAlaAspArgIeGIuAspSerAnIyVleuYrAspSer 400
DB 1727 TCAATGGGCTGACCTTATCCGACAGCGTGAAGAGCAATTAAGCTCAAGCTTCT 1786
QY 400 heSerIeAspIleIySerValSerTySerAlaserMeIalaserIeHsIlegIy 420
DB 1787 TCTCTGAGATATCAATCAATGATTCAATTCAGCCAGCATGGCAGATCTTACATGAGCT 1846
QY 420 heSerSerSerGIuAspAlaIleuGIuTyIyIyProSerThrThrIleuAspGIyThrA 440
DB 1847 TCTCTATCAAGAGAGCTTGTGAATTAATCAAACTTCACTGATGGAGCA 1906
QY 440 snIyIeCyGIuInPheSerProValGIuGIuIeSerGIuInThrProGIuThrSer 460
DB 1907 ACAAGTATGCCAGTCTCCCTGTTCAAGAACTATCGAGAGACTCCGAAACAGTCC 1966
QY 460 roAspIySeGIuGIuAlaserIleProLyVleuGIuThrAlaArgProSerApsSer 480
DB 1967 CTATTAAGAGAGAGCAACATCCCAAGAGCTGCAAGCCGCTTCAAGAGCC 2026
QY 480 InSerIyAspIleuHsIleSerValArgThrSerSerGIyThrAlaGIuAspSerIe 500
DB 2027 AGAGCAATGATTTGATTCGTCAGACACAGCAAGAGCAAGCCGCAAGGATCCCTTT 2086
QY 500 euSerProIeHsIleArgSerGIySerValGIuAspAsnTyHsIleThrSerPheLeu 520
DB 2087 TATCTCACTGTATGAAGTGGAGCGTGGAGCAATTAACCAACAGGCTCTTTTTCG 2146
QY 520 IyLeuSerThrSerGIuInHsIleuThrIySerAlaGIyLeuGIyLeuIySIIyTrp 540
DB 2147 GCCTTTCACAGCAAGAGACACTCAAGAGTGTGCTGAGCTTGAAGGCTGAGC 2206
QY 540 IaserAspIleuAlaProGIuInThrSerThrProSerIeLeuThrSerSerIyTrpPhe 560
DB 2207 ACTCGAATATTTGGCCCCCAGACCTTACCCCTTCCGACAGAGAGCTGATATTTCG 2266
QY 560 IATHGIuSerSerHsIlePheTySerAlaserAlaIleTyrGIyGIySerAlaserTyS 580
DB 2267 CCAGAGATCTTCACTTCTAATCTGCTTCAAGCAATTAAGAGGCAAGGCAAGTTACT 2326
QY 580 eraIaIyTySerCySerGIuLeuProThrCySIIyAspGIuValIyTySerValArgAr 600
DB 2327 CTGCTCAAGTGAAGCACTGCCCACTGGGAGAACCAAGCTATTTCTGTGCGAGGCG 2386
QY 600 rgGIuLyProSerAspArgAlaAspSerArgSerTrpHsIlegIuIySerProPheG 620

Db 1787 TCTCTGGAATCAATCAGTTTCATATTCAGCCAGACGACATCTTTCATGAGCT 1846
Qy heserSerSerGluAspAlaLeuGluTyrTyrProSerThrThrLeuAspGlyThra 440
Db TCTCTCATTCAGAAAGAGCTTTGGAAATACAAACCTTCACATCTCGAAGGGAACA 1906
Qy snlyLeuCySgInPheSerProValGlnGluLeuSerGlnGlnThrProGlnThrSerP 460
Db ACAAGCTATGCGCAGTTCTCCCTGTTTCAGAACTATTCGAGAGAGACTCCCGAAACAGTTC 1966
Qy roaApLySgInGluAlaSerLeuProLysLeuGlnThrAlaArgProSerAspSerG 480
Db CTGATTAAGAGAAAGCCAGATCCCGCAAGAGCTGACACCGCAGCTTCAGACAGCC 2026
Qy 480 InSerLySgArgLeuHisSerValArgThrSerSerSerLysThrAlaGlnAspSerLeu 500
Db AGAGCAAGCAGATTGCANTGCTGTCAGAACAGAGAGAGCTGACCGCCAGAGTCCCTTT 2086
Qy 500 euserProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520
Db TATCTCACTGCAATCCAGAGTGGAGCGTGGAGAGACATTACACACAGCTTCCTTTTCG 2146
Qy 520 LysSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrP 540
Db GCCTTTCACAGCCAGAGAGACCTGACAGAGTCTGCTGGCTTAAAGGCTGGC 2206
Qy 540 iserSerAspLeuAlaProGlnThrSerThrProSerLeuThrSerSerThrPhePheA 560
Db ACTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCTTCAACAGAGCTGGATTTTG 2266
Qy 560 laThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerLysSerTyrS 580
Db CCACAGAGTCCCTCACTTCTTCTGCTGACATCTACGAGAGGAGGAGGAGGAGTACT 2326
Qy 580 eHlaTyrSerCySgSerGlnLeuProThrCySgLyAspGlnValTyrSerValArgArgA 600
Db CTGCTCAAGCTGACGACGACGCTGCTCCACTTCGCGAGACCAAGTCTATTCGTTCGAGG 2386
Qy 600 TGGInLysProSerAspArgAlaAspSerArgAspSerTyrPheGlnGluSerProPheG 620
Db GGCAAGAGCCAGAGAGAGAGCTGACCTGCGGCGAGAGCTGGCATGAAAGAGAGCCCTTTG 2446
Qy 620 luluSgInPheLysArgArgSerCySgInMetGlnPheGlyGlnSerIleMetSerGlnVal 640
Db AAAAGCAGTTTAAACGACAGAGCTGCCAATGGAATTGGAGAGAGACATCATGTCAGAGA 2506
Qy 640 snArgSerArgGlnGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetG 660
Db AAGGTCAACGGAAGAGCTGGGAAAGTGGGAGTCACTAGCTTTTCGCGACAGCATGG 2566
Qy 660 lullellegluValSer 665
Db 2567 AAATCATGAGTCTCC 2583

RESULT 29
US-10-357-930-27149
; Sequence 27149, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: HUMAN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862

; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27149
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-27149

Alignment Scores:

Pred. No.:	0	Length:	5145
Score:	472.00	Matches:	663
Percent Similarity:	99.40%	Conservative:	0
Best Local Similarity:	99.40%	Mismatches:	2
Query Match:	70.98%	Indels:	4
DB:	18	Gaps:	0

US-10-029-345A-109 (1-665) x US-10-357-930-27149 (1-5145)

Qy 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuGln 20
Db 589 ATGGCCCATGAGATGATTGGAACTCAATTGTTACTGAGAGGTTGGCTGCTGGAGA 648
Qy 21 SerGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGlnTyrAsnThrSer 40
Db 649 AGTGGAGCGAAAGAGCTGCTTAATGATACCGGCACTTGTGGAAATACATATCATCC 708
Qy 41 HisIleLeuGlnAlaIleAsnIleAsnCySerLysSerLysMetLysArgArgLeuGln 60
Db 709 CACATTTTGGAGCCATTATATCACTGCTCCAGGCTTATGAGAGGAGTTGCACAG 768
Qy 61 AspLysValLeuIleThrGlnLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
Db 769 GACAAAGTATATACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 828
Qy 81 CySerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCAGTCAGAAAGTTGTGATTACATCAAGCTCCCAAGATGTGCTCTCTCTTCA 888
Qy 101 AspCyPheLeuThrValLeuLeuGlnLysLeuGlnLysSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTCTCATCTGATCTTCTGGTAACTGGAGAAAGAGCTTCACTGTTCACTG 948
Qy 121 LeuAlaGlyGlyPheAlaGluPheSerArgCyPheProGlyLeuCySgInGlyLysSer 140
Db 949 CTTCAGAGTGGTTTTCGAGTTCTCTGTTGTTTCTCTGCTGCTGTAAGAAATATCC 1008
Qy 141 ThrLeuValProThrCySgInSerGlnProCySgLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTGATGCTCTTACCTGATTCATCTTCAGCTTGCCTTACTGTTGCCAACAATGGGCCAAC 1068
Qy 161 ArgIleLeuProLeuLeuTyrLysGlyCySgInArgAspValLeuAsnLysGluLeuIle 180
Db 1069 CGAATTTCTCCCATCTTATATCTTGGCTGCAAGAGATGCTCTCAACAAGAGCTGAT- 1127
Qy 181 -GlnGlnAsnGlyTyrIleGlyTyrValLeuAsnAlaSerTyr-ThrCySgProLysProAsp 200
Db 1128 GCACAGAAATGGAGTGGTATGTGTTAATGCACAA-TACGTCTCAAGAGCTGACT 1186
Qy 200 helLeProGlnSerHisPheLeuArgValProValAsnAspSerPheCySgInLysIle 220

Db	1187	TTATCCCGGAGCTCATTTCTCGGCTGAGCTGGAATGACAGCTTTTGAGAAAATT	1246
Qy	220	euprOTfPLeuAapLySeRvAlaApheIlleGluVAlaLyuAlaSeRAnGlyCyv	240
Db	1247	TGCGGTGGTTGGACAAATCAAGTAGATTTCATTGAGAAAGCAAAAGCCCTCAATGAGATGTG	1306
Qy	240	allLeuValHlCyAeuuAlaGlyLlSeRvAgSeRvAlaThThlAlaAlleAlTyrllem	260
Db	1307	TTCTHGTCACTGTTTAACTGGGATCTCCGGTCCGACCAATGGCTATGGCTTACATCA	1366
Qy	260	eLyvArGMeLApMeSeRleuApGluAlaTyArzArPheValLyvGluLyvArGProT	280
Db	1367	TGAAGAGATGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAGAAAGACTTA	1426
Qy	280	hrLlSeRvProApNpheAnPheleuGlyLInLeuLeuApTyGluLyvAllyeLya	300
Db	1427	CTAATATCTCCAAACTTCATATTTCGTGGCGCAACTCTTGAGCTTAGAGAAAGAAATTAGA	1486
Qy	300	engInThGjAlaSeRglYProLyvSeRvlyeLyuVleuLyuLeuHlSteuLyuLyvProA	320
Db	1487	ACCGAGCTGGAGCATTCAAGGCGCAAAAGACAAATCAAGCTGTGACTTGAGAAAGCCAA	1546
Qy	320	engLyuProValProAlaValSeRgluglyGlyLInLyvSeRglThThrProLeuSeRProp	340
Db	1547	ATGAACCTGTCCCTCTCTCTCTCAAGGTTGACAGAAAGGAGAAAGCCGCTTCAGTCCAC	1606
Qy	340	roCyAlaApSeRvAlaThSeRgluaAlaGlyLInArGProValHlApProAlaSeRv	360
Db	1607	CCTGGCGGCACTGTCTACTCAAGAGGACAGAGGACAAAGCCGCTGATCCCGCCAGCG	1666
Qy	360	alProSeRvAlProSeRvAlGlnProSeRleuLeuGluApSeRvProLeuValGlnAlaL	380
Db	1667	TGCCACGGGTGCCACGCGTGACCGCTGTGTATGAGAGACGCGCTGTGTACAGCGGC	1726
Qy	380	eusSeRglYleuHlSteuSeRvAlaApAryLeuGluApSeRvAluLyvleuLyvArGSeRv	400
Db	1727	TCAGTGGGCTGACCTGTCTCCGACAGAGGCTGGAGAGACAAATAGCTTAAGGCTTCTT	1786
Qy	400	heSeRleuApTyLeLyvSeRvAlSeTyRSeRvAlaSeRMeLAlaSeRleuHlAglyP	420
Db	1787	TCTGCTCGATATCAATCAATCAAGTTCAATTCAGCGACAGATGGAGCATCTTACATGGCT	1846
Qy	420	heSeRSeRSeRgluApAlaLeuGluTyTyLyvProSeRThThrleuApGlyThra	440
Db	1847	TCTCTCATCAAGAGATCCTTGGAAATCTCAAAACCTTCCATCACTCTGATGGAGCA	1906
Qy	440	enLyvleuCyGlnPheSeRProValGlnLyvSeRgluGlnThThrProLyuThSeRv	460
Db	1907	ACAAGCTATVGCAGATTCTCCCTCTTCCAGAACTATCGAGACAACTCCGAAACCAAGTC	1966
Qy	460	roApLyvGluGluAlaSeRlleProLyvLyvleuGlnThAlaArGProSeRvArGSeRv	480
Db	1967	CTGATTAAGAGAGAACCAAGCATCCCAAGAAAGCTGACAGCCGACGGCTTCAACACACC	2026
Qy	480	InSeRlyvArGleuHlSeRvAlaArgThSeRSeRSeRglYThAlaGlnArGSeRleuL	500
Db	2027	AGAGCAACGATTGCATTCGGTTCAGAAACCAACAGACAGTGCACCGCCACAGATGCCCTTT	2086
Qy	500	eusSeRProLeuHlArGSeRglYSeRvAlGluApArAlTyHlStHSeRvheLeuPheG	520
Db	2087	TATCTCCACTCATCGAAGTGGAGCGTGGAGGACAAATTTACCAACCAAGCTTCCTTTTTCG	2146
Qy	520	lyLeuSeRThSeRglngInHlSteuThLyvSeRvAlaGlyLeuGlyLeuLyvGlyTrpH	540
Db	2147	GCGTTTCCACCAAGCAAGACACCTCAAGAAATGTCTGTGGCTTGGGCTTAAAGGGCTGGC	2206
Qy	540	lAsSeRvAlleuAlaProGlnThSeRThThrProSeRleuThSeRSeRTrpTyRPha	560
Db	2207	ACTCGGATATCTTGGCCCCCAGACACTTACCCCTTCCCTGACACAGCAGCTGATATTGG	2266
Qy	560	laThGluSeRSeRtlApheTySeRvAlaSeRvAlaAlleTyGlyGlySeRvAlaSeRvTyS	580
Db	2267	CCACAGATCTCCACACTTCTAATCTGTGCTTAGCCATTTAGGAGGACAGTCCAGTTACT	2326

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OY      580  exlaIYrSrCYseSrGlnLePrOThCYeGIyApGlnValYrSrVaLArGaRGA 60
Db      2327  CTGCTACACCTCAGCAGCTCCCACTTGCAGACCAAGCTTATCTTGCGCAGGC 23
OY      600  rGlnYrPSeSrAsPaRgAlAAsPSeArGhYrSeTrPhIaGInGInSePrPheG 62
Db      2387  GGCAAGACCAAGTGAACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGCCCTTGG 24
OY      620  lYlYsGlnPheLYbAghYrSeCYeGImeGlnPheGlyGInSeRlIeMeSeRGlAa 64
Db      2447  AAAAGCGITTTAAACGACAGAGCTGCCCAATGGAATTTGAGAGACATCATGTGAGA 25
OY      640  snArSeArGhGInGInLeuGlyLYeValGlySeRInSeSrPheSeRGIySeMeRG 66
Db      2507  ACAGGTACGGAGAAAGACTGGGGAAAGTGGGCACTGACGTACGTCTTTTCGGGCGATGG 25
OY      660  lYlLeIleGlnValSeR 66S
Db      2567  AAATCATTTGAGGTCTCC 2583

RESULT 30
US-10-357-930-28675
; Sequence 28675, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY O
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28675
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28675

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-28675 (1-5145)
OY      1  MetAlAhIeGInuMeTlIeGlyThrGlnIleValThGlnAArgLeuValAlaLeuLeuGlu 20

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Db	589	ATGCCCCATGATGATGATGGAATCTCAAAATTTGTAAGAGAGTTGGTGGCTCTGCTGGAA	648
Qy	21	SeG1YThrG1uLySeVal1LeuLeu1LeaSerArygProPheValG1uTyraEnThSer	40
Db	649	AGTGAACCGGAAAAAAGTGTCTGCTTAATTAATGACCGGCAATTTGGAAATCAATACATCC	708
Qy	41	His1LeuGluL1a1LeaEn1LeaenCySer1yS1eUeC1ySArG1eUeG1n	60
Db	709	CACATTTTGAAAGCCAAATTAAATCAACGCTCCAAAGCTTAAGAAGCAAGTTGGCAACG	768
Qy	61	AspLySeVal1Leu1LeThrG1uLeu1LeG1nH1SeSer1aLySH1S1yVa1aP11LeaP	80
Db	769	GACAAAGTGTATATACAGAGCTCATCCAGATTCACGAAACATYAAAGTTGACATTTGAT	828
Qy	81	CysSerG1nLySeVal1Val1TyraPgl1nSeSerG1nAspVal1aSe1LeuSeSer	100
Db	829	TCCAGTCCAGAGGTGTGTATGATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA	888
Qy	101	AspCySphLeuThrVal1LeuLeuG1Y1yLeuG1uLySeSerPheAsnSerValH1S1eu	120
Db	889	GACTGTTTCTCATCTGATCTTCTGGTAACTGGAGAAGACTTCAACTCTTCACTG	948
Qy	121	Leu1aG1yG1yPhe1aG1uPheSeSerAryCySphProG1Y1eUcYSeG1uG1ySeSer	140
Db	949	CTTGCAAGGTGGTGTGGCTGAGTCTCTCGTTGTTCCGTGGCCTCTGTGAAGAAATCC	1008
Qy	141	ThrLeuValProThrCyS1eSeSerG1nProCySeLeuProVal1aAsn1LeG1yProThr	160
Db	1009	ACTCAAGTCCCTACTGCTCATTTCTCAAGCTCTGTTACCTGTGGCCAAATTTGGGCAAC	1068
Qy	161	Arg1LeuProAsnLeuTyLeuG1Y1yG1nArGAspVal1LeuAsnLyG1uLeu1Le	180
Db	1069	CGAATCTTCCCAATCTTAATCTTGTGGCTCCAGCAGAGATGCTCTCAACAGACTCAT	1127
Qy	181	-G1nG1nAsnG1Y1eG1YTyraVal1LeuAsn1aSeSerYr-ThrCySProLySProAsp	200
Db	1128	GCAGCAGAAATGGGATTTGGTTATGTGTAAATGCCAGCAA-TACCTGTCCAAAGCTTACT	1186
Qy	200	he1LeProG1uSeTh1sPheLeuArGValProValaAsnAspSerPheCyG1uLyS1Le	220
Db	1187	TTATCCCAAGTCTCAATTTCTCGCGTGGCTGTGAATGACAGCTTTTGTGAAGAAATTT	1246
Qy	220	eubPro1rPheLeuAspLySeSerValaAspPhe1LeG1uLySa1aLySa1aSeSaSnG1Cyav	240
Db	1247	TGCGCGTGTGGCAAAATCAGTAAATTCATTGGAAGAAAGCCCTCCAAATGGATGTCG	1306
Qy	240	allLeuValH1eCyS1eUe1aG1Y1eSeSaRySeSer1aThr1Lea1Lea1aTy1Lea	260
Db	1307	TTCTATGTGACGTGTATGCTGGATCTCCGCTCCGCCCAACATCGCATGCTTACATCA	1366
Qy	260	eLySaRySeSerPheSeSer1eUeAspG1u1aTyraGPhSeVal1yG1uLySaRyProT	280
Db	1367	TGAAGAGGATGACATGTCTTAATGAAGCTTACAAATTTGGAAAGAAAAAGCCTTA	1426
Qy	280	he1LeSeProAsnPhAsnPhLeuG1yG1nLeuLeuAspTyrg1uLySa1yS1eLySa	300
Db	1427	CTAATCTCCAAACTCAATTTCTGGGCCAACCTCGACATATGGAAGAAAGATTAAAG	1486
Qy	300	snG1nThG1Y1aSeG1YProLySeSer1ySe1eUe1yS1eUeG1uLySProa	320
Db	1487	ACCAGACTGAGCATCAGGCGCCAAAGGCAAACCTCAAGCTGCTGCACTGGAGAAAGCCAA	1546
Qy	320	snG1uProValPro1aValaSeG1uG1YG1uLySeSerG1uThrProLeuSeSerProp	340
Db	1547	ATGAACCTGTCCCTGCTGCTCAGAGAGGTGACAGAAAAGCCAGAGCGCCCTCAGTCAAC	1606
Qy	340	roCySa1aAspSer1aThrSeSerGlu1a1aG1YG1nArGProValH1sPro1aSeerv	360
Db	1607	CTGTGTCCGACTGTCTACTCAGAGAGCGACAGAAAGGCGCGTGTGATCCCGCCAGCG	1666
Qy	360	alProSeSerValProSeSerValG1nProSeSer1eUeG1uAspSeSerProLeuValG1n1aL	380
Db	1667	TGCCACGCGTCCACAGCTGACGCGCTGTGTAGAGACAGCGCCGTGTGTACAGCGC	1726

QY	380	eUsErg1YLeuH1sLeuSer1aAePaTgLeuG1uAaPSeRaSmLyLeuLyvAArgSeR	400
Db	1727	TCAGTGGGCTGCACCTGTCCGACAGACGCTGGAAAGACAGAAATACCTCAAGCGTCTC	178
QY	400	hSeSer1euaAp11eYSeSeRValSeRyTSer1aSeRMeR1a1aSeR1euh1sg1Yp	420
Db	1787	TCTCTCTGATATTCAAATCAAGATTCAATATTCAGCACACATCGGACAGATCTCTCATATGCT	184
QY	420	hSeSeSeSeSeR1uAaP1aLeuG1uY1Y1Y1YpSeSeRThRThR1euaApG1YThR	440
Db	1847	TCTCTCTCATGAAAGATGCTTGGAAATCAACAACTTCCACTACTCTGGATGGAGCA	190
QY	440	enLyLeuCYG6InPhSeSeRProT1G1nG1uLeuSeRg1uG1nThRProG1uThRSeR	460
Db	1907	ACAAGCTATGCCAGATGTCTCCCTGGTTCAGGAATCATCGAGGACAGATCTCCGAAACAGTC	196
QY	460	roApLyvG1uG1uA1SeR1eProLyvLeuG1nThR1aApGProSeRaPSeRg	480
Db	1967	CTGTAAAGAGAGAAAGCCAGCATCCCAAGAGCTGCAGACCGCGAGCCTTCAAGACAGC	202
QY	480	1nSeR1ySAg1euh1aSeSeRValArgThSeSeSeRg1YThR1aG1nA1gSeR1eU	500
Db	2027	AGACAAAGCATTTGCATTCGGTTCAGAACACAGACAGCATGTGGACCGCCAGAGTCCCTT	208
QY	500	eUsESeRProLeuH1aASeSeRg1YSeSeR1eV1G1uAaPAnTh1ePhSeRheLeuPheG	520
Db	2087	TATCTCACTGCATTCAGATGGAGAGGTGTGAAGACAAATTCACACCAAGCTTCTTTTCG	214
QY	520	1Y1eUsEaThRSeSeRg1nG1nH1sLeuThR1YSeSeR1aG1YLeuG1YLeuYsg1YThR	540
Db	2147	GCCCTTCCACCAAGCCAGACACCTTCAGAGTCTGCGCTGGGCTTAAAGGCTTGGC	220
QY	540	1aSeSeRaP1eLeuA1aProG1nThRSeRThRProSeSeRLeuThRSeSeRThRThRPha	560
Db	2207	ACTCGGATATCTTTGGCCCCCAAGACTTCACTTCCCTTCCATCACCAAGACGCTGATATTTG	226
QY	560	1aThnG1uSeSeRTh1sPhEYSeR1aSeR1a1eY1YG1YG1YSeR1aSeRThRS	580
Db	2267	CCACAGAGCTTCACACCTTCACTGCTCAGCACATCTACGGAGGAGAGTCCAGTTACT	232
QY	580	eR1a1YSeSeCYSeSeRg1nLeuProThRProYsg1YaaP1nVal1YSeSeRValArgA	600
Db	2327	CTGCCACAGCTGCAGACCGACCTGCCACTTGGGAGACCAAGCTTATCTGTCCGACAGC	238
QY	600	rg1nLyvProSeRaSPaRg1aAaPSeRa1rgASeSeRTPh1sG1uG1uSeRProPhG	620
Db	2387	GGCACAAACCAAGTACAGAGCTGACTCGCGCGCGAGCTGCATGAAGAGAGCCCTTTG	244
QY	620	1uLyvG1nPhE1YARgARgSeSeCYG1nMeRg1uPhEg1Yg1uSeR11eWetSeRg1uA	640
Db	2447	AAAAGCATTTAAACGACAAAGCTGCGCAAAATTTGAGAGAGCAATCATGTCAGAGA	250
QY	640	enA1gSeRaRg1uG1uLeuG1Y1YvA1G1YSeRg1nSeSeRPhSeSeRg1YSeRMeRg	660
Db	2507	ACAGGTACCGGAGAGAGCTGGGAAAGTGGGACAGTCAgTCAgCTTTTCGGGACAGATGG	256
QY	660	1u1e1e1eG1uV1a1SeR	665
Db	2567	AAATCATTTAGAGTCTCC	2583
RESULT 31			
US-10-072-012-255			
; Sequence 255, Application US/10072012			
; Publication No. US20040033493A1			
; GENERAL INFORMATION:			
; APPLICANT: Tcherev, Velizar			
; APPLICANT: Spytek, Kimberly			
; APPLICANT: Zernusen, Bryan			
; APPLICANT: Patuturajan, Meera			
; APPLICANT: Shimkets, Richard			
; APPLICANT: Li, Li			
; APPLICANT: Gannoli, Esha			


```

Db      1133  --CC-AGCGTACCCAGCGTGACGCCGCTGTTAGAGCAGACCCGCTGTACAGGCCG 1189
Qy      380  euSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerArgLeuValLeuValArgSerP 400
Db      1190  TCAGTGGCGTGCACCTGTCGGCAGACAGGTGGAAAGCAGCAATTAAGCTCAAGCGTTCTCC 1249
Qy      400  heSerLeuAspIleValSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyP 420
Db      1250  TCTCTGTGATATCAATCAAGTTTCAATTACAGCCAGCATGCGACATCTTACATGCT 1309
Qy      420  heSerSerSerGluAspAlaLeuGluTyrTyrIleAspProSerThrThrLeuAspGlyThra 440
Db      1310  TCTCTCATCAGAAAGATGCTTGGAAATCAACAACCTTCACTACCTGATGAGGAGCA 1369
Qy      440  enuValLeuCyArgInpHeSerProValGlnGluLeuSerGluGlnThrProGlnThrSerP 460
Db      1370  ACAAGCTATGCGAGTCTCCCTCCCTGTTCAAGAACTATCGAGCACTCCCGAAACCAAGTC 1429
Qy      460  roAspArgGluGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSerG 480
Db      1430  CTGATTAAGAGAAAGCCAGCATCTCCAGAAAGCTGACAGCCAGGCTTCCAGACAGCC 1489
Qy      480  InSerValArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db      1490  AGAGCAAGCGATGATGATTCGGTCAAGAACAGCAGCAGATGGCAGCCGACAGAGGTCCTTT 1549
Qy      500  euSerProLeuHisAspSerGlySerValGluAspAspThrThrSerPheLeuPheG 520
Db      1550  TATCTCCTACCTGCACTCAAGAGGGAGCGTGGAGACAAATTAACAACAGCTTCTCTTTGG 1609
Qy      520  1LeuSerThrSerGlnGlnHisLeuThrIleValSerAlaGlyLeuGlyLeuValTyrP 540
Db      1610  GCTTTTCCACCAAGCCAGCAGCAGCTCAAGAGTCTGCTGGCTGGCTTTAAGGCGTGGC 1669
Qy      540  1AspArgIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheA 560
Db      1670  ACTCGGATATCTTGGCCCCCAGACCTCACTACCTCCCTGACAGCAGAGTGGTATTTTGG 1729
Qy      560  1AthrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrS 580
Db      1730  CCACAAAGTCTTCACTACTCTGCTGCTCAGCCATCAAGGAGCAGAGCCAGCTTACT 1789
Qy      580  erAlaTyrSerCySerGlnLeuProThrCyArgIleAspGlnValTyrSerValArgArgA 600
Db      1790  CTGCCCTACAGCTGACAGCAGCTGCCCACTTGGGAAACCAAGCTCATCTCTGTCGAGGC 1849
Qy      600  rGlnIleAspProSerAspArgAlaAspSerArgArgSerTyrPheIleGluSerProPheG 620
Db      1850  GCGAAGAGCGCAAGTGAAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGCCCTTTG 1909
Qy      620  1uValGlnPheValArgArgSerCyArgInMetGluPheGlyGluSerIleMetSerGluA 640
Db      1910  AAAAGAGATTAAACCCAGAGCTGCCAATGGAATTTGGAGAGACATCATGTACAGAA 1969
Qy      640  snArgSerArgGluGluLeuGlyValValGlySerGlnSerSerPheSerGlySerMetG 660
Db      1970  ACGAGTCACGGGAAGAGCTGGGGAAAGTGGGCACTGATGCTTTCGGGAGCATGG 2029
Qy      660  1uIleIleGluValSer 665
Db      2030  AAATCATTTGAGCTCTCC 2046

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RESULT 33

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US-10-108-260A-2429
; Sequence 2429, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458

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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2429
; LENGTH: 1916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2429

Alignment Scores:
pred. No.:      2 866-168      Length:      1916
Score:          178.00      Matches:      278
Percent Similarity: 99.29%      Conservative: 0
Beet Local Similarity: 99.29%      Mismatches: 1
Query Match:      26.77%      Indels:      2
DB:              17          Gaps:      0

US-10-029-345A-109 (1-665) x US-10-108-260A-2429 (1-1916)

Qy      387  AlaAspArgLeuGluAspSerAnuValLeuValArgSerPheSerLeuAspIleValSer 406
Db      142  GCAAGAGGCTGGAGAGACAGCATTAAGCTCAAGCGTTCTTCTCTGTGATATCAATCA 201
Qy      407  ValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAla 426
Db      202  GTTTCATATTCAAGCCAGCATGCGAGCATCTTACATGCGCTTCTCATCAGAAAGATGCT 261
Qy      427  LeuGluTyrTyrIleValProSerThrThrLeuAspGlyThraAnuValLeuCyArgInpHeSer 446
Db      262  TTGGAAATTAACAACCTTCACTACTGTGAAGGAGCAACAAGCTATGCCAGTCTCC 321
Qy      447  ProValGlnGluLeuSerGluGlnThrProGlnThrSerProAspIleValGluAlaSer 466
Db      322  CCTGTTCAAGGAATATCCGAGCAGACTCCGAAACAGTCTGATTAAGAGAGAGCCAGC 381
Qy      467  1LeuProValLeuGlnThrAlaArgProSerAspSerGlnSerValArgLeuHisSer 486
Db      382  ATCCCAAGAAAGCTGAGACCCGCGCTTCAAGCAGCAGCAAGCAGATTCGATTCG 441
Qy      487  ValArgThrSerSerSerGlyThrAlaArgProSerAspSerLeuSerProLeuHisAspSer 506
Db      442  GTTCAGAAACAGAGCAGGTGGACCCGCGAGAGTCTTTATCTCAGCTGACATCGAAGT 501
Qy      507  GlySerValGluAspAspThrThrIleThrSerPheLeuPheGlyLeuSerThr-SerGlnG 526
Db      502  GGGAGCGTGGAGAGCAATTAACAACAGCTTCTTTGGCTTTCAT-CAGCCAGCA 560
Qy      526  nHisLeuThrIleValSerAlaGlyLeuGlyLeuValTyrPheIleAspIleLeuAlaP 546
Db      561  GCACTCAAGAGTCTGCTGGCTGGCTTAAAGGCTGGCACTCGAATATCTTGGCCCC 620
Qy      546  OGlnThrSerThrProSerLeuThrSerSerTyrPheAlaThrGluSerSerIleP 566
Db      621  CCAGAGCTCTTACCTTCCCTTCAAGCAGCGTGGATTTTGGCACAGAGTCTCAACAT 680
Qy      566  eTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSerAlaTyrSerCySerG 586
Db      681  CTACTCTGCTCAGGCATTTACGAGGAGCTGCACTTACTGCTTACAGCTGAGCCA 740
Qy      586  nLeuProThrCyArgIleAspGlnValTyrSerValArgArgArgGlnLeuProSerAsp 606
Db      741  GCTGCCCACTTGCAGGAGCAAGTCTATCTGTGCGCAGGCGGAGAAACCAAGTGAAG 800
Qy      606  gAlaAspSerArgArgSerTyrPheIleGluGluSerProPheGlyValArgArg 626
Db      801  ACTCACTGCGCGGAGCTGGCATGAAGAGAGCCCTTTGAAAGAGCAATTAACAGCAG 860
Qy      626  gSerCyArgInMetGluPheGlyGluSerIleMetSerGluAsnArgSerArgGluGlu 646
Db      861  AAGCTGCCAAATGGAATTTGAGAGAGCATCATGTCAGAGAACAGTCCGGAAGAGCT 920
Qy      646  uGlyValValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 665
Db      921  GGGGAAAGGCGCAGTCACTGCTTTCGGGAGCAGATGAATCATTTGAGGTCTCC 978

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RESULT 34

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US-10-357-930-10717/c
/ Sequence 10717, Application US/10357930
/ Publication No. US20040259086A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Endege, Wilson
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ FILE REFERENCE: MRL-007B/CN
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10717
/ LENGTH: 425
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-357-930-10717

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Alignment Scores:	
Pred. No.:	1,188-128
Score:	138.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	20.75%
DB:	18
	Gaps:
	0

US-10-029-345A-109 (1-665) × US-10-357-930-10717 (1-425)

QY	240	ValLeuValIhIscYsLeuValagIyIleSerArxSerAlaThrIleAlaAlaTyrlle	250
Db	423	GIITCAAGGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACATGCGTATGCGCTTACATC	364
QY	260	MelTybATgMTaSPMeTSerLeuAapGluAlaTyTArgPhaVallyGluValArgPro	279
Db	363	ATGAAAGAGATGACATGCTCTTTAGATGAAGCTTACAGATTGTGTAAAGAAAAAAGACT	304
QY	280	ThrlleSerProAenPhaenPhelenuGIyInLeuLeuApyTyGluTybIleTyb	299
Db	303	ACTATATCTCCAAACTTCATTTTCTGGGCCAACTCTGGACTATGAGAAAGAAATTAAAG	244
QY	300	AsnGlnhncIyIlaSerGIyPpolybSerTybLeuTybLeuLeuHslLeuGIuTybPro	319
Db	243	AACCAAGACTGAGCATCTAGGGCCMAAGAACCAACTCAAGCTGTCGACCTGGAGAAAGCCA	184
QY	320	AsnGIuProValProAlaValSerGIuGIyGIuTybSerGIuThrrProLeuSerPro	339
Db	183	AATGAACCTGTCCCTGCTGTCTTCAGAGGTGGACAGAAAGCGAGAGCGCCCTCAATGTCA	124
QY	340	ProCYAlaAspSerAlaThrsSerGIuAlaAlaGIyInArgProValIhIsProAlaSer	359
Db	123	CCCTGGCCGCACTGTGCTACCTCAAGGCAACAGACAAAGAGCCCGTGACATCCCGGACAC	64
QY	360	ValIProSerValIProSerValGIInProSerLeuenuGIuAspProLeuValI	377
Db	63	GTGCCACAGGTGCCAGCGTGCAGCCGTGCTGTTTAAAGACAGCCCGCTGGTGA	10

RESULT 35
US-10-357

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US-10-357-930-31909/c
Sequence 31909, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-00780N
CURRENT APPLICATION NUMBER: US/10/357,930
PENDING FILING DATE: 2003-02-04
PRIORITY APPLICATION NUMBER: 09/785,276
PRIORITY FILING DATE: 2003-02-16
PRIORITY APPLICATION NUMBER: 60/183,319
PRIORITY FILING DATE: 2000-02-17
PRIORITY APPLICATION NUMBER: 60/189,862
PRIORITY FILING DATE: 2000-03-16
PRIORITY APPLICATION NUMBER: 60/207,454
PRIORITY FILING DATE: 2000-05-25
PRIORITY APPLICATION NUMBER: 60/211,314
PRIORITY FILING DATE: 2000-06-09
PRIORITY APPLICATION NUMBER: 60/219,007
PRIORITY FILING DATE: 2000-07-18
PRIORITY APPLICATION NUMBER: 60/255,281
PRIORITY FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31909
LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-31909

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Alignment Scores:	
Pred. NO.:	1.3e-127
Score:	137.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	20.60%
DB:	18
Length:	44
Matches:	1
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-029-345A-109 (1-665) x US-10-357-930-31909 (1-467)

QY	241	LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet	266
Db	465	CTAGTGCACCTGTTTACTGGAGATCTCCGCTCCGACACATCGCTATCGCTACATCATG	406
QY	261	LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr	288
Db	405	AAGAGATGGACATGCTCTTAGATAGACTTCACATTTTGGAAGAAAAAGCCTCACT	346
QY	281	IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLeuAsn	300
Db	345	ATATCTCCAACTTCATATTTCTGGGCCCACTCCCTGAGCTATGGAAGAAAGATTAGAAC	286
QY	301	GlnThrGluValSerGlyProLysSerLysLeuLysLeuGlnLysGluLysProAsn	320
Db	285	CAGACTGGAGCATCGGGCCAAAGGCMAACTCAAGCTGCTGCACCTGGAGAAGCCAAAT	226
QY	321	GlnProValProAlaValSerGluGlyGlnLysSerGlnThrProLeuSerProPro	340
Db	225	GAACCTGTCCTCGCTGCTTCAGAGGGTGGACAGAAAAGCAGAGCGCCCTCACTCCACCC	166
QY	341	CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal	360
Db	165	TGTGGCGACTCTGCTACCTCAGAGGACGAGACAAAGGCCCTGCAATCCCGCCAAAGCTG	106
QY	361	ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuVal	377

DB 105 CCCAGGTCGCCAGCGTGACGCGCTGTTAGAGAGACAGCCGCGTGGTA 55
 RESULT 36
 US-10-357-930-40868/c
 ; Sequence 40868, Application US/10357930
 ; Publication No. US20040259086A1
 GENERAL INFORMATION:
 APPLICANT: Schlegel, Robert
 APPLICANT: Endege, Wilson
 APPLICANT: Monahan, John
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 TITLE OF INVENTION: HUMAN PROSTATE CANCER
 FILE REFERENCE: MRI-007BCN
 CURRENT APPLICATION NUMBER: US/10/357, 930
 CURRENT FILING DATE: 2003-02-04
 PRIOR APPLICATION NUMBER: 09/785, 276
 PRIOR FILING DATE: 2003-02-16
 PRIOR APPLICATION NUMBER: 60/183, 319
 PRIOR FILING DATE: 2000-02-17
 PRIOR APPLICATION NUMBER: 60/189, 862
 PRIOR FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/207, 454
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/211, 314
 PRIOR FILING DATE: 2000-06-09
 PRIOR APPLICATION NUMBER: 60/219, 007
 PRIOR FILING DATE: 2000-07-18
 PRIOR APPLICATION NUMBER: 60/255, 281
 PRIOR FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 62232
 SOFTWARE: FASTSeq for Windows Version 4.0
 SEQ ID NO 40868
 LENGTH: 467
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-357-930-40868
 Alignment Scores:
 Pred. No.: 1.3e-127 Length: 467
 Score: 137.00 Matches: 137
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 20.60% Indels: 0
 DB: 18 Gaps: 0
 US-10-029-345A-109 (1-665) x US-10-357-930-40868 (1-467)
 QY 241 LeuValIhIsCyLeuValaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrlleMet 260
 DB 465 CTAGTGCACTGTTTGGCTGGAGTCTCCCGCTCCGACCACTCGCTATCGCTCATCATG 406
 QY 261 LysAsgMetAsgMetSerLeuaspGuaIaTyArgPhaValyGluYasArgProThr 280
 DB 405 AAGAGAGATGAGACATGCTTTAGTGAAGCTTACAGATTGTGAAAGAAAAGAACCTACT 346
 QY 281 ILeSerProAsnPhaAsnPhaLeuGlyGlnLeuLeuAspTyrgIuIySylIeYAsn 300
 DB 345 ATATCTCCAACTCAATTTTCTGCGCCAACTCTTGACATGAGAAAGATTAAAGAAC 286
 QY 301 GlnThrGlyAlaSerGlyProlySerlybLeuLybLeuLeuHlIeugIuLybProAsn 320
 DB 285 CAGACTGAGGCAATCGGGCCAAAGACAACTCAACTCTGCACTCGAGGAAAGCCAAAT 226
 QY 321 GluProValProAlaValSerGluGlyGlnIySerGluThrProLeuSerProPro 340
 DB 225 GAACCTGTCCCTGCTGTCTCAAGGGGTGGACGAAAAAGGAGCGCCCTCACTCAACC 166
 QY 341 CysAlaAspSerAlaThrSerGluIaIaIaGlyGlnArgProValhIspProAlaSerVal 360
 DB 165 TGTGGCGACTCTGCTACCTCAAGAGGACAGACAAAGGCCCTGTGATCCCGCACCGTG 106
 QY 361 ProSerValProSerValGlnProSerLeuLeuIaAspSerProLeuVal 377

Db	105	CCGACGTCGCCAGCGTCGACGCGCTGCTTTAGAGACAGCCCCGCTGTA	55
		RESULT 37	
		US-10-357-930-41017/c	
		; Sequence 41017, Application US/10357930	
		; Publication No. US20040259086A1	
		GENERAL INFORMATION:	
		; APPLICANT: Schlegel, Robert	
		; APPLICANT: Endege, Wilson	
		; APPLICANT: Monahan, John	
		TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR	
		IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF	
		TITLE OF INVENTION: HUMAN PROSTATE CANCER	
		FILE REFERENCE: MRI-007BCN	
		CURRENT APPLICATION NUMBER: US/10/357,930	
		CURRENT FILING DATE: 2003-02-04	
		PRIOR APPLICATION NUMBER: 09/785,276	
		PRIOR FILING DATE: 2003-02-16	
		PRIOR APPLICATION NUMBER: 60/183,319	
		PRIOR FILING DATE: 2000-02-17	
		PRIOR APPLICATION NUMBER: 60/189,862	
		PRIOR FILING DATE: 2000-03-16	
		PRIOR APPLICATION NUMBER: 60/207,454	
		PRIOR FILING DATE: 2000-05-25	
		PRIOR APPLICATION NUMBER: 60/211,314	
		PRIOR FILING DATE: 2000-06-09	
		PRIOR APPLICATION NUMBER: 60/219,007	
		PRIOR FILING DATE: 2000-07-18	
		PRIOR APPLICATION NUMBER: 60/255,281	
		PRIOR FILING DATE: 2000-12-13	
		NUMBER OF SEQ ID NOS: 62232	
		SOFTWARE: FastSeq for Windows Version 4.0	
		SEQ ID NO 41017	
		LENGTH: 467	
		TYPE: DNA	
		ORGANISM: Homo sapiens	
		US-10-357-930-41017	
		Alignment Scores:	
		Pred. No.: 1,3e-127	Length: 467
		Score: 137.00	Matches: 137
		Percent Similarity: 100.00%	Conservative: 0
		Best Local Similarity: 100.00%	Mismatches: 0
		Query Match: 20.60%	Indels: 0
		DB: 18	Gaps: 0
		US-10-029-345A-109 (1-665) x US-10-357-930-41017 (1-467)	
Qy	241	LeuValIhIaCYsLeuValIGlyIleSerArgSerAlaThrIleAlaIleAlaTyIleMet	266
Db	465	CTAGTGCACCTGTTTAGTGTGGGATCTCCGCTCGCCACCATGCTATCGCTATCATCATG	406
Qy	261	LySarMetLarPmeSerLeuAspGluAlaTyArgPheValIlyGluLySarProThr	280
Db	405	AAGAGGATGAGCACTCTCTTGTAGTAACTTACCAATTTGTAAAGAAAAAGAACTTACT	346
Qy	281	IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyGlyIlyLySarIleLyAsn	300
Db	345	ATATCTCCAACTTCAATTTTCTGGGCCCACTCTCGACTATGAGAAAGATTAAAGAAC	286
Qy	301	GlnThrGlyAlaSerGlyProIlySerIlyLeuIlyLeuIlyIleGluIlyyProAsn	320
Db	285	CAGACTGGAGCATCGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAAGCAAAAT	226
Qy	321	GluProValProAlaValSerGlyGlyGlnIlyySerGlyThrProLeuSerProPro	340
Db	225	GAACCTGTCCTGCTGCTCTCAGAGGGGTGAGCAAGAAAGGAAAGCCCTTCAGTCCACCC	166
Qy	341	CysAlaAspSerAlaThrSerGlyAlaIleAGlyGlnArgProValIleProAlaSerVal	360
Db	165	TGTGCCGACTCTGCTACTCTCAGAGGCAAGACAAAGGCCCTGTGATCTCCGCCACGCTG	106

Db	137	ACCTCAGAGGACAGGACAAGAGCCCGTGCATCCCGCCAGCGTGCACAGCGTGCCAGC	78
Qy	366	VaIGLnProSerLeuLeuGIuAappSerProLeuVa1	377
Db	77	GTGCAAGCCGTGCTGCTTTAGAGAGACAGCCCGCTGATA	42

Search completed: February 14, 2005, 16:00:26
Job time : 974 secs

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